

```
BLAST score
E value
                  1.0e-65
Match length
                  133
                  87
% identity
NCBI Description tubulin beta-2 chain - garden pea (fragment)
                  203812
Seq. No.
Seq. ID
                  LIB3083-023-Q1-L1-G7
Method
                  BLASTX
NCBI GI
                  g4371292
BLAST score
                  477
E value
                  5.0e-48
Match length
                  132
                  70
% identity
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]
                  203813
Seq. No.
                  LIB3083-023-Q1-L1-H1
Seq. ID
Method
                  BLASTX
                  g3202042
NCBI GI
BLAST score
                  181
E value
                  2.0e-13
Match length
                  119
% identity
                  42
                 (AF069324) 26S proteasome regulatory subunit S5A
NCBI Description
                  [Mesembryanthemum crystallinum]
Seq. No.
                  203814
Seq. ID
                  LIB3083-023-Q1-L1-H11
Method
                  BLASTX
NCBI GI
                  g4098874
BLAST score
                  487
E value
                  3.0e-49
Match length
                  131
                  76
% identity
                 (U80967) heat shock protein 70 [Pneumocystis carinii f. sp.
NCBI Description
                  carinii]
                  203815
Seq. No.
Seq. ID
                  LIB3083-023-Q1-L1-H12
Method
                  BLASTX
NCBI GI
                  q135427
BLAST score
                  244
                  5.0e-21
E value
Match length
                  63
                  70
% identity
                 TUBULIN ALPHA CHAIN, TESTIS-SPECIFIC
NCBI Description
                  >gi_1079254_pir__A56622 alpha-tubulin, testis-specific -
                  rainbow trout >gi_213862 (M36623) alpha-tubulin
                  [Oncorhynchus mykiss]
```

Seq. No. 203816

Seq. ID LIB3083-023-Q1-L1-H2

Method BLASTX NCBI GI g266989 BLAST score 453 E value 3.0e-45



```
Match length
                  72
% identity
                  GTP-BINDING PROTEIN SAR1B >gi 322517 pir S28603
NCBI Description
                  GTP-binding protein - Arabidopsis thaliana >gi 166734
                  (M95795) GTP-binding protein [Arabidopsis thaliana]
                  203817
Seq. No.
                  LIB3083-023-Q1-L1-H3
Seq. ID
                  BLASTX
Method
                  g3193298
NCBI GI
                  172
BLAST score
                  2.0e-12
E value
                  100
Match length
                  40
% identity
NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
                  203818
Seq. No.
```

LIB3083-023-Q1-L1-H8 Seq. ID BLASTX Method g1703108 NCBI GI

601 BLAST score E value 1.0e-62 Match length 119 97 % identity

ACTIN 2/7 >gi 2129525 pir\_\_S71210 actin 2 - Arabidopsis NCBI Description thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis thaliana >qi 1049307 (U37281) actin-2 (Arabidopsis thaliana] >gi\_1943863 (U27811) actin7 [Arabidopsis

thaliana]

203819 Seq. No.

Seq. ID LIB3083-024-Q1-L1-A1

BLASTXMethod g4406819 NCBI GI 172 BLAST score 3.0e-12 E value 86 Match length 47 % identity

NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

203820 Seq. No.

Seq. ID LIB3083-024-Q1-L1-A10

Method BLASTX NCBI GI g129881 BLAST score 657 4.0e-69 E value 136 Match length 89 % identity

NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi\_482294\_pir\_\_A36094

pyrophosphate--fructose-6-phosphate 1-phosphotransferase

(EC 2.7.1.90) alpha chain - potato (cv. Kennebec)

>qi 169538 (M55190) pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit [Solanum tuberosum]

```
Seq. No.
                   203821
                   LIB3083-024-Q1-L1-A11
Seq. ID
                   BLASTX
Method
                   g4098331
NCBI GI
BLAST score
                   306
E value
                   8.0e-44
                   98
Match length
                   91
% identity
                   (U76896) beta-tubulin 5 [Triticum aestivum]
NCBI Description
                   203822
Seq. No.
Seq. ID
                   LIB3083-024-Q1-L1-A12
Method
                   BLASTX
NCBI GI
                   g1684857
BLAST score
                   547
E value
                   3.0e-56
Match length
                   120
% identity
                   37
                  (U77940) polyubiquitin [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   203823
Seq. ID
                   LIB3083-024-Q1-L1-A2
Method
                   BLASTX
NCBI GI
                   q2065531
BLAST score
                   607
E value
                   3.0e-63
Match length
                   139
                   76
% identity
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
                   203824
Seq. No.
                   LIB3083-024-Q1-L1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g974294
BLAST score
                   323
                   6.0e-30
E value
                   106
Match length
                   60
% identity
NCBI Description
                   (U31309) LP6 [Pinus taeda]
                   203825
Seq. No.
Seq. ID
                   LIB3083-024-Q1-L1-A6
                   BLASTX
Method
NCBI GI
                   g4263695
BLAST score
                   383
E value
                   5.0e-37
Match length
                   148
                   9
% identity
                   (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                   thaliana]
                   203826
Seq. No.
Seq. ID
                   LIB3083-024-Q1-L1-A9
```

Method BLASTX NCBI GI g2129495 BLAST score 555 E value 4.0e-58



```
Match length
% identity
                   82
                  fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi 1000090
                   (U30508) E6 [Gossypium barbadense]
Seq. No.
                   203827
Seq. ID
                  LIB3083-024-Q1-L1-B1
Method
                  BLASTX
NCBI GI
                   a4580461
BLAST score
                   148
                   2.0e-09
E value
Match length
                   42
% identity
                   74
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                  203828
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-B10
Method
                  BLASTX
NCBI GI
                   g4371292
BLAST score
                   551
                   1.0e-56 ·
E value
                   139
Match length
% identity
                   71
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                  203829
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-B11
Method
                  BLASTN
NCBI GI
                   g1143223
BLAST score
                   110
E value
                   6.0e-55
Match length
                   373
                   50
% identity
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
                   203830
Seq. No.
                  LIB3083-024-Q1-L1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1143223
BLAST score
                   110
                   7.0e-55
E value
Match length
                   323
                   54
% identity
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                   203831
Seq. ID
                   LIB3083-024-Q1-L1-B3
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3176098
BLAST score 493
E value 7.0e-50
Match length 143
% identity 38

NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No. 203832

NCBI Description

thalianal



```
Seq. ID
                   LIB3083-024-Q1-L1-B4
Method
                   BLASTX
                   g3033388
NCBI GI
                   206
BLAST score
E value
                   3.0e-16
Match length
                   95
% identity
                   41
NCBI Description
                   (AC004238) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   203833
Seq. ID
                   LIB3083-024-Q1-L1-B5
Method
                   BLASTX
NCBI GI
                   g1703108
BLAST score
                   703
E value
                   2.0e-74
                   136
Match length
                   99
% identity
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                   thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   203834
Seq. No.
Seq. ID
                   LIB3083-024-Q1-L1-B6
Method
                   BLASTX
NCBI GI
                   q2642443
BLAST score
                   213
                   5.0e-17
E value
                   128
Match length
% identity
                   32
NCBI Description (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
                   203835
Seq. No.
Seq. ID
                   LIB3083-024-Q1-L1-B8
Method
                   BLASTX
NCBI GI
                   q464840
BLAST score
                   216
E value
                   2.0e-17
Match length
                   59
                   75
% identity
NCBI Description
                   TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
                   alpha-1 chain - fern (Anemia phyllitidis)
                   >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia
                   phyllitidis]
Seq. No.
                   203836
                   LIB3083-024-Q1-L1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2961356
BLAST score
                   395
E value
                   2.0e-38
Match length
                   131
% identity
                   60
```

(AL022140) alcohol dehydrogenase like protein [Arabidopsis



```
203837
Seq. No.
Seq. ID
                   LIB3083-024-Q1-L1-C10
Method
                   BLASTX
NCBI GI
                   g4336436
BLAST score
                   205
                   4.0e-16
E value
Match length
                   60
% identity
                   70
NCBI Description
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
Seq. No.
                   203838
Seq. ID
                   LIB3083-024-Q1-L1-C3
Method
                   BLASTX
NCBI GI
                   q730456
BLAST score
                   475
E value
                   9.0e-48
Match length
                   129
% identity
                   67
NCBI Description
                  40S RIBOSOMAL PROTEIN S19
                   203839
Seq. No.
                  LIB3083-024-Q1-L1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2736286
BLAST score
                   285
E value
                   2.0e-25
Match length
                   59
                   86
% identity
NCBI Description
                   (AF031079) isopentenyl diphosphate isomerase I [Camptotheca
                   acuminata]
Seq. No.
                   203840
Seq. ID
                   LIB3083-024-Q1-L1-C5
Method
                   BLASTX
NCBI GI
                   g3128477
BLAST score
                   505
E value
                   3.0e-51
Match length
                   144
% identity
                   66
NCBI Description
                  (AF062640) metalloproteinase [Arabidopsis thaliana]
Seq. No.
                   203841
                   LIB3083-024-Q1-L1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g626598
BLAST score
                   149
E value
                   2.0e-09
                  92
Match length
                   39
% identity
NCBI Description
                  hypothetical protein YHR016c - yeast (Saccharomyces
                   cerevisiae) >gi_500710 (U10400) Ysc84p [Saccharomyces
                   cerevisiae]
Seq. No.
                   203842
```

Seq. ID LIB3083-024-Q1-L1-D1

Method BLASTX NCBI GI g2271477



```
BLAST score
                  4.0e-73
E value
Match length
                  144
                  92
% identity
                  (AF009631) AP47/50p [Arabidopsis thaliana]
NCBI Description
                  203843
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-D10
Method
                  BLASTX
                  g4206112
NCBI GI
                  293
BLAST score
E value
                  2.0e-26
Match length
                  61
% identity
                  92
                  (AF097662) alpha tubulin [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                  203844
                  LIB3083-024-Q1-L1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1737222
BLAST score
                  625
E value
                  2.0e-65
Match length
                  130
% identity
                  82
                  (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]
NCBI Description
                  203845
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-D3
Method
                  BLASTX
NCBI GI
                  g3327868
BLAST score
                  154
                   4.0e-10
E value
Match length
                  68
                  56
% identity
                   (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
NCBI Description
                  thaliana]
                  203846
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-E1
Method
                  BLASTN
                  g1480456
NCBI GI
BLAST score
                  34
E value
                  1.0e-09
                  50
Match length
                  92
% identity
NCBI Description
                  Hevea brasiliensis latex allergen Hev b 5 mRNA, complete
                  cds
Seq. No.
                  203847
Seq. ID
                  LIB3083-024-Q1-L1-E10
Method
                  BLASTX
NCBI GI
                  q4544412
BLAST score
                  224
E value
                  2.0e-18
Match length
                  114
                  39
% identity
```

NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

NCBI GI

BLAST score



```
203848
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-E11
                  BLASTX
Method
NCBI GI
                  g3763932
                  552
BLAST score
                  8.0e-57
E value
                  134
Match length
                  78
% identity
NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]
                  203849
Seq. No.
                  LIB3083-024-Q1-L1-E12
Seq. ID
                  BLASTX
Method
                  g2244732
NCBI GI
                  248
BLAST score
                  3.0e-21
E value
                  45
Match length
                  98
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.
                  203850
Seq. ID
                  LIB3083-024-Q1-L1-E2
Method
                  BLASTX
                  q4105696
NCBI GI
                  313
BLAST score
                  9.0e-29
E value
                  64
Match length
                  95
% identity
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
                  203851
Seq. No.
                  LIB3083-024-Q1-L1-E3
Seq. ID
Method
                  BLASTX
                  g2662469
NCBI GI
                  554
BLAST score
                  5.0e-57
E value
                  128
Match length
                  84
% identity
NCBI Description (AF034217) ribosomal protein S6 [Arabidopsis thaliana]
                  203852
Seq. No.
                  LIB3083-024-Q1-L1-E4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g166919
                  51
BLAST score
                  1.0e-19
E value
Match length
                  63
% identity
                  Arabidopsis thaliana alpha-6 tubulin (TUA6) gene, complete
NCBI Description
                  cds
                  203853
Seq. No.
                  LIB3083-024-Q1-L1-E5
Seq. ID
Method
                  BLASTX
```

27803

q2494113



E value 5.0e-68 Match length 130 % identity (AC002376) Strong similarity to Musa pectate lyase NCBI Description (gb X92943). ESTs gb AA042458, gb ATTS4502, gb N38552 come from this gene. [Arabidopsis thaliana] 203854 Seq. No. LIB3083-024-Q1-L1-E6 Seq. ID Method BLASTX NCBI GI q2827143 BLAST score 388 E value 1.0e-37 Match length 81 86 % identity (AF027174) cellulose synthase catalytic subunit NCBI Description [Arabidopsis thaliana] Seq. No. 203855 LIB3083-024-Q1-L1-E7 Seq. ID Method BLASTX g4580395 NCBI GI BLAST score 383 5.0e-37 E value Match length 142 % identity 59 (AC007171) putative kinesin-related protein [Arabidopsis NCBI Description thalianal Seq. No. 203856 LIB3083-024-Q1-L1-E8 Seq. ID Method BLASTX g3193303 NCBI GI BLAST score 306 5.0e-28 E value Match length 117 % identity 54 (AF069298) similar to several proteins containing a tandem NCBI Description repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana] Seq. No. 203857 Seq. ID LIB3083-024-Q1-L1-E9 Method BLASTX NCBI GI g4544412

BLAST score 318 E value 2.0e-29 Match length 116 % identity 47

(AC006955) hypothetical protein [Arabidopsis thaliana] NCBI Description

203858 Seq. No.

Seq. ID LIB3083-024-Q1-L1-F2

Method BLASTX NCBI GI g82734 BLAST score 412



```
2.0e-40
E value
                  83
Match length
% identity
                  ubiquitin precursor - maize (fragment)
NCBI Description
                  >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
                  203859
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-F3
Method
                  BLASTX
                  g1076737
NCBI GI
                  623
BLAST score
                  4.0e-65
E value
                  141
Match length
                  83
% identity
NCBI Description beta-tubulin R1623 - rice
                  203860
Seq. No.
                  LIB3083-024-Q1-L1-F4
Seq. ID
                  BLASTX
Method
                  g2129499
NCBI GI
                  430
BLAST score
E value
                  1.0e-42
Match length
                  112
                  72
% identity
                  fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  203861
Seq. No.
                  LIB3083-024-Q1-L1-F5
Seq. ID
                  BLASTX
Method
                  g2497543
NCBI GI
BLAST score
                  599
                  8.0e-66
E value
                  147
Match length
                  90
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061_pir__S41379
NCBI Description
                  pyruvate kinase - common tobacco >gi 444023 emb CAA82628
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                  203862
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-F6
                  BLASTX
Method
                  g2739381
NCBI GI
BLAST score
                   515
                   2.0e-52
E value
                  130
Match length
                   75
% identity
                  (AC002505) putative patatin [Arabidopsis thaliana]
NCBI Description
                   203863
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-F8
```

BLASTX Method q3377813 NCBI GI 289 BLAST score E value 6.0e-26 Match length 101 57 % identity

NCBI Description



```
NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]
                  203864
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-F9
Method
                  BLASTX
                  g294845
NCBI GI
BLAST score
                  386
E value
                  2.0e-37
                  127
Match length
                  57
% identity
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
                  203865
Seq. No.
                  LIB3083-024-Q1-L1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1699024
BLAST score
                  481
E value
                  1.0e-48
Match length
                  125
% identity
                  66
NCBI Description
                   (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
                   (U78870) unknown [Arabidopsis thaliana]
                  203866
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-G11
Method
                  BLASTX
NCBI GI
                  g2388564
BLAST score
                  201
E value
                  1.0e-15
Match length
                  126
% identity
                   40
                  (AC000098) ESTs gb AA042402, gb_ATTS1380 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                  203867
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-G2
Method
                  BLASTX
NCBI GI
                  g1330401
BLAST score
                  207
                  2.0e-16
E value
                  127
Match length
% identity
                  36
NCBI Description
                  (U58762) T27F7.1 gene product [Caenorhabditis elegans]
                  203868
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-G9
Method
                  BLASTX
                  g464849
NCBI GI
BLAST score
                  204
                  5.0e-16
E value
                   42
Match length
                  90
% identity
```

27806

alpha-tubulin [Prunus dulcis]

chain - almond >gi 20413 emb CAA47635 (X67162)

TUBULIN ALPHA CHAIN >gi\_486847\_pir\_\_S36232 tubulin alpha

Seq. ID

Method



```
Seq. No.
                  203869
Seq. ID
                  LIB3083-024-Q1-L1-H12
Method
                  BLASTX
                  q2252828
NCBI GI
BLAST score
                  113
E value
                  8.0e-12
Match length
                  80
                  48
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  203870
Seq. ID
                  LIB3083-024-Q1-L1-H3
Method
                  BLASTX
NCBI GI
                  q2129473
BLAST score
                  242
E value
                  2.0e-20
Match length
                  89
% identity
                  52
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                  203871
Seq. ID
                  LIB3083-024-Q1-L1-H4
Method
                  BLASTX
NCBI GI
                  q4204300
BLAST score
                  194
E value
                   4.0e-15
Match length
                  72
% identity
                   60
NCBI Description
                  (AC003027) Unknown protein [Arabidopsis thaliana]
                  203872
Seq. No.
Seq. ID
                  LIB3083-024-Q1-L1-H7
Method
                  BLASTX
NCBI GI
                  q4235430
BLAST score
                   428
                   5.0e-44
E value
                  143
Match length
% identity
                   63
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
                  203873
Seq. No.
Seq. ID
                  LIB3083-027-Q1-L1-A1
Method
                  BLASTX
NCBI GI
                  g1730171
BLAST score
                   462
                   3.0e-46
E value
Match length
                   114
                   78
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi 1370066 emb CAA61574 (X89394)
                   glucose-6-phosphate isomerase [Clarkia williamsonii]
                   203874
Seq. No.
```

27807

LIB3083-027-Q1-L1-A3

BLASTX



```
q3451071
NCBI GI
BLAST score
                  198
                  3.0e-15
E value
                  110
Match length
                  42
% identity
                  (AL031326) beta adaptin - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  203875
Seq. No.
                  LIB3083-027-Q1-L1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  539
                  3.0e-55
E value
                  125
Match length
                  81
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
                  203876
Seq. No.
                  LIB3083-027-Q1-L1-A7
Seq. ID
Method
                  BLASTX
                  g3218396
NCBI GI
BLAST score
                   255
                   6.0e-22
E value
                   99
Match length
                   49
% identity
NCBI Description (AL023860) hypothetical protein [Schizosaccharomyces pombe]
                   203877
Seq. No.
                  LIB3083-027-Q1-L1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q498038
                   424
BLAST score
E value
                   7.0e-42
Match length
                   128
                   59
% identity
NCBI Description (L33792) lipid transfer protein [Senecio odorus]
                   203878
Seq. No.
                   LIB3083-027-Q1-L1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1542941
BLAST score
                   238
                   5.0e-20
E value
                   88
Match length
% identity
                   (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
Seq. No.
                   203879
                   LIB3083-027-Q1-L1-B2
Seq. ID
Method
                   BLASTX
                   g3513727
NCBI GI
BLAST score
                   114
                   3.0e-12
E value
```

101

Match length



Seq. ID LIB3083-027-Q1-19
Method BLASTX
NCBI GI g3024127
BLAST score 546
E value 2.0e-58
Match length 132
% identity 83

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi\_1655578\_emb\_CAA95857\_ (Z71272) S-adenosyl-L-methionine

synthetase 2 [Catharanthus roseus]

 Seq. No.
 203881

 Seq. ID
 LIB3083-027-Q1-L1-B7

 Method
 BLASTX

 NCBI GI
 g2995990

 BLAST score
 315

 E value
 5.0e-29

 Match length
 105

 % identity
 61

NCBI Description (AF053746) dormancy-associated protein [Arabidopsis

thaliana] >gi\_2995992 (AF053747) dormancy-associated

protein [Arabidopsis thaliana]

Seq. No. 203882

Seq. ID LIB3083-027-Q1-L1-C1

Method BLASTX
NCBI GI g3152598
BLAST score 454
E value 3.0e-45
Match length 138
% identity 64

NCBI Description (AC002986) Contains similarity to C2-HC type zinc finger

protein C.e-MyT1 gb U67079 from C. elegans and to

hypersensitivity-related gene 201 isolog T28M21.14 from A.

thaliana BAC gb\_AF002109. [Arabidopsis thaliana]

Seq. No. 203883

Seq. ID LIB3083-027-Q1-L1-C2

Method BLASTX
NCBI GI g2507455
BLAST score 255
E value 3.0e-22
Match length 75
% identity 67

NCBI Description FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

SYNTHETASE) (FHS) (FTHFS) >gi\_322401\_pir\_\_A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi\_170145 (M83940) 10-formyltetrahydrofolate synthetase



## [Spinacia oleracea]

```
203884
Seq. No.
                  LIB3083-027-Q1-L1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3694872
BLAST score
                  532
E value
                  1.0e-54
Match length
                  110
                  89
% identity
                  (AF092547) profilin [Ricinus communis]
NCBI Description
Seq. No.
                  203885
                  LIB3083-027-Q1-L1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q172945
BLAST score
                  270
E value
                  9.0e-24
Match length
                  132
                  42
% identity
                  (J03964) Phe-RNA synthetase [Saccharomyces cerevisiae]
NCBI Description
Seq. No.
                  203886
                  LIB3083-027-Q1-L1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2864625
BLAST score
                   471
E value
                  2.0e-47
Match length
                  121
                  79
% identity
                  (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  203887
                  LIB3083-027-Q1-L1-C7
Seq. ID
Method
                  BLASTX
                  g2511689
NCBI GI
                   553
BLAST score
                   6.0e-57
E value
Match length
                   136
                   74
% identity
                  (Z99952) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
                   203888
Seq. No.
                   LIB3083-027-Q1-L1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4325282
                   399
BLAST score
                   6.0e-39
E value
                   83
Match length
% identity
                   89
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi 4325286 gb AAD17314 (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
```

Seq. No.

203889

Seq. ID LIB3083-027-Q1-L1-D1

Method BLASTX

Seq. ID



```
q3297814
NCBI GI
BLAST score
                  301
                  2.0e-27
E value
Match length
                  142
% identity
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
                  203890
Seq. No.
                  LIB3083-027-Q1-L1-D10
Seq. ID
                  BLASTX
Method
                  g1155261
NCBI GI
                  179
BLAST score
                  5.0e-13
E value
                  99
Match length
                   45
% identity
                   (U40217) eukaryotic release factor 1 homolog [Arabidopsis
NCBI Description
                  thaliana]
                  203891
Seq. No.
Seq. ID
                  LIB3083-027-Q1-L1-D3
                  BLASTX
Method
                  g130720
NCBI GI
                   164
BLAST score
E value
                   2.0e-11
                   68
Match length
                   47
% identity
                  PROTEOLIPID PROTEIN PPA1 >gi 101508 pir_A34633 probable
NCBI Description
                   H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein
                   - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294)
                   proteolipid protein of proton ATPase [Saccharomyces
                   cerevisiae] >gi 500700 (U10399) Ppalp: Proteolipid protein
                   of proton ATPase [Saccharomyces cerevisiae]
                   203892
Seq. No.
                   LIB3083-027-Q1-L1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g606942
BLAST score
                   409
                   1.0e-45
E value
                   142
Match length
                   68
% identity
                   (U13760) unknown [Gossypium hirsutum]
NCBI Description
                   203893
Seq. No.
                   LIB3083-027-Q1-L1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g135449
                   650
BLAST score
                   3.0e-68
E value
                   138
Match length
% identity
                   TUBULIN BETA-1 CHAIN >gi 100932 pir_S14701 tubulin beta-1
NCBI Description
                   chain - maize >gi 295851 emb CAA37060 (X52878) beta 1
                   tubulin [Zea mays]
Seq. No.
                   203894
```

27811

LIB3083-027-Q1-L1-D7



```
Method BLASTX
NCBI GI 94469007
BLAST score 210
E value 1.0e-16
Match length 139
% identity 37
NCBI Description (NL03560
```

NCBI Description (AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

 Seq. No.
 203895

 Seq. ID
 LIB3083-027-Q1-L1-D8

 Method
 BLASTX

 NCBI GI
 g267069

 BLAST score
 476

 F value
 4 0e-48

BLAST score 476
E value 4.0e-48
Match length 91
% identity 96

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 203896

Seq. ID LIB3083-027-Q1-L1-E1

Method BLASTX
NCBI GI g4337175
BLAST score 438
E value 2.0e-43
Match length 131
% identity 64

NCBI Description (AC006416) ESTs gb T20589, gb\_T04648, gb\_AA597906,

gb\_T04111, gb\_R841\overline{80}, gb\_R654\overline{28}, gb\_T444\overline{39}, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb\_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 203897

Seq. ID LIB3083-027-Q1-L1-E5

Method BLASTX
NCBI GI g4455222
BLAST score 278
E value 1.0e-24
Match length 116
% identity 53

NCBI Description (AL035440) hypothetical protein [Arabidopsis thaliana]

Seq. No. 203898

Seq. ID LIB3083-027-Q1-L1-E6

Method BLASTX
NCBI GI g1706958
BLAST score 410
E value 2.0e-40
Match length 111
% identity 71

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 203899

Seq. ID LIB3083-027-Q1-L1-E7



```
BLASTN
Method
                  g3449322
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   160
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC17, complete sequence [Arabidopsis thaliana]
                   203900
Seq. No.
                  LIB3083-027-Q1-L1-E8
Seq. ID
                   BLASTN
Method
                   g995906
NCBI GI
BLAST score
                   55
                   2.0e-22
E value
                   75
Match length
                   93
% identity
                   Gossypium hirsutum nonspecific lipid transfer protein
NCBI Description
                   precursor mRNA, complete cds
Seq. No.
                   203901
                   LIB3083-027-Q1-L1-F1
Seq. ID
                   BLASTX
Method
                   g1706958
NCBI GI
                   572
BLAST score
E value
                   3.0e-59
                   135
Match length
                   77
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   203902
Seq. No.
Seq. ID
                   LIB3083-027-Q1-L1-F3
                   BLASTX
Method
                   q3367536
NCBI GI
                   253
BLAST score
E value
                   8.0e-22
                   65
Match length
                   78
% identity
                   (ACO04392) Contains similarity to symbiosis-related like
NCBI Description
                   protein F1N20.80 gi_2961343 from A. thaliana BAC
                   gb AL022140. EST gb T04695 comes from this gene.
                   [Arabidopsis thaliana]
                   203903
Seq. No.
                   LIB3083-027-Q1-L1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2494115
BLAST score
                   313
                   8.0e-29
E value
Match length
                   90
```

70 % identity

(AC002376) Strong similarity to Arabidopsis ATHSAR1 NCBI Description

(gb M90418). ESTs gb T44122, gb N65276, gb AA041135 come from

this gene. [Arabidopsis thaliana]

203904 Seq. No.

LIB3083-027-Q1-L1-F6 Seq. ID



```
BLASTX
Method
                  q1706958
NCBI GI
                  521
BLAST score
                  2.0e-53
E value
                  101
Match length
% identity
                   96
                   (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  203905
Seq. No.
                  LIB3083-027-Q1-L1-G11
Seq. ID
                  BLASTX
Method
                  g3126967
NCBI GI
BLAST score
                   161
                   6.0e-11
E value
Match length
                   131
% identity
                  (AF061807) polyubiquitin [Elaeagnus umbellata]
NCBI Description
                   203906
Seq. No.
                   LIB3083-027-Q1-L1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2239091
BLAST score
                   219
E value
                   9.0e-18
Match length
                   133
                   40
% identity
                   (Z84571) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus]
                   203907
Seq. No.
                   LIB3083-027-Q1-L1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4510345
                   141
BLAST score
                   1.0e-08
E value
                   46
Match length
                   54
% identity
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   203908
Seq. No.
                   LIB3083-027-Q1-L1-G4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g166818
                   36
BLAST score
                   9.0e-11
E value
                   52
Match length
                   92
% identity
NCBI Description Arabidopsis thaliana protein kinase mRNA, complete cds
                   203909
Seq. No.
                   LIB3083-027-Q1-L1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g218157
                   521
BLAST score
                   3.0e-53
E value
```

115

90

Match length % identity





```
(D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
                  203910
Seq. No.
                  LIB3083-027-Q1-L1-G8
Seq. ID
                  BLASTX
Method
                  g4098323
NCBI GI
BLAST score
                  659
                  2.0e-69
E value
                  128
Match length
                  95
% identity
                  (U76746) beta-tubulin 3 [Triticum aestivum]
NCBI Description
                  203911
Seq. No.
                  LIB3083-027-Q1-L1-H1
Seq. ID
                  BLASTX
Method
                   g2832625
NCBI GI
                   506
BLAST score
                   2.0e-51
E value
                   129
Match length
                   71
% identity
                   (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                   203912
Seq. No.
                   LIB3083-027-Q1-L1-H2
Seq. ID
                   BLASTX
Method
                   q4115925
NCBI GI
                   178
BLAST score
                   6.0e-13
E value
                   49
Match length
                   39
% identity
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >gi 4539439 emb_CAB40027.1_ (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
                   203913
Seq. No.
                   LIB3083-027-Q1-L1-H3
Seq. ID
Method
                   BLASTX
                   g3377812
NCBI GI
                   482
BLAST score
                   1.0e-48
E value
                   134
Match length
                   71
% identity
                   (AF076275) contains similarity to heavy-metal-associated
NCBI Description
                   domain containing proteins (Pfam: HMA.hm, score: 12.02)
                   [Arabidopsis thaliana]
                   203914
Seq. No.
Seq. ID
                   LIB3083-027-Q1-L1-H4
                   BLASTX
Method
                   g3511285
NCBI GI
BLAST score
                   247
                   5.0e-21
E value
                   118
Match length
% identity
                   (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
```

tremula]

```
Seq. No. 203915
Seq. ID LIB3083-027-Q1-L1-H5
Method BLASTX
NCBI GI g3929364
BLAST score 390
E value 7.0e-38
Match length 104
% identity 75
```

dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi\_666977\_emb\_CAA59061\_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi\_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb\_X84318 from A.thaliana. ESTs gb\_Z27005, gb\_T04711, gb\_T45078 and gb\_Z28689 come

from this gene. [Arabidopsis thaliana]

 Seq. No.
 203916

 Seq. ID
 LIB3083-027-Q1-L1-H8

 Method
 BLASTX

 NCBI GI
 g549060

 BLAST score
 315

 E value
 4.0e-29

 Match length
 108

% identity 57

NCBI Description T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)

>gi\_631656\_pir\_\_S43058 CCTeta protein eta chain - mouse
>gi\_468504\_emb\_CAA83274\_ (Z31399) CCTeta, eta subunit of
the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No. 203917

Seq. ID LIB3083-028-Q1-L1-A1

Method BLASTX
NCBI GI g2920839
BLAST score 348
E value 7.0e-33
Match length 127
% identity 52

NCBI Description (U95136) Os-FIERG2 gene product [Oryza sativa]

Seq. No. 203918

Seq. ID LIB3083-028-Q1-L1-A2

Method BLASTX
NCBI GI g1669573
BLAST score 657
E value 4.0e-69
Match length 134
% identity 91

NCBI Description (D88399) endosperm kinase [Oryza sativa]

Seq. No. 203919

Seq. ID LIB3083-028-Q1-L1-A3

Method BLASTX
NCBI GI g2920839
BLAST score 373
E value 8.0e-36



Match length % identity 53

(U95136) Os-FIERG2 gene product [Oryza sativa] NCBI Description

Seq. No.

203920

Seq. ID LIB3083-028-Q1-L1-A4 BLASTX Method

NCBI GI q2944446 BLAST score 393 3.0e-38 E value 92 Match length 76 % identity

(AF050756) cysteine endopeptidase precursor [Ricinus NCBI Description

communis]

203921 Seq. No.

LIB3083-028-Q1-L1-A5 Seq. ID

Method BLASTX g2920839 NCBI GI BLAST score 344 E value 2.0e-32 127 Match length 52 % identity

NCBI Description (U95136) Os-FIERG2 gene product [Oryza sativa]

Seq. No. 203922

Seq. ID LIB3083-028-Q1-L1-A7

BLASTX Method NCBI GI g2506139 BLAST score 385 E value 3.0e-37 Match length 101 % identity 75

COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) NCBI Description

(ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)

archain/delta-COP [Oryza sativa]

203923 Seq. No.

LIB3083-028-Q1-L1-B1 Seq. ID

BLASTX Method NCBI GI q135434 BLAST score 244 E value 1.0e-20 55 Match length % identity 84

TUBULIN ALPHA-1B CHAIN (TUBULIN ALPHA-N CHAIN) NCBI Description

> >qi 84170 pir S02130 tubulin alpha chain - slime mold (Physarum polycephalum) >gi 1213632 emb CAA28712 (X05039)

alpha-tubulin [Physarum polycephalum]

203924 Seq. No.

LIB3083-028-Q1-L1-B2 Seq. ID

Method BLASTX NCBI GI g4539301 BLAST score 143 2.0e-09 E value Match length 76



% identity (AL049480) putative mitochondrial protein [Arabidopsis NCBI Description thaliana] 203925 Seq. No. LIB3083-028-Q1-L1-B4 Seq. ID Method BLASTX q3122232 NCBI GI BLAST score 156 2.0e-10 E value Match length 99 51 % identity MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR NCBI Description >gi 1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi\_4454008\_emb\_CAA23061\_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana] 203926 Seq. No. LIB3083-028-Q1-L1-B5 Seq. ID BLASTX Method q3776560 NCBI GI BLAST score 366 5.0e-35 E value Match length 84 87 % identity (AC005388) Similar to gb U51990 hPrp18 (splicing factor) NCBI Description gene from Homo sapiens. [Arabidopsis thaliana] 203927 Seq. No. LIB3083-028-Q1-L1-B6 Seq. ID BLASTX Method g4097547 NCBI GI BLAST score 217 2.0e-17 E value Match length 113 % identity (U64906) ATFP3 [Arabidopsis thaliana] NCBI Description 203928 Seq. No. LIB3083-028-Q1-L1-B7 Seq. ID BLASTX Method g308906 NCBI GI 275 BLAST score 2.0e-24 E value 103 Match length % identity (L18909) thioredoxin [Lilium longiflorum] NCBI Description

Seq. No. 203929

LIB3083-028-Q1-L1-C3 Seq. ID Method BLASTN

g2829205 NCBI GI BLAST score 116 E value 1.0e-58 Match length 226 % identity 68



Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No. 203930

NCBI Description

Seq. ID LIB3083-028-Q1-L1-C4

Method BLASTX
NCBI GI g3702332
BLAST score 172
E value 2.0e-12

Match length 63 % identity 51

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 203931

Seq. ID LIB3083-028-Q1-L1-C6

Method BLASTX
NCBI GI g2459445
BLAST score 233
E value 2.0e-19
Match length 87
% identity 25

NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis

thaliana]

Seq. No. 203932

Seq. ID LIB3083-028-Q1-L1-C7

Method BLASTX
NCBI GI 94008159
BLAST score 594
E value 7.0e-62
Match length 117
% identity 93

NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]

Seq. No. 203933

Seq. ID LIB3083-028-Q1-L1-C8

Method BLASTX
NCBI GI g3831451
BLAST score 482
E value 4.0e-51
Match length 123
% identity 80

NCBI Description (AC005700) putative O-GlcNAc transferase [Arabidopsis

thaliana]

Seq. No. 203934

Seq. ID LIB3083-028-Q1-L1-E2

Method BLASTX
NCBI GI g4336436
BLAST score 411
E value 2.0e-40
Match length 106
% identity 71

NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No. 203935

Seq. ID LIB3083-028-Q1-L1-E3



```
Method
                   BLASTX
NCBI GI
                   g1706956
BLAST score
                   521
E value
                   3.0e-53
Match length
                   103
% identity
                   94
NCBI Description
                   (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   203936
Seq. ID
                   LIB3083-028-Q1-L1-E4
Method
                   BLASTX
NCBI GI
                   g3482910
BLAST score
                   318
E value
                   5.0e-30
Match length
                   60
% identity
                   87
NCBI Description
                   (AC003970) Similar to rice water stress induced protein
                   gi_537404 [Arabidopsis thaliana]
Seq. No.
                   203937
Seq. ID
                   LIB3083-028-Q1-L1-E7
Method
                   BLASTX
NCBI GI
                   g2723477
BLAST score
                   289
E value
                   5.0e-26
Match length
                   67
% identity
                   85
NCBI Description
                   (D89824) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                   203938
Seq. ID
                   LIB3083-028-Q1-L1-E8
Method
                   BLASTX
NCBI GI
                   g4406780
BLAST score
                   653
E value
                   1.0e-68
Match length
                   138
% identity
                   86
NCBI Description
                   (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                   203939
Seq. ID
                  LIB3083-028-Q1-L1-F1
Method
                  BLASTX
                  g3334147
                  351
                  3.0e-33
                  125
                  48
NCBI Description
                  ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
```

NCBI GI BLAST score E value Match length % identity

chitinase [Gossypium hirsutum]

Seq. No. 203940

Seq. ID LIB3083-028-Q1-L1-F3

Method BLASTX NCBI GI q3608171 BLAST score 452 E value 4.0e-45



Match length 115 % identity 78

NCBI Description (D86306) proton-translocating inorganic pyrophosphatase

[Cucurbita moschata]

Seq. No. 203941

Seq. ID LIB3083-028-Q1-L1-F4

Method BLASTX
NCBI GI g2811025
BLAST score 145
E value 3.0e-09
Match length 58
% identity 52

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi\_1944181\_dbj\_BAA19607\_

(AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 203942

Seq. ID LIB3083-028-Q1-L1-F5

Method BLASTX
NCBI GI g2924520
BLAST score 455
E value 2.0e-45
Match length 105
% identity 86

NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)

[Arabidopsis thaliana]

Seq. No. 203943

Seq. ID LIB3083-028-Q1-L1-F7

Method BLASTX
NCBI GI g2129495
BLAST score 647
E value 6.0e-68
Match length 136
% identity 89

NCBI Description fiber protein E6 (clone SIE6-2A) - sea-island cotton

>gi\_1000088 (U30507) E6 [Gossypium barbadense] >gi\_1000090

(U30508) E6 [Gossypium barbadense]

Seq. No. 203944

Seq. ID LIB3083-028-Q1-L1-G1

Method BLASTX
NCBI GI g2129495
BLAST score 311
E value 2.0e-33
Match length 139
% identity 57

NCBI Description fiber protein E6 (clone SIE6-2A) - sea-island cotton

>gi\_1000088 (U30507) E6 [Gossypium barbadense] >gi\_1000090

(U30508) E6 [Gossypium barbadense]

Seq. No. 203945

Seq. ID LIB3083-028-Q1-L1-G11

Method BLASTX
NCBI GI g1706956
BLAST score 159
E value 1.0e-10



```
Match length
                  41
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  203946
Seq. No.
                  LIB3083-028-Q1-L1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3785995
                  366
BLAST score
                  4.0e-35
E value
Match length
                  118
% identity
                   60
                   (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                  203947
Seq. No.
                  LIB3083-028-Q1-L1-G3
Seq. ID
Method
                  BLASTX
                  g3128176
NCBI GI
                   244
BLAST score
                   1.0e-20
E value
                   86
Match length
% identity
                   57
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                   203948
Seq. No.
                  LIB3083-028-Q1-L1-G5
Seq. ID
                  BLASTX
Method
                   g2980767
NCBI GI
                   426
BLAST score
                   5.0e-42
E value
                   135
Match length
                   67
% identity
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   203949
Seq. No.
                   LIB3083-028-Q1-L1-G7
Seq. ID
                   BLASTN
Method
                   g1143223
NCBI GI
BLAST score
                   180
                   1.0e-96
E value
                   375
Match length
                   49
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                   203950
Seq. ID
                   LIB3083-028-Q1-L1-H2
                   BLASTX
Method
                   g1174592
NCBI GI
BLAST score
                   619
                   9.0e-65
E value
Match length
                   119
                   97
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
```

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin - garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No.



```
LIB3083-028-Q1-L1-H3
Seq. ID
                  BLASTX
Method
                  g2098709
NCBI GI
                  491
BLAST score
                  1.0e-49
E value
Match length
                  137
% identity
                  76
NCBI Description (U82975) pectinesterase [Citrus sinensis]
                  203952
Seq. No.
                  LIB3083-028-Q1-L1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2098709
                  296
BLAST score
                  7.0e-27
E value
                  126
Match length
% identity
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
                  203953
Seq. No.
                  LIB3083-028-Q1-L1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1019946
BLAST score
                   607
                   3.0e-63
E value
                   123
Match length
% identity
                  (U37060) ascorbate peroxidase [Gossypium hirsutum]
NCBI Description
                   203954
Seq. No.
                   LIB3083-029-Q1-L1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455217
BLAST score
                   309
                   2.0e-28
E value
Match length
                   64
% identity
                   75
                   (AL035440) Avr9 elicitor response like protein [Arabidopsis
NCBI Description
                   thaliana]
                   203955
Seq. No.
                   LIB3083-029-Q1-L1-E11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1403523
BLAST score
                   48
                   6.0e-18
E value
Match length
                   104
% identity
                   87
NCBI Description Plasmid pIJ2581 tsr & glkA genes
                   203956
Seq. No.
                   LIB3083-029-Q1-L1-F12
Seq. ID
                   BLASTX
Method
                   g2500520
NCBI GI
                   552
BLAST score
```

5.0e-61

141

E value

Match length

NCBI Description



```
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-14 (EIF-4A-14)
NCBI Description
                  >qi 485943 emb CAA55742_ (X79141) NeIF-4A14 [Nicotiana
                  tabacum]
                  203957
Seq. No.
                  LIB3083-029-Q1-L1-F4
Seq. ID
Method
                  BLASTX
                  q4314390
NCBI GI
                  153
BLAST score
E value
                  5.0e-10
Match length
                   61
% identity
                   (AC006232) putative calcium binding protein [Arabidopsis
NCBI Description
                  thalianal
                  203958
Seq. No.
                  LIB3083-029-Q1-L1-G10
Seq. ID
                  BLASTX
Method
                   q3643594
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   52
Match length
% identity
                   81
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                   203959
Seq. No.
                   LIB3083-029-Q1-L1-G11
Seq. ID
Method
                   BLASTX
                   q3264761
NCBI GI
                   548
BLAST score
                   2.0e-56
E value
                   130
Match length
                   78
% identity
NCBI Description (AF071890) sulfite reductase [Prunus armeniaca]
                   203960
Seq. No.
                   LIB3083-029-Q1-L1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q451544
BLAST score
                   206
                   3.0e-16
E value
                   43
Match length
                   91
% identity
                   (U04267) proline-rich cell wall protein [Gossypium
NCBI Description
                   barbadense]
Seq. No.
                   203961
                   LIB3083-029-Q1-L1-G5
Seq. ID
Method
                   BLASTX
                   q630801
NCBI GI
                   194
BLAST score
                   7.0e-15
E value
                   43
Match length
% identity
                   86
                   tubulin beta chain - common limpet
```

27824

>gi 1335661 emb CAA55979 (X79469) beta tubulin [Patella



## vulgata]

```
203962
Seq. No.
                  LIB3083-029-Q1-L1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462931
BLAST score
                  207
                  2.0e-16
E value
                  77
Match length
                   57
% identity
                   (Z83833) UDP-glucose:sterol glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   203963
Seq. No.
                   LIB3083-029-Q1-L1-H4
Seq. ID
                   BLASTX
Method
                   g2829204
NCBI GI
BLAST score
                   364
                   9.0e-35
E value
                   87
Match length
% identity
                   (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                   hirsutum]
                   203964
Seq. No.
                   LIB3083-029-Q1-L1-H5
Seq. ID
                   BLASTX
Method
                   q3451075
NCBI GI
BLAST score
                   152
                   5.0e-10
E value
                   114
Match length
                   28
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   203965
Seq. No.
                   LIB3083-029-Q1-L1-H6
Seq. ID
Method
                   BLASTX
                   q2104681
NCBI GI
BLAST score
                   182
                   1.0e-15
E value
                   108
Match length
                   55
% identity
                   (X97907) transcription factor [Vicia faba]
NCBI Description
                   203966
Seq. No.
                   LIB3083-030-Q1-L1-A2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3108252
BLAST score
                   187
                   1.0e-101
E. value
                   329
Match length
                   90
% identity
NCBI Description Gossypium barbadense clone pXP039 repetitive DNA sequence
                   203967
Seq. No.
                   LIB3083-030-Q1-L1-A3
Seq. ID
```

27825

BLASTX

Method



```
g4559381
NCBI GI
                  449
BLAST score
                  8.0e-45
E value
                  122
Match length
                  70
% identity
                  (AC006526) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  203968
Seq. No.
                  LIB3083-03Q-Q1-L1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q421941
                  326
BLAST score
                  3.0e-30
E value
                  75
Match length
                  83
% identity
                  GTP-binding protein, ras-related - common tobacco
NCBI Description
                  >gi 296878 emb CAA50609 (X71609) ras-related GTP-binding
                  protein [Nicotiana tabacum]
                  203969
Seq. No.
Seq. ID
                  LIB3083-030-Q1-L1-A7
Method
                  BLASTX
NCBI GI
                  g1125691
                  161
BLAST score
                  7.0e-11
E value
                   54
Match length
                   59
% identity
NCBI Description (X94301) DnaJ protein [Solanum tuberosum]
                   203970
Seq. No.
                  LIB3083-030-Q1-L1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1143223
                   265
BLAST score
                   1.0e-147
E value
                   303
Match length
                   28
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   203971
Seq. No.
                   LIB3083-030-Q1-L1-B1
Seq. ID
Method
                   BLASTX
                   g3482918
NCBI GI
BLAST score
                   164
E value
                   2.0e-11
                   32
Match length
                   97
% identity
                   (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   203972
Seq. No.
Seq. ID
                   LIB3083-030-Q1-L1-B2
                   BLASTX
Method
                   q4406780
NCBI GI
BLAST score
                   322
E value
                   8.0e-30
```

59

Match length



```
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                  203973
Seq. No.
                  LIB3083-030-Q1-L1-B3
Seq. ID
                  BLASTX
Method
                  g2914703
NCBI GI
                  258
BLAST score
                  3.0e-22
E value
                  78
Match length
% identity
                   62
                  (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
                  203974
Seq. No.
                  LIB3083-030-Q1-L1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2244735
                   300
BLAST score
E value
                   1.0e-168
Match length
                   368
                   96
% identity
NCBI Description Cotton mRNA for expansin, clone CF631, partial cds
                   203975
Seq. No.
                   LIB3083-030-Q1-L1-C2
Seq. ID
Method
                   BLASTN
                   g2921331
NCBI GI
                   77
BLAST score
                   2.0e-35
E value
Match length
                   181
                   85
% identity
                   Gossypium hirsutum MYB-like DNA-binding domain protein
NCBI Description
                   (Cmy-D) mRNA, complete cds
                   203976
Seq. No.
                   LIB3083-030-Q1-L1-C3
Seq. ID
                   BLASTX
Method
                   g3335349
NCBI GI
                   365
BLAST score
                   4.0e-37
E value
                   122
Match length
% identity
                   65
                   (ACO04512) Similar to gb U46691 putative chromatin
NCBI Description
                   structure regulator (SUPT6H) from Homo sapiens. ESTs
                   gb T42908, gb_AA586170 and gb_AA395125 come from this gene.
                   [Arabidopsis thaliana]
                   203977
Seq. No.
Seq. ID
                   LIB3083-030-Q1-L1-C7
                   BLASTN
Method
NCBI GI
                   q4220631
BLAST score
                   34
                   2.0e-09
E value
```

E value 2.0e-Match length 53 % identity 25

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



## K5J14, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  LIB3083-030-Q1-L1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3511285
BLAST score
                  596
                  6.0e-62
E value
                  145
Match length
                  78
% identity
                  (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
                  203979
Seq. No.
                  LIB3083-030-Q1-L1-D5
Seq. ID
                  BLASTX
Method
                  g2104959
NCBI GI
BLAST score
                   337
                   2.0e-31
E value
                  73
Match length
                   85
% identity
                  (U96925) immunophilin [Vicia faba]
NCBI Description
Seq. No.
                   203980
                   LIB3083-030-Q1-L1-D7
Seq. ID
Method
                   BLASTX
                   q2098709
NCBI GI
                   256
BLAST score
E value
                   1.0e-28
                   75
Match length
% identity
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
                   203981
Seq. No.
                   LIB3083-030-Q1-L1-D8
Seq. ID
Method
                   BLASTX
                   g2369714
NCBI GI
BLAST score
                   602
E value
                   9.0e-63
                   115
Match length
                   97
% identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   203982
Seq. No.
                   LIB3083-030-Q1-L1-E4
Seq. ID
                   BLASTX
Method
                   g1354849
NCBI GI
                   381
BLAST score
                   1.0e-36
E value
                   111
Match length
                   62
% identity
                   (U57350) epoxide hydrolase [Nicotiana tabacum]
NCBI Description
                   203983
Seq. No.
                   LIB3083-030-Q1-L1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2501572
```

Seq. ID

Method



```
BLAST score
                     566
                     2.0e-58
  E value
                     155
  Match length
                     72
  % identity
                     LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
  NCBI Description
                     (L47118) EMB8 gene product [Picea glauca]
                     203984
  Seq. No.
                     LIB3083-030-Q1-L1-F1
  Seq. ID
                     BLASTX
Method
  NCBI GI
                     q4140398
  BLAST score
                     198
  E value
                     3.0e-15
                     52
  Match length
  % identity
                     (AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]
  NCBI Description
                     203985
  Seq. No.
                     LIB3083-030-Q1-L1-F2
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q267070
  BLAST score
                     298
                      6.0e-27
  E value
  Match length
                      57
  % identity
                     TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699)
  NCBI Description
                      TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_
                      (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis
                      thaliana]
                      203986
  Seq. No.
  Seq. ID
                      LIB3083-030-Q1-L1-F4
  Method
                      BLASTX
  NCBI GI
                      g1173209
  BLAST score
                      482
  E value
                      2.0e-48
                      99
  Match length
                      95
  % identity
                      40S RIBOSOMAL PROTEIN S16 >gi 541835_pir__S41193 ribosomal
  NCBI Description
                      protein S16 protein - upland cotton
                      >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                      [Gossypium hirsutum]
  Seq. No.
                      203987
                      LIB3083-030-Q1-L1-G1
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      g2995949
  BLAST score
                      506
  E value
                      2.0e-51
                      109
  Match length
                      76
   % identity
                     (AF053563) ubiquitin [Mesembryanthemum crystallinum]
  NCBI Description
                      203988
   Seq. No.
```

27829

LIB3083-030-Q1-L1-G2

BLASTX

BLAST score

284



```
g3914559
NCBI GI
                  275
BLAST score
                  3.0e-24
E value
                  74
Match length
                  74
% identity
                  RAS-RELATED PROTEIN RAB7 >gi_414834 (L14930) Rab7p [Glycine
NCBI Description
                  max]
                  203989
Seq. No.
                  LIB3083-030-Q1-L1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3157931
                   456
BLAST score
                   2.0e-45
E value
                   99
Match length
                   89
% identity
                   (AC002131) Similar to pyrophosphate-dependent
NCBI Description
                   phosphofuctokinase beta subunit gb_Z32850 from Ricinus
                   communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come
                   from this gene. [Arabidopsis thaliana]
                   203990
Seq. No.
                   LIB3083-030-Q1-L1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500378
BLAST score
                   383
                   6.0e-37
E value
                   89
Match length
% identity
                   79
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                   203991
                   LIB3083-030-Q1-L1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1915960
                   157
BLAST score
                   4.0e-17
E value
                   88
Match length
% identity
                   64
                   (Y07636) peptidylprolyl isomerase [Triticum aestivum]
NCBI Description
                   203992
Seq. No.
                   LIB3083-030-Q1-L1-H3
Seq. ID
                   BLASTX
Method
                   g3688181
NCBI GI
BLAST score
                   564
                   4.0e-58
E value
                   157
Match length
                   71
% identity
                   (ALO31804) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   203993
Seq. No.
                   LIB3083-030-Q1-L1-H4
Seq. ID
                   BLASTX
Method
                   g1652591
NCBI GI
```



```
3.0e-25
E value
                  127
Match length
                  43
% identity
                  (D90906) chloroplast import-associated channel IAP75
NCBI Description
                  [Synechocystis sp.]
                  203994
Seq. No.
                  LIB3083-030-Q1-L1-H7
Seq. ID
                  BLASTX
Method
                  g1518540
NCBI GI
                  205
BLAST score
                  5.0e-16
E value
                  56
Match length
                  71
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                   203995
Seq. No.
                   LIB3083-031-Q1-L1-A1
Seq. ID
                   BLASTX
Method
                   g464840
NCBI GI
                   285
BLAST score
                   1.0e-25
E value
                   55
Match length
                   100
% identity
                  TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin
NCBI Description
                   alpha-1 chain - fern (Anemia phyllitidis)
                   >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia
                   phyllitidis]
                   203996
Seq. No.
                   LIB3083-031-Q1-L1-A2
Seq. ID
                   BLASTX
Method
                   g1162986
NCBI GI
                   186
BLAST score
                   6.0e-14
E value
                   34
Match length
                   100
% identity
                   (M32430) beta-2 tubulin [Lytechinus pictus]
NCBI Description
                   203997
Seq. No.
                   LIB3083-031-Q1-L1-A5
 Seq. ID
Method
                   BLASTX
                   g3421123
NCBI GI
                   163
 BLAST score
                   2.0e-11
E value
                   38
Match length
 % identity
                   79
                    (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
 NCBI Description
                   thaliana]
                   203998
 Seq. No.
                   LIB3083-031-Q1-L1-A9
 Seq. ID
                   BLASTX
 Method
                   q3212879
 NCBI GI
                    330
 BLAST score
```

8.0e-31

70

E value

Match length

NCBI Description



```
% identity
                  (AC004005) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                  thalianal
                  203999
Seq. No.
                  LIB3083-031-Q1-L1-B12
Seq. ID
                  BLASTX
Method
                  q4544403
NCBI GI
                  241 -
BLAST score
                  2.0e-20
E value
                  67
Match length
                  63
% identity
NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase
                  precursor [Arabidopsis thaliana]
                  204000
Seq. No.
                  LIB3083-031-Q1-L1-B2
Seq. ID
                  BLASTX
Method
                  *g267079
NCBI GI
                  252
BLAST score
                  1.0e-21
E value
                   47
Match length
                  100
% identity
                  TUBULIN BETA-6 CHAIN >gi_320187_pir JQ1590 tubulin beta-6
NCBI Description
                   chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6
                   tubulin [Arabidopsis thaliana]
                   204001
Seq. No.
                   LIB3083-031-Q1-L1-B4
Seq. ID
                   BLASTX
Method
                   g2304971
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
                   78
Match length
                   47
% identity
NCBI Description (U82828) ATM [Homo sapiens]
                   204002
Seq. No.
                   LIB3083-031-Q1-L1-B5
Seq. ID
Method
                   BLASTX
                   q1706956
NCBI GI
                   611
BLAST score
                   1.0e-63
E value
                   139
Match length
% identity
                   (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204003
Seq. No.
                   LIB3083-031-Q1-L1-B9
Seq. ID
Method
                   BLASTX
                   q4454043
NCBI GI
                   422
BLAST score
                   1.0e-41
E value
                   118
Match length
 % identity
                   69
```

(AL035394) putative receptor kinase [Arabidopsis thaliana]



```
Seq. No.
                  204004
Seq. ID
                  LIB3083-031-Q1-L1-C12
Method
                  BLASTN
NCBI GI
                  g18483
BLAST score
                  43
                  4.0e-15
E value
Match length
                  83
% identity
                  88
NCBI Description
                 Cotton mRNA for cottonseed catalase subunit 1 (EC 1.11.1.6)
                  204005
Seq. No.
                  LIB3083-031-Q1-L1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  256
E value
                  1.0e-142
Match length
                  335
% identity
                  62
NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
                  precursor (PRP) mRNA, complete cds
Seq. No.
                  204006
Seq. ID
                  LIB3083-031-Q1-L1-C8
Method
                  BLASTX
NCBI GI
                  q2661840
BLAST score
                  240
E value
                  3.0e-20
Match length
                  59
% identity
                  76
                 (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
Seq. No.
                  204007
Seq. ID
                  LIB3083-031-Q1-L1-C9
Method
                  BLASTX
NCBI GI
                  g3395440
BLAST score
                  170
E value
                  4.0e-12
Match length
                  78
% identity
                  40
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  204008
Seq. ID
                  LIB3083-031-Q1-L1-D11
Method
                  BLASTX
NCBI GI
                  q217909
BLAST score
                  350
                  3.0e-33
E value
Match length
                  74
                  95
% identity
NCBI Description
                  (D14044) glycolate oxidase [Cucurbita sp.]
                  204009
Seq. No.
Seq. ID
                  LIB3083-031-Q1-L1-D12
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2583126
BLAST score 424
E value 3.0e-48

% identity

NCBI Description



```
Match length
% identity
                   71
                   (AC002387) putative DNA repair protein (RAD57) [Arabidopsis
NCBI Description
                   thaliana]
                   204010
Seq. No.
                   LIB3083-031-Q1-L1-D4
Seq. ID
Method
                   BLASTX
                   g3036811
NCBI GI
                   270
BLAST score
                   2.0e-31
E value
Match length
                   105
% identity
                   (AL022373) Calcium-dependent serine/threonine protein
NCBI Description
                   kinase [Arabidopsis thaliana]
                   204011
Seq. No.
                   LIB3083-031-Q1-L1-D8
Seq. ID
                   BLASTX
Method
                   q3935181
NCBI GI
                   203
BLAST score
                   5.0e-16
E value
Match length
                   41
% identity
                   90
                   (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                   204012
Seq. No.
                   LIB3083-031-Q1-L1-E4
Seq. ID
Method
                   BLASTX
                   g4455198
NCBI GI
                   296
BLAST score
                   9.0e-27
E value
                   103
Match length
% identity
                   64
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   204013
Seq. No.
                   LIB3083-031-Q1-L1-E8
Seq. ID
Method
                   BLASTX
                   g3434971
NCBI GI
                   202
BLAST score
                   7.0e-16
E value
                   95
Match length
                   54
 % identity
                    (AB008105) ethylene responsive element binding factor 3
NCBI Description
                    [Arabidopsis thaliana]
                   204014
Seq. No.
                   LIB3083-031-Q1-L1-F10
 Seq. ID
                   BLASTX
Method
                   g3822036
NCBI GI
                   198
BLAST score
                   2.0e-15
 E value
                   112
 Match length
                    43
```

(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. ID

Method

BLASTX



```
Seq. No.
                  LIB3083-031-Q1-L1-F6
Seq. ID
                  BLASTX
Method
                  a4490735
NCBI GI
                  142
BLAST score
                  1.0e-08
E value
                  46
Match length
                  61
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                  204016
Seq. No.
                  LIB3083-031-Q1-L1-F9
Seq. ID
                  BLASTX
Method
                  q3201554
NCBI GI
                   465
BLAST score
                  1.0e-46
E value
                  109
Match length
                   75
% identity
                  (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
                   204017
Seq. No.
                   LIB3083-031-Q1-L1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q729508
                   247
BLAST score
                   3.0e-21
E value
                   77
Match length
                   65
% identity
                   NARINGENIN, 2-OXOGLUTARATE 3-DIOXYGENASE
NCBI Description
                   (FLAVONONE-3-HYDROXYLASE) (FHT) >gi_499020_emb_CAA53579_
                   (X75965) flavanone 3-hydroxylase [Vītis vinifera]
                   204018
Seq. No.
                   LIB3083-031-Q1-L1-G7
Seq. ID
                   BLASTX
Method
                   q2244860
NCBI GI
                   212
BLAST score
                   5.0e-17
E value
                   91
Match length
                   53
% identity
                   (Z97337) cucumisin [Arabidopsis thaliana]
NCBI Description
                   204019
Seq. No.
                   LIB3083-031-Q1-L1-G8
Seq. ID
Method
                   BLASTX
                   q1717950
NCBI GI
                   283
BLAST score
E value
                   3.0e-25
Match length
                   52
 % identity
                   90
                   UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 2
 NCBI Description
                   PRECURSOR (RIESKE IRON-SULFUR PROTEIN 2) (RISP2) >gi_530052
                    (L16810) Rieske iron-sulfur protein [Nicotiana tabacum]
                    204020
 Seq. No.
                    LIB3083-031-Q1-L1-H3
```

Method

BLASTX



```
q1076696
NCBI GI
BLAST score
                  261
E value
                  1.0e-22
                  57
Match length
                  79
% identity
                  cyprosin - cardoon >gi_556819_emb_CAA57510_ (X81984)
NCBI Description
                  cyprosin [Cynara cardunculus]
                  204021
Seq. No.
                  LIB3083-031-Q1-L1-H5
Seq. ID
                  BLASTX
Method
                  g2829204
NCBI GI
BLAST score
                  273
                  2.0e-24
E value
                  51
Match length
                  100
% identity
                   (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
                   204022
Seq. No.
                  LIB3083-031-Q1-L1-H7
Seq. ID
                   BLASTX
Method
                   g1346172
NCBI GI
                   143
BLAST score
                   7.0e-09
E value
                   37
Match length
                   81
% identity
                   78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)
NCBI Description
                   (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)
                   >gi 170384 (L08830) glucose-regulated protein 78
                   [Lycopersicon esculentum]
                   204023
Seq. No.
                   LIB3083-037-Q1-G1-A11
Seq. ID
                   BLASTX
Method
                   g2129495
NCBI GI
                   652
BLAST score
                   1.0e-68
E value
                   135
Match length
% identity
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                   (U30508) E6 [Gossypium barbadense]
                   204024
 Seq. No.
                   LIB3083-037-Q1-G1-A2
 Seq. ID
                   BLASTN
 Method
                   q343239
 NCBI GI
 BLAST score
                   139
 E value
                   3.0e-72
 Match length
                   385
                   87
 % identity
NCBI Description Mustard (S.alba) chloroplast 16S rRNA, 5' end, and Val-tRNA
                   204025
 Seq. No.
                   LIB3083-037-Q1-G1-A4
 Seq. ID
```

Match length

108



```
g2500194
NCBI GI
                  703
BLAST score
                  2.0e-74
E value
Match length
                  140
% identity
                  94
                 RAC-LIKE GTP BINDING PROTEIN ARAC5 >gi 1293668 (U52350)
NCBI Description
                  GTP-binding protein [Arabidopsis thaliana]
                  204026
Seq. No.
                  LIB3083-037-Q1-G1-A6
Seq. ID
                  BLASTX
Method
                  q1747296
NCBI GI
                  509
BLAST score
                  8.0e-52
E value
                  131
Match length
% identity
                  73
NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
                   >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
                   204027
Seq. No.
                   LIB3083-037-Q1-G1-A7
Seq. ID
Method
                   BLASTX
                   g3421090
NCBI GI
BLAST score
                   624
                   3.0e-65
E value
Match length
                   126
% identity
                   95
                   (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
NCBI Description
                   thaliana]
                   204028
Seq. No.
                   LIB3083-037-Q1-G1-A8
Seq. ID
Method
                   BLASTX
                   g1402888
NCBI GI
                   403
BLAST score
                   2.0e-39
E value
                   125
Match length
                   66
 % identity
NCBI Description (X98130) unknown [Arabidopsis thaliana]
                   204029
 Seq. No.
                   LIB3083-037-Q1-G1-B1
 Seq. ID
                   BLASTX
 Method
                   q3063448
 NCBI GI
                   456
 BLAST score
                   1.0e-45
 E value
                   117
 Match length
                   71
 % identity
 NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]
                   204030
 Seq. No.
                   LIB3083-037-Q1-G1-B12
 Seq. ID
                   BLASTX
 Method
                   g4417283
 NCBI GI
                   242
 BLAST score
                   1.0e-20
 E value
```

Seq. ID



```
% identity
                  (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                  204031
Seq. No.
                  LIB3083-037-Q1-G1-B3
Seq. ID
Method
                  BLASTX
                  g4539330
NCBI GI
                  214
BLAST score
                  4.0e-17
E value
                  98
Match length
                  53
% identity
                   (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                   204032
Seq. No.
                  LIB3083-037-Q1-G1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4371292
                   359
BLAST score
E value
                   3.0e - 34
                   134
Match length
% identity
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204033
Seq. No.
                   LIB3083-037-Q1-G1-B7
Seq. ID
                   BLASTX
Method
                   a4049349
NCBI GI
BLAST score
                   418
                   4.0e-41
E value
Match length
                   122
                   66
% identity
                   (AL034567) ubiquinol-cytochrome c reductase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   204034
                   LIB3083-037-Q1-G1-C10
Seq. ID
                   BLASTX
Method
                   q1619602
NCBI GI
BLAST score
                   154
                   1.0e-10
E value
                   62
Match length
% identity
                   56
                   (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                   204035
Seq. No.
                   LIB3083-037-Q1-G1-C11
 Seq. ID
Method
                   BLASTX
                   q4115377
NCBI GI
BLAST score
                   454
                   2.0e-45
E value
Match length
                   106
                   79
 % identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   204036
 Seq. No.
```

27838

LIB3083-037-Q1-G1-C3



```
BLASTX
Method
NCBI GI
                                                               q464849
                                                               379
BLAST score
                                                               5.0e-37
E value
                                                               79
Match length
% identity
                                                               96
                                                              TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                                                               chain - almond >gi_2041\overline{3}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CAA47\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447\overline{635}_{emb_CA447
                                                               alpha-tubulin [Prunus dulcis]
                                                               204037
Seq. No.
                                                               LIB3083-037-Q1-G1-C5
Seq. ID
Method
                                                               BLASTX
                                                               q1465818
NCBI GI
BLAST score
                                                               141
                                                               7.0e-15
E value
Match length
                                                               49
                                                               72
% identity
                                                               (U64855) coded for by C. elegans cDNA CEESS16F; coded for
NCBI Description
                                                               by C. elegans cDNA yk76b10.3; coded for by C. elegans cDNA
                                                               yk14d4.3; coded for by C. elegans cDNA CEESS16F; coded for
                                                               by C. elegans cDNA yk49a11.5; coded for by C. elegans cDNA
                                                               yk48c6
Seq. No.
                                                               204038
Seq. ID
                                                               LIB3083-037-Q1-G1-C6
Method
                                                               BLASTX
NCBI GI
                                                               q4510383
BLAST score
                                                               440
                                                               1.0e-43
E value
                                                               90
Match length
% identity
                                                               91
NCBI Description
                                                              (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                                                               204039
Seq. ID
                                                               LIB3083-037-Q1-G1-C7
Method
                                                               BLASTX
                                                               q870711
NCBI GI
BLAST score
                                                               261
                                                               3.0e-23
E value
                                                               66
Match length
                                                               71
% identity
                                                               (L39267) biotin carboxylase [Ricinus communis]
NCBI Description
                                                               >gi 1582355 prf 2118337B Ac-CoA carboxylase:SUBUNIT=biotin
                                                               carboxylase [Ricinus communis]
                                                               204040
Seq. No.
Seq. ID
                                                               LIB3083-037-Q1-G1-C8
                                                               BLASTX
Method
                                                               g4490758
NCBI GI
BLAST score
                                                               187
                                                               5.0e-14
E value
```

Match length 66 % identity 48

(AL035708) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 204041



```
LIB3083-037-Q1-G1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1143223
                  115
BLAST score
                  6.0e-58
E value
                  343
Match length
% identity
                  50
                  Gossypium barbadense FbLate-2 gene, complete cds
NCBI Description
                  204042
Seq. No.
                  LIB3083-037-Q1-G1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3757514
BLAST score
                  254
E value
                   3.0e-22
                   62
Match length
% identity
                   (AC005167) putative plasma membrane intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                   204043
Seq. No.
                   LIB3083-037-Q1-G1-D5
Seq. ID
Method
                   BLASTX
                   q3135277
NCBI GI
                   154
BLAST score
E value
                   3.0e-10
                   94
Match length
                   44
% identity
                   (AC003058) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4191776 (AC005917) hypothetical protein [Arabidopsis
                   thaliana]
                   204044
Seq. No.
Seq. ID
                   LIB3083-037-Q1-G1-D7
                   BLASTX
Method
                                                              .....
NCBI GI
                   g4467111
BLAST score
                   460
                   5.0e-46
E value
Match length
                   138
% identity
                   69
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   204045
Seq. No.
                   LIB3083-037-Q1-G1-D8
Seq. ID
Method
                   BLASTX
                   q267069
NCBI GI
BLAST score
                   670
                   1.0e-70
E value
                   126
Match length
                   98
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

204046

LIB3083-037-Q1-G1-E10

Seq. No. Seq. ID



```
BLASTX
Method
NCBI GI
                  q267069
                  403
BLAST score
                  1.0e-39
E value
                  84
Match length
                  88
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  204047
Seq. No.
                  LIB3083-037-Q1-G1-E2
Seq. ID
Method
                  BLASTX
                  q3882081
NCBI GI
                   653
BLAST score
                   1.0e-68
E value
                   136
Match length
% identity
NCBI Description (AJ012552) polyubiquitin [Vicia faba]
                   204048
Seq. No.
                   LIB3083-037-Q1-G1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2459448
                   280
BLAST score
                   3.0e-25
E value
                   82
Match length
                   66
% identity
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   204049
Seq. No.
                   LIB3083-037-Q1-G1-F10
Seq. ID
                   BLASTX
Method
NCBI GI.
                   q3201969
BLAST score
                   354
E value
                   8.0e-34
                   87
Match length
                   68
% identity
                   (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
                   204050
Seq. No.
                   LIB3083-037-Q1-G1-F11
Seq. ID
Method
                   BLASTX
                   q2739365
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
Match length
                   82
                   51
 % identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   204051
 Seq. No.
                   LIB3083-037-Q1-G1-F12
 Seq. ID
 Method
                   BLASTX
```

g2129499

152

NCBI GI

BLAST score



```
3.0e-10
E value
                  97
Match length
                  44
% identity
                  fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  204052
Seq. No.
                  LIB3083-037-Q1-G1-F2
Seq. ID
                  BLASTX
Method
                  g1199467
NCBI GI
BLAST score
                   317
                   2.0e-29
E value
Match length
                   100
% identity
                   (D64155) possible aldehyde decarbonylase [Arabidopsis
NCBI Description
                   thaliana]
                   204053
Seq. No.
                   LIB3083-037-Q1-G1-F6
Seq. ID
                   BLASTX
Method
                   q3914449
NCBI GI
                   583
BLAST score
                   2.0e-60
E value
                   123
Match length
                   93
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus
                   persica]
                   204054
Seq. No.
                   LIB3083-040-Q1-G1-A1
Seq. ID
                   BLASTX
Method
                   g4522009
NCBI GI
BLAST score
                   315
E value
                   5.0e-29
Match length
                   94
 % identity
                   60
                   (AC007069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204055
 Seq. No.
                   LIB3083-040-Q1-G1-A2
 Seq. ID
                   BLASTX
 Method
                   g100226
 NCBI GI
                   222
 BLAST score
                   4.0e-18
 E value
                   130
 Match length
                   40
 % identity
                   hypothetical protein - tomato >gi_19275_emb_CAA78112_
 NCBI Description
                    (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                    [Lycopersicon esculentum]
                   204056
 Seq. No.
```

Seq. ID LIB3083-040-Q1-G1-A3

Method BLASTN NCBI GI g434344 BLAST score 63



```
8.0e-27
E value
Match length
                  103
% identity
                  A.thaliana (Columbia) mRNA for S18 ribosomal protein
NCBI Description
                  (641bp)
                  204057
Seq. No.
                  LIB3083-040-Q1-G1-A4
Seq. ID
Method
                  BLASTX
                  g4567310
NCBI GI
                  207
BLAST score
                  2.0e-16
E value
                  100
Match length
% identity
                  47
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                  204058
Seq. No.
                  LIB3083-040-Q1-G1-A6
Seq. ID
                  BLASTX
Method
                  g1705678
NCBI GI
BLAST score
                  242
                  1.0e-20
E value
                   57
Match length
                   86
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                   valosin-containing protein [Glycine max]
                   204059
Seq. No.
                   LIB3083-040-Q1-G1-B1
Seq. ID
                   BLASTX
Method
                   g2661840
NCBI GI
BLAST score
                   172
                   2.0e-21
E value
                   99
Match length
                   57
% identity
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                   204060
Seq. No.
Seq. ID
                   LIB3083-040-Q1-G1-B3
                   BLASTX
Method
                   q2827699
NCBI GI
                   215
BLAST score
E value
                   2.0e-17
Match length
                   105
                   48
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204061
                   LIB3083-040-Q1-G1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129533
BLAST score
                   492
                   9.0e-50
E value
Match length
                   139
 % identity
                   68
NCBI Description adenine nucleotide translocase - Arabidopsis thaliana
```



>gi\_1051109\_emb\_CAA89201\_ (Z49227) adenine nucleotide
translocase [Arabidopsis thaliana]

translocase [Arabidopsis thaliana] Seq. No. 204062 LIB3083-040-Q1-G1-D2 Seq. ID Method BLASTX NCBI GI g2618701 BLAST score 168 E value 3.0e-18 Match length 111 % identity NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana] Seq. No. 204063 Seq. ID LIB3083-040-Q1-G1-D5 Method BLASTX NCBI GI g4539422 BLAST score 499 E value 2.0e-59 Match length 133 % identity NCBI Description (AL049171) putative protein [Arabidopsis thaliana] Seq. No. 204064 Seq. ID LIB3083-040-Q1-G1-E3 Method BLASTX NCBI GI g2911075 BLAST score 249 E value 3.0e-21

% identity 58
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 204065

Match length

Seq. ID LIB3083-040-Q1-G1-E5

86

Method BLASTX
NCBI GI g134613
BLAST score 239
E value 4.0e-20
Match length 46
% identity 98

NCBI Description SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi\_82727\_pir\_\_A29077

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize >gi\_168620 (M54936) superoxide dismutase 2 [Zea mays]

>gi\_168622 (M15175) SOD2 protein [Zea mays]

Seq. No. 204066

Seq. ID LIB3083-040-Q1-G1-F3

Method BLASTX
NCBI GI g3024501
BLAST score 257
E value 3.0e-22
Match length 65
% identity 75

NCBI Description RAS-RELATED PROTEIN RAB11C >gi\_1370146\_emb\_CAA98179

(Z73951) RAB11C [Lotus japonicus]

BLAST score

199



```
204067
Seq. No.
                  LIB3083-040-Q1-G1-F5
Seq. ID
                  BLASTX
Method
                  g2764574
NCBI GI
                   430
BLAST score
                  1.0e-42
E value
                  117
Match length
                   68
% identity
NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
                   204068
Seq. No.
                   LIB3083-040-Q1-G1-F7
Seq. ID
                   BLASTX
Method
                   g2980788
NCBI GI
                   148
BLAST score
                   2.0e-09
E value
                   87
Match length
                   40
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   204069
Seq. No.
                   LIB3083-040-Q1-G1-G1
Seq. ID
                   BLASTX
Method
                   g1729851
NCBI GI
                   178
BLAST score
                   1.0e-13
E value
                   42
Match length
                   79
% identity
                   TUBULIN BETA CHAIN >gi_1263904 emb_CAA56936_ (X81046)
NCBI Description
                   beta-tubulin [Rhynchosporium secalis]
                   204070
Seq. No.
                   LIB3083-040-Q1-G1-G2
Seq. ID
                   BLASTX
Method
                   g231496
NCBI GI
                   666
BLAST score
                   4.0e-70
E value
                   144
Match length
                   90
% identity
                   ACTIN 58 >gi 100421 pir S20094 actin - potato
NCBI Description
                   >gi 21536 emb CAA39278 (X55749) actin [Solanum tuberosum]
                   204071
Seq. No.
                   LIB3083-040-Q1-G1-G3
 Seq. ID
                   BLASTX
Method
                   q3269288
NCBI GI
                   480
BLAST score
                   2.0e-48
E value
                   131
Match length
 % identity
                   (AL030978) putative protein [Arabidopsis thaliana]
 NCBI Description
                   204072
 Seq. No.
                   LIB3083-040-Q1-G1-H10
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g2695711
```

NCBI Description



```
5.0e-16
E value
                  54
Match length
                  70
% identity
                   (AJ001370) cytochome b5 [Olea europaea]
NCBI Description
                  204073
Seq. No.
                  LIB3083-040-Q1-G1-H2
Seq. ID
                  BLASTX
Method
                  g1706958
NCBI GI
                   517
BLAST score
                   1.0e-52
E value
                   98
Match length
                   99
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204074
Seq. No.
                   LIB3083-040-Q1-G1-H4
Seq. ID
                   BLASTX
Method
                   q4263786
NCBI GI
                   655
BLAST score
E value
                   7.0e-69
                   142
Match length
% identity
                   87
                   (AC006068) putative acyl coenzyme A oxidase, peroxisomal
NCBI Description
                   component [Arabidopsis thaliana]
                   204075
Seq. No.
                   LIB3083-040-Q1-G1-H5
Seq. ID
                   BLASTX
Method
                   q4127456
NCBI GI
BLAST score
                   399
                   6.0e-39
E value
                   139
Match length
                   38
% identity
                   (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
                   204076
Seq. No.
                   LIB3083-040-Q1-G1-H7
Seq. ID
                   BLASTX
Method
                   g3036816
NCBI GI
BLAST score
                   293
                   2.0e-26
E value
                   148
Match length
                   42
% identity
                   (AL022373) myosin-like protein [Arabidopsis thaliana]
NCBI Description
                   204077
Seq. No.
                   LIB3083-041-Q1-G1-D10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2829203
BLAST score
                   97
                   2.0e-47
E value
                   161
Match length
 % identity
```

protein precursor (LTP) mRNA, complete cds

Gossypium hirsutum cultivar Siokra 1-2 lipid transfer

% identity

NCBI Description

53



```
Seq. No.
Seq. ID
                  LIB3083-041-Q1-G1-D12
                  BLASTX
Method
                  g120669
NCBI GI
BLAST score
                   435
                   2.0e-43
E value
                   88
Match length
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   204079
Seq. No.
                   LIB3083-041-Q1-G1-G12
Seq. ID
                   BLASTX
Method
                   g2499710
NCBI GI
BLAST score
                   495
                   4.0e-56
E value
                   130
Match length
                   84
% identity
                   PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                   >gi 1438075 (L33686) phospholipase D [Ricinus communis]
                   204080
Seq. No.
                   LIB3083-042-Q1-G1-A8
Seq. ID
                   BLASTX
Method
                   q1518540
NCBI GI
                   180
BLAST score
                   9.0e-14
E value
                   49
Match length
                   71
% identity
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   204081
Seq. No.
Seq. ID
                   LIB3083-042-Q1-G1-A9
                   BLASTX
Method
NCBI GI
                   q2811025
BLAST score
                   317
                   1.0e-29
E value
                   82
Match length
                   66
% identity
                   ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
NCBI Description
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
                   204082
Seq. No.
                   LIB3083-042-Q1-G1-B9
Seq. ID
                   BLASTX
Method
                   g2129575
NCBI GI
                   203
BLAST score
                   1.0e-16
E value
                   91
Match length
```

DNA repair protein homolog XPBara - Arabidopsis thaliana

E value

Match length

NCBI Description

% identity

2.0e-53 119

17



```
204083
Seq. No.
                  LIB3083-042-Q1-G1-C11
Seq. ID
                  BLASTX
Method
                  q2935416
NCBI GI
                  276
BLAST score
                  7.0e-25
E value
                  67
Match length
                  78
% identity
                  (AF047896) isoflavone reductase homolog [Betula pendula]
NCBI Description
Seq. No.
                  204084
                  LIB3083-042-Q1-G1-C9
Seq. ID
Method
                  BLASTX
                  g543715
NCBI GI
BLAST score
                  322
E value
                  3.0e-30
Match length
                  78
% identity
                  PROTEIN PHOSPHATASE PP2A REGULATORY SUBUNIT A (PR65)
NCBI Description
                  >gi 541969 pir S40171 phosphoprotein phosphatase 2A 65K
                  regulatory chain - garden pea >gi_629639_pir__$43776
                  phosphoprotein phosphatase 2A 65kDa regulatory subunit -
                   garden pea (fragment) >gi_437901_emb_CAA81107_ (Z25888)
                  phosphoprotein phosphatase 2A 65kDa regulatory subunit
                   [Pisum sativum]
Seq. No.
                   204085
                   LIB3083-042-Q1-G1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4103342
BLAST score
                   474
                   8.0e-48
E value
Match length
                   111
                   86
% identity
                   (AF022377) agamous-like putative transcription factor
NCBI Description
                   [Cucumis sativus]
                   204086
Seq. No.
                   LIB3083-042-Q1-G1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3236240
                   213
BLAST score
                   1.0e-17
E value
Match length
                   57
                   72
% identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204087
                   LIB3083-042-Q1-G1-F6
Seq. ID
                   BLASTX
Method
                   q576773
NCBI GI
                   522
BLAST score
```

27848

(U16956) polyubiquitin [Filobasidiella neoformans]



```
Seq. Nó.
                  204088
                  LIB3083-042-Q1-G1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191152
BLAST score
                  240
E value
                  5.0e-24
Match length
                  83
% identity
                  (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
Seq. No.
                  204089
                  LIB3083-042-Q1-G1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1706956
BLAST score
                   446
E value
                  2.0e-59
Match length
                  124
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204090
Seq. No.
Seq. ID
                  LIB3083-042-Q1-G1-G2
Method
                  BLASTX
NCBI GI
                   q1706958
                   329
BLAST score
                   9.0e-38
E value
                   121
Match length
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   204091
Seq. ID
                   LIB3083-042-Q1-G1-G6
Method
                   BLASTX
NCBI GI
                   g2213623
BLAST score
                   166
                   4.0e-12
E value
                   49
Match length
% identity
                   61
NCBI Description (AC000103) F21J9.15 [Arabidopsis thaliana]
                   204092
Seq. No.
                   LIB3083-042-Q1-G1-G8
Seq. ID
Method
                   BLASTX
                   g2739365
NCBI GI
                   349
BLAST score
                   2.0e-33
E value
Match length
                   82
                   78
% identity
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
                   204093
Seq. No.
Seq. ID
                   LIB3083-042-Q1-G1-H12
Method
                   BLASTX
                   g3023816
NCBI GI
BLAST score
                   151
```

8.0e-14

E value



Match length 58 % identity 68

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 204094

Seq. ID LIB3083-042-Q1-G1-H3

Method BLASTX
NCBI GI g3047117
BLAST score 363
E value 5.0e-35
Match length 85

Match length 85 % identity 84

NCBI Description (AF058919) similar to ATP-dependent RNA helicases

[Arabidopsis thaliana]

Seq. No. 204095

Seq. ID LIB3083-042-Q1-G1-H7

Method BLASTX
NCBI GI g2739046
BLAST score 314
E value 5.0e-29
Match length 117

% identity 55

NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p

[Glycine max]

Seq. No. 204096

Seq. ID LIB3083-042-Q1-G1-H8

Method BLASTX
NCBI GI g2935416
BLAST score 401
E value 3.0e-39
Match length 104

% identity 78

NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No.

Seq. ID LIB3083-046-Q1-G1-A6

204097

Method BLASTX
NCBI GI g267069
BLAST score 389
E value 7.0e-38
Match length 104
% identity 74

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 204098

Seq. ID LIB3083-046-Q1-G1-A7

Method BLASTX
NCBI GI g4185509
BLAST score 294
E value 1.0e-26



Match length 90 % identity (AF102821) actin depolymerizing factor 3 [Arabidopsis NCBI Description thaliana] 204099 Seq. No. Seq. ID LIB3083-046-Q1-G1-A8 Method BLASTX q2842493 NCBI GI 229 BLAST score E value 5.0e-19 Match length 96 % identity 56 (AL021749) predicted protein [Arabidopsis thaliana] NCBI Description 204100 Seq. No. LIB3083-046-Q1-G1-B11 Seq. ID Method BLASTX g2340108 NCBI GI BLAST score 559 1.0e-57 E value 105 Match length 97 % identity (U65948) starch branching enzyme IIa [Zea mays] NCBI Description 204101 Seq. No. LIB3083-046-Q1-G1-B2 Seq. ID Method BLASTX NCBI GI q119350 556 BLAST score 3.0e-57 E value 126 Match length % identity 85 ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608\_pir\_\_JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi\_16271\_emb\_CAA41114\_ (X58107) enolase [Arabidopsis thaliana] Seq. No. 204102 LIB3083-046-Q1-G1-B6 Seq. ID BLASTX Method NCBI GI q1168446 BLAST score 214 E value 3.0e-17 Match length 134 % identity AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) NCBI Description >qi 1073840 pir F64132 aminopeptidase N (pepN) homolog -Haemophilus influenzae (strain Rd KW20) >gi 1574460 (U32835) aminopeptidase N (pepN) [Haemophilus influenzae Rd]

204103 Seq. No.

LIB3083-046-Q1-G1-C10 Seq. ID

BLASTX Method NCBI GI g3163946

NCBI Description



```
BLAST score
E value
                  4.0e-65
                  136
Match length
% identity
                   (AJ005599) alpha-tubulin 1 [Eleusine indica]
NCBI Description
Seq. No.
                  204104
                  LIB3083-046-Q1-G1-C12
Seq. ID
                  BLASTX
Method
                   q3281853
NCBI GI
                   246
BLAST score
                   8.0e-21
E value
                   73
Match length
% identity
                   64
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   204105
Seq. No.
                   LIB3083-046-Q1-G1-C3
Seq. ID
Method
                   BLASTX
                   g2213882
NCBI GI
                   152
BLAST score
                   3.0e-12
E value
                   76
Match length
                   57
% identity
                   (AF004165) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                   pennellii]
                   204106
Seq. No.
                   LIB3083-046-Q1-G1-C4
Seq. ID
                   BLASTX
Method
                   g4262226
NCBI GI
                   162
BLAST score
                   4.0e-11
E value
                   104
Match length
                   45
% identity
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   204107
Seq. No.
                   LIB3083-046-Q1-G1-C6
Seq. ID
                   BLASTX
Method
                   q3157932
NCBI GI
                   509
BLAST score
                   8.0e-52
E value
                   129
Match length
                   78
 % identity
                   (AC002131) Similar to hypothetical protein HYP1 gb Z97338
NCBI Description
                   from A. thaliana. [Arabidopsis thaliana]
                   204108
 Seq. No.
                   LIB3083-046-Q1-G1-C7
 Seq. ID
 Method
                   BLASTX
                   q2213882
 NCBI GI
                   605
 BLAST score
                   5.0e-63
 E value
                   144
 Match length
                   78
 % identity
                   (AF004165) 2-isopropylmalate synthase [Lycopersicon
```

Seq. ID



## pennellii]

```
Seq. No.
                  204109
                  LIB3083-046-Q1-G1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2317910
BLAST score
                  197
E value
                   1.0e-15
Match length
                   71
                  51
% identity
NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]
Seq. No.
                  204110
Seq. ID
                  LIB3083-046-Q1-G1-D3
Method
                  BLASTX
                   q3660467
NCBI GI
                   302
BLAST score
E value
                   6.0e-28
                                                      X._
                   72
Match length
                   79
% identity
                   (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   204111
                  LIB3083-046-Q1-G1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2435517
                   274
BLAST score
E value
                   2.0e-24
                   89
Match length
                   61
% identity
                   (AF024504) contains similarity to peptidase family A1
NCBI Description
                   [Arabidopsis thaliana]
                   204112
Seq. No.
Seq. ID
                   LIB3083-046-Q1-G1-D5
Method
                   BLASTX
NCBI GI
                   q3136336
BLAST score
                   451
E value
                   4.0e-45
Match length
                   94
                   52
% identity
                  (AF064552) calmodulin; Cam [Apium graveolens]
NCBI Description
Seq. No.
                   204113
                   LIB3083-046-Q1-G1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3660467
BLAST score
                   158
E value
                   3.0e-11
Match length
                   40
% identity
                   75
                   (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
                   204114
Seq. No. 😓
```

27853

LIB3083-046-Q1-G1-D8



```
BLASTX
Method
NCBI GI
                  q1170373
                  281
BLAST score
                  3.0e-25
E value
                   99
Match length
                   59
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302
NCBI Description
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                   >gi 397482_emb_CAA52684_ (X74604) heat shock protein 70
                   cognate [Arabidopsis thaliana]
                   204115
Seq. No.
                  LIB3083-046-Q1-G1-E8
Seq. ID
Method
                  BLASTX
                   q4008159
NCBI GI
                   209
BLAST score
                   2.0e-19
E value
                   87
Match length
                   58
% identity
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
                   204116
Seq. No.
                   LIB3083-046-Q1-G1-F1
Seq. ID
Method
                   BLASTX
                   g3834321
NCBI GI
                   158
BLAST score
                   5.0e-11
E value
                   67
Match length
                   58
% identity
                   (AC005679) Strong similarity to F13P17.9 gi 3337356
NCBI Description
                   transport protein SEC61 alpha subunit homolog from
                   Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis
                   thaliana]
                   204117
Seq. No.
                   LIB3083-046-Q1-G1-F10
Seq. ID
Method
                   BLASTX
                   q4432807
NCBI GI
                   130
BLAST score
E value
                   3.0e-15
                   130
Match length
                   46
% identity
                  (AC006570) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   204118
Seq. No.
                   LIB3083-046-Q1-G1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3122053
BLAST score
                   354
                   7.0e-34
E value
Match length
                   95
                   68
% identity
```

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description

>gi 1235582\_emb\_CAA65391\_ (X96555) elongation factor

1-alpha [Pisum sativum]

204119 Seq. No.

```
Seq. ID
                  LIB3083-046-Q1-G1-F7
Method
                  BLASTX
NCBI GI
                  q4567286
BLAST score
                  614
                  4.0e-64
E value
                  136
Match length
% identity
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                  thaliana]
                  204120
Seq. No.
Seq. ID
                  LIB3083-046-Q1-G1-G1
Method
                  BLASTX
                  g407992
NCBI GI
BLAST score
                  177
                  7.0e-13
E value
                  84
Match length
                  46
% identity
NCBI Description
                  (L25125) RNA helicase [Mus musculus]
                  204121
Seq. No.
                  LIB3083-046-Q1-G1-G12
Seq. ID
Method
                  BLASTX
                  g4510345
NCBI GI
BLAST score
                  162
                  3.0e-11
E value
Match length
                  57
                  51
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204122
Seq. No.
                  LIB3083-046-Q1-G1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q832876
BLAST score
                   558
E value
                   1.0e-57
Match length
                   122
                   89
% identity
                   (L41345) ascorbate free radical reductase [Solanum
NCBI Description
                   lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                   radical reductase [Lycopersicon esculentum]
Seq. No.
                   204123
Seq. ID
                  LIB3083-046-Q1-G1-G6
Method
                  BLASTX
NCBI GI
                   g2351374
BLAST score
                   418
E value
                   3.0e-41
```

98 Match length % identity 83

(U54560) putative 26S proteasome subunit athMOV34 NCBI Description

[Arabidopsis thaliana]

Seq. No. 204124

Seq. ID LIB3083-046-Q1-G1-H12

BLASTX Method NCBI GI g2065531

BLAST score

440



```
BLAST score
E value
                   3.0e-19
Match length
                   54
% identity
                   80
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   204125
Seq. ID
                   LIB3083-046-Q1-G1-H2
Method
                   BLASTX
NCBI GI
                   q1408471
BLAST score
                   170
E value
                   4.0e-13
Match length
                   73
% identity
                   62
NCBI Description
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
Seq. No.
                   204126
Seq. ID
                   LIB3083-046-Q1-G1-H6
Method
                   BLASTX
NCBI GI
                   g2129915
BLAST score
                   337
E value
                   1.0e-31
Match length
                   103
% identity
                   63
NCBI Description
                   ferredoxin precursor - sweet orange
                   >gi_1360725 emb CAA87068 (Z46944) non-photosynthetic
                   ferredoxin [Citrus sinensis]
Seq. No.
                   204127
Seq. ID
                   LIB3083-046-Q1-G1-H8
Method
                   BLASTX
NCBI GI
                   q3687237
BLAST score
                   143
E value
                   7.0e-09
Match length
                   100
% identity
                   39
NCBI Description
                   (AC005169) putative Cys3His zinc-finger protein
                   [Arabidopsis thaliana]
Seq. No.
                   204128
Seq. ID
                   LIB3083-047-Q1-G1-C1
Method
                   BLASTX
NCBI GI
                   q3641837
BLAST score
                   401
E value
                   2.0e-39
Match length
                   104
% identity
NCBI Description
                   (AL023094) Nonclathrin coat protein gamma - like protein
                   [Arabidopsis thaliana]
Seq. No.
                  204129
Seq. ID
                  LIB3083-047-Q1-G1-D2
Method
                  BLASTX
NCBI GI
                  g3643609
```



E value 4.0e-44
Match length 82
% identity 87
NCBI Description (AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No. 204130
Seq. ID LIB3083-047-Q1-G1-E2
Method BLASTX
NCBI GI g3953456
RLAST score 349

BLAST score 349 E value 3.0e-33 Match length 124 % identity 59

NCBI Description (AC002328) F20N2.1 [Arabidopsis thaliana]

Seq. No. 204131

Seq. ID LIB3083-047-Q1-G1-G7

Method BLASTX
NCBI GI g4580398
BLAST score 166
E value 5.0e-20
Match length 92
% identity 57

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

Seq. No. 204132

Seq. ID LIB3083-047-Q1-G1-G8

Method BLASTX
NCBI GI g3927825
BLAST score 291
E value 1.0e-26
Match length 69
% identity 78

NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana]

Seq. No. 204133

Seq. ID LIB3083-047-Q1-G1-H2

Method BLASTX
NCBI GI g2129753
BLAST score 560
E value 7.0e-58
Match length 119
% identity 87

NCBI Description threonine synthase (EC 4.2.99.2) precursor - Arabidopsis

thaliana (fragment) >gi\_1448917 (L41666) threonine synthase

[Arabidopsis thaliana]

Seq. No. 204134

Seq. ID LIB3083-047-Q1-G1-H5

Method BLASTX
NCBI GI g1706956
BLAST score 662
E value 8.0e-70
Match length 122

```
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  204135
Seq. No.
                  LIB3083-047-Q1-G1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4039152
                  150
BLAST score
                  6.0e-10
E value
                  38
Match length
                  74
% identity
                  (AF104221) low temperature and salt responsive protein
NCBI Description
                  LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303
                  (AF122006) hydrophobic protein [Arabidopsis thaliana]
                  204136
Seq. No.
                  LIB3083-047-Q1-G1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3421096
                  505
BLAST score
                  2.0e-51
E value
                  108
Match length
                  92
% identity
                  (AF043528) 20S proteasome subunit PAG1 [Arabidopsis
NCBI Description
                  thaliana] >gi 3885332 (AC005623) proteasome component
                   [Arabidopsis thaliana]
                   204137
Seq. No.
                  LIB3083-048-Q1-G1-A1
Seq. ID
                  BLASTX
Method
                   q4056403
NCBI GI
                   165
BLAST score
                   8.0e-12
E value
                   61
Match length
% identity
                   57
                  (AD001673) lipoxygenase [Persea americana]
NCBI Description
                   204138
Seq. No.
                   LIB3083-048-Q1-G1-A12
Seq. ID
Method
                   BLASTX
                   a2627181
NCBI GI
                   167
BLAST score
E value
                   5.0e-12
                   59
Match length
% identity
                   56
                  (D89619) cycloartenol synthase [Pisum sativum]
NCBI Description
                   204139
Seq. No.
Seq. ID
                   LIB3083-048-Q1-G1-C9
                   BLASTX
Method
NCBI GI
                   q1076746
                   106
BLAST score
                   4.0e-10
E value
                   83
Match length
                   53
% identity
NCBI Description heat shock protein 70 - rice (fragment)
```

>gi\_763160\_emb\_CAA47948\_ (X67711) heat shock protein 70

Seq. No.

Seq. ID

Method



## [Oryza sativa]

```
204140
Seq. No.
                  LIB3083-048-Q1-G1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924520
BLAST score
                  292
                  9.0e-28
E value
                  91
Match length
                  75
% identity
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                  [Arabidopsis thaliana]
                  204141
Seq. No.
                  LIB3083-048-Q1-G1-E1
Seq. ID
                  BLASTX
Method
                  g2832623
NCBI GI
BLAST score
                  333
                  3.0e-31
E value
                  101
Match length
% identity
                   (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                   204142
Seq. No.
                  LIB3083-048-Q1-G1-E3
Seq. ID
                  BLASTX
Method
                   a1084481
NCBI GI
BLAST score
                   556
                   2.0e-57
E value
Match length
                   126
                   88
% identity
NCBI Description heat shock protein 70 - Maize
                   204143
Seq. No.
                   LIB3083-048-Q1-G1-F6
Seq. ID
Method
                   BLASTX
                   q445613
NCBI GI
BLAST score
                   313
                   6.0e-29
E value
Match length
                   89
                   72
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                   204144
Seq. No.
                   LIB3083-048-Q1-G1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1136122
                   486
BLAST score
E value
                   5.0e-49
                   135
Match length
                   77
% identity
                  (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                   204145
```

27859

LIB3083-048-Q1-G1-F8

BLASTX

```
Side A
```

```
NCBI GI
                  169
BLAST score
E value
                  2.0e-12
                  51
Match length
                   67
% identity
                  TUBULIN BETA-1 CHAIN >gi 100072 pir S20868 tubulin beta-1
NCBI Description
                  chain - garden pea >gi 20758 emb CAA38613 (X54844)
                  beta-tubulin 1 [Pisum sativum]
                  204146
Seq. No.
Seq. ID
                  LIB3083-048-Q1-G1-F9
Method
                  BLASTX
NCBI GI
                  q629541
BLAST score
                  100
E value
                  1.0e-09
                  59
Match length
% identity
                   64
                  plasma membrane intrinsic protein 1c - Arabidopsis thaliana
NCBI Description
                  >gi 472875 emb CAA53476 (X75882) plasma membrane intrinsic
                  protein 1c [Arabidopsis thaliana]
Seq. No.
                  204147
Seq. ID
                  LIB3083-048-Q1-G1-G3
Method
                  BLASTX
NCBI GI
                  g1370174
BLAST score
                  250
                  7.0e-22
E value
Match length
                  58
% identity
                   83
NCBI Description (Z73936) RAB1Y [Lotus japonicus]
Seq. No.
                  204148
Seq. ID
                  LIB3083-048-Q1-G1-G4
Method
                  BLASTN
NCBI GI
                  g2154714
BLAST score
                   46
                   9.0e-17
E value
                  90
Match length
                  88
% identity
NCBI Description A.thaliana mRNA for CDPK-related protein kinase
Seq. No.
                  204149
Seq. ID
                  LIB3083-048-Q1-G1-G5
Method
                  BLASTX
NCBI GI
                  g322525
BLAST score
                   468
E value
                   3.0e-47
Match length
                  103
% identity
NCBI Description
                  omnipotent suppressor protein SUP1 homolog (clone A18) -
                  Arabidopsis thaliana (fragment) >gi 16512 emb CAA49171
```

(X69374) similar to yeast omnipotent suppressor protein

SUP1 (SUP45); ORF [Arabidopsis thaliana]

Seq. No. 204150

Seq. ID LIB3083-048-Q1-G1-G6

Method BLASTX



```
q3068809
NCBI GI
                   243
BLAST score
                   4.0e-21
E value
                   60
Match length
% identity
                   (AF059295) Skp1 homolog [Arabidopsis thaliana]
NCBI Description
                   204151
Seq. No.
           18,
                   LIB3083-048-Q1-G1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g466160
BLAST score
                   267
                   2.0e-23
E value
Match length
                   83
% identity
                   HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi 630771_pir__S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi_289769 (L14429) putative [Caenorhabditis
                   elegans]
Seq. No.
                   204152
Seq. ID
                   LIB3083-048-Q1-G1-G8
Method
                   BLASTX
NCBI GI
                   g2129630
BLAST score
                   224
                   2.0e-20
E value
Match length
                   75
                   54
% identity
                   lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thaliana] >gi 33\overline{9}5760 (U7\overline{7}721)
                   unknown [Arabidopsis thaliana]
Seq. No.
                   204153
                   LIB3083-048-Q1-G1-H1
Seq. ID
Method
                   BLASTN
                   g1143223
NCBI GI
                   264
BLAST score
                   1.0e-147
E value
                   408
Match length
                   48
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                   204154
                   LIB3083-048-Q1-G1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3860277
BLAST score
                   515
E value
                   2.0e-52
Match length
                   111
                   91
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
```

Seq. No. 204155

Seq. ID LIB3083-048-Q1-G1-H3

Method BLASTX

Method

NCBI GI

BLASTX

g3915737

```
NCBI GI
                    g2815246
BLAST score
                    213
                    3.0e-17
E value
Match length
                    55
% identity
                    71
NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.
                    204156
Seq. ID
                    LIB3083-048-Q1-G1-H4
Method
                    BLASTX
NCBI GI
                    q4538897
BLAST score
                    273
E value
                    4.0e-24
Match length
                    83
% identity
                    61
NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]
Seq. No.
                    204157
Seq. ID
                    LIB3083-048-Q1-G1-H5
Method
                    BLASTX
NCBI GI
                    g1702983
BLAST score
                    363
E value
                    1.0e-34
Match length
                    116
% identity
                    60
                    AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850
NCBI Description
                    hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein
                    [Fragaria ananassa]
Seq. No.
                    204158
Seq. ID
                    LIB3083-048-Q1-G1-H7
Method
                    BLASTX
NCBI GI
                    q2811025
BLAST score
                    1,78
E value
                    4.0e-13
Match length
                    69
% identity
                    58
                    ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607
NCBI Description
                    (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                    204159
Seq. ID
                    LIB3083-048-Q1-G1-H8
Method
                    BLASTX
NCBI GI
                    g4185509
BLAST score
                    230
E value
                    4.0e-19
Match length
                    53
% identity
                    87
NCBI Description
                   (AF102821) actin depolymerizing factor 3 [Arabidopsis
                    thaliana]
Seq. No.
                    204160
                    LIB3083-049-Q1-L1-G6
Seq. ID
```



```
230
BLAST score
                   2.0e-19
E value
                   80
Match length
% identity
                   60
```

IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP NCBI Description ALPHA) >gi 3228370 (AF017252) importin alpha [Lycopersicon

esculentum]

204161 Seq. No.

LIB3083-049-Q1-L1-H12 Seq. ID

BLASTX Method g1155261 NCBI GI 641 BLAST score 3.0e-67 E value 135 Match length % identity 94

(U40217) eukaryotic release factor 1 homolog [Arabidopsis NCBI Description

thaliana]

204162 Seq. No.

LIB3083-050-Q1-L1-A1 Seq. ID

Method BLASTX g1702983 NCBI GI BLAST score 293 1.0e-26 E value 105 Match length % identity 53

AUXIN-REPRESSED 12.5 KD PROTEIN >gi\_99855\_pir\_\_S11850 NCBI Description

hypothetical protein - garden strawberry >gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

204163 Seq. No.

LIB3083-050-Q1-L1-A2 Seq. ID

BLASTX Method g2499879 NCBI GI 468 BLAST score 5.0e-47 E value 121 Match length 74 % identity

CYSTEINE PROTEINASE 3 PRECURSOR >gi\_2129935\_pir\_\_S66348 NCBI Description senescence-associated cysteine proteinase precursor (clone

SENU3) - tomato >gi\_1235545\_emb\_CAA88629\_ (Z48736) pre-pro-cysteine proteinase [Lycopersicon esculentum]

204164 Seq. No.

LIB3083-050-Q1-L1-A3 Seq. ID

BLASTX Method q3668092 NCBI GI BLAST score 394 2.0e-38 E value 126 Match length % identity

(AC004667) unknown protein [Arabidopsis thaliana] NCBI Description

204165 Seq. No.



```
LIB3083-050-Q1-L1-A4
Seq. ID
Method
                  BLASTX
                  g2281115
NCBI GI
                  319
BLAST score
                  1.0e-29
E value
                  69
Match length
% identity
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                  thaliana]
                  204166
Seq. No.
                  LIB3083-050-Q1-L1-A7
Seq. ID
Method
                  BLASTN
                  g1143223
NCBI GI
                  239
BLAST score
                  1.0e-132
E value
                   401
Match length
                   35
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   204167
Seq. No.
                  LIB3083-050-Q1-L1-B3
Seq. ID
                  BLASTX
Method
                   g4432844
NCBI GI
BLAST score
                   276
E value
                   2.0e-24
                   131
Match length
                   40
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                   204168
Seq. No.
                   LIB3083-050-Q1-L1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1174592
                   483
BLAST score
E value
                   7.0e-51
Match length
                   106
% identity
                   TUBULIN ALPHA-1 CHAIN >qi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   204169
Seq. No.
                   LIB3083-050-Q1-L1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4510383
BLAST score
                   214
                   4.0e-17
E value
Match length
                   42
                   95
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                   204170
Seq. No.
                   LIB3083-050-Q1-L1-B6
Seq. ID
Method
                   BLASTX
```

g2979545

192

NCBI GI BLAST score



```
E value
                  1.0e-14
                  113
Match length
% identity
                  47
                   (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  204171
                  LIB3083-050-Q1-L1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169585
BLAST score
                  389
E value
                   1.0e-37
Match length
                   130
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >qi 885894 (U20179) fructose 1,6-bisphosphatase [Brassica
                  napus]
                   204172
Seq. No.
Seq. ID
                  LIB3083-050-Q1-L1-C12
Method
                   BLASTX
NCBI GI
                   q542850
BLAST score
                   227
E value
                   1.0e-34
                   115
Match length
                   68
% identity
NCBI Description hnRNP G protein - human
Seq. No.
                   204173
Seq. ID
                   LIB3083-050-Q1-L1-C3
Method
                   BLASTX
NCBI GI
                   g1762914
BLAST score
                   259
E value
                   2.0e-22
Match length
                   66
% identity
                   71
                   (U65973) alcohol dehydrogenase A [Washingtonia robusta]
NCBI Description
Seq. No.
                   204174
                   LIB3083-050-Q1-L1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1399275
BLAST score
                   525
E value
                   1.0e-53
                   125
Match length
                   82
% identity
                   (U31835) calmodulin-domain protein kinase CDPK isoform 6
NCBI Description
                   [Arabidopsis thaliana] >gi 2623752 (AC002329) CDPK6
                   (calmodulin-domain protein kinase isoform 6) [Arabidopsis
                   thaliana]
                   204175
Seq. No.
Seq. ID
                   LIB3083-050-Q1-L1-D1
Method
                   BLASTX
```

g2827555

411 3.0e-40

NCBI GI BLAST score

E value



91

Match length

% identity

```
Match length
% identity
                  60
                   (AL021635) Translation factor EF-1 alpha - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  204176
Seq. No.
                  LIB3083-050-Q1-L1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204300
BLAST score
                  334
E value
                   3.0e-31
Match length
                   107
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   204177
Seq. No.
                  LIB3083-050-Q1-L1-D12
Seq. ID
Method
                   BLASTX
                   g2058282
NCBI GI
                   202
BLAST score
                   2.0e-16
E value
                   64
Match length
% identity
                  (X97377) atranbpla [Arabidopsis thaliana]
NCBI Description
                   204178
Seq. No.
Seq. ID
                   LIB3083-050-Q1-L1-D3
                   BLASTX
Method
NCBI GI
                   g2982432
                   334
BLAST score
                   2.0e-31
E value
                   76
Match length
                   80
% identity
                   (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204179
                   LIB3083-050-Q1-L1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q416758
BLAST score
                   377
E value
                   2.0e-36
Match length
                   108
                   66
% identity
                   SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130)
NCBI Description
                   carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
                   204180
Seq. No.
                   LIB3083-050-Q1-L1-D5
Seq. ID
                   BLASTX
Method
                   q2501449
NCBI GI
                   154
BLAST score
                   3.0e-19
E value
```

27866

NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi\_1668773\_emb\_CAA67922\_





## (X99608) ubiquitin-like protein [Oryza sativa]

```
Seq. No.
                  LIB3083-050-Q1-L1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166899
BLAST score
                  36
                  7.0e-11
E value
                  56
Match length
                  91
% identity
                  Arabidopsis thaliana bete-3 tubulin (TUB3) gene, complete
NCBI Description
                  204182
Seq. No.
Seq. ID
                  LIB3083-050-Q1-L1-D9
Method
                  BLASTX
                  q559684
NCBI GI
BLAST score
                  587
                   6.0e-61
E value
                  142
Match length
% identity
                  (L36097) aquaporin [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                  204183
                  LIB3083-050-Q1-L1-E11
Seq. ID
                  BLASTX
Method
                   q279675
NCBI GI
                   169
BLAST score
E value
                   5.0e-17
                   96
Match length
                   50
% identity
NCBI Description fibronectin precursor - human
Seq. No.
                   204184
                   LIB3083-050-Q1-L1-E3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3046906
BLAST score
                   43
E value
                   5.0e-15
Match length
                   95
                   87
% identity
                   Onchocerca volvulus beta-tubulin (tub) gene, complete cds
NCBI Description
Seq. No.
                   204185
                   LIB3083-050-Q1-L1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3549669
                   297
BLAST score
                   5.0e-29
E value
Match length
                   84
% identity
                   80
                   (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
                   204186
Seq. No.
                   LIB3083-050-Q1-L1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129473
```



BLAST score 190 E value 8.0e-22 Match length 105 % identity 56 NCBI Description arabinogalactan-like protein - loblolly pine >gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda] Seq. No. 204187 Seq. ID LIB3083-050-Q1-L1-E7 Method BLASTX NCBI GI q2827143 BLAST score 475 E value 6.0e-48 Match length 109 % identity NCBI Description (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana] Seq. No. 204188 Seq. ID LIB3083-050-Q1-L1-E9 Method BLASTX NCBI GI g267069 BLAST score 622 E value 5.0e-65 Match length 116 % identity 98 TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 204189 LIB3083-050-Q1-L1-F1 Seq. ID Method BLASTX NCBI GI q3702333 BLAST score 333 E value 4.0e-31 Match length 106 % identity NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana] Seq. No. 204190 Seq. ID LIB3083-050-Q1-L1-F11 Method BLASTX NCBI GI q3176098 BLAST score 391 E value 6.0e-38 Match length 116 % identity

NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No. 204191

Seq. ID LIB3083-050-Q1-L1-F2

Method BLASTN NCBI GI q3335331 BLAST score 38 E value 6.0e-12



```
Match length
                  81
% identity
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  204192
Seq. No.
                  LIB3083-050-Q1-L1-F4
Seq. ID
                  BLASTN
Method
                  g606941
NCBI GI
                  201
BLAST score
                  1.0e-109
E value
                  331
Match length
                  96
% identity
                  Gossypium hirsutum C312 clone Fb-B6 unidentified fiber
NCBI Description
                  mRNA, complete cds
                  204193
Seq. No.
                  LIB3083-050-Q1-L1-F6
Seq. ID
                  BLASTX
Method
                   q1495251
NCBI GI
BLAST score
                   215
                   2.0e-17
E value
                   129
Match length
                   41
% identity
                   (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   204194
Seq. No.
                   LIB3083-050-Q1-L1-F8
Seq. ID
Method
                   BLASTX
                   q4204315
NCBI GI
                   187
BLAST score
                   5.0e-14
E value
                   98
Match length
                   39
% identity
                   (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   204195
Seq. No.
                   LIB3083-050-Q1-L1-F9
Seq. ID
                   BLASTX
Method
                   g31397
NCBI GI
                   436
BLAST score
                   3.0e-43
E value
                   124
Match length
                   69
% identity
                   (X02761) fibronectin precursor [Homo sapiens]
NCBI Description
                   204196
Seq. No.
                   LIB3083-050-Q1-L1-G11
Seq. ID
                   BLASTX
Method
                   g4115364
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
                   50
Match length
                   58
 % identity
                   (AC005957) putative fatty acid elongase [Arabidopsis
NCBI Description
```

NCBI GI

BLAST score



```
Seq. No.
                  LIB3083-050-Q1-L1-G3
Seq. ID
                  BLASTX
Method
                  q4490330
NCBI GI
                  556
BLAST score
                  2.0e-57
E value
                  116
Match length
                  96
% identity
NCBI Description (AL035656) splicing factor-like protein [Arabidopsis
                  thaliana]
                  204198
Seq. No.
                  LIB3083-050-Q1-L1-G4
Seq. ID
Method
                  BLASTX
                  g3687223
NCBI GI
                  274
BLAST score
                  7.0e-25
E value
                  80
Match length
                  78
% identity
NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]
                  204199
Seq. No.
                  LIB3083-050-Q1-L1-G5
Seq. ID
                  BLASTX
Method
                  g807698
NCBI GI
                   219
BLAST score
                   6.0e-18
E value
                   96
Match length
                   50
% identity
NCBI Description (D32206) prepro-cucumisin [Cucumis melo]
                   204200
Seq. No.
                   LIB3083-050-Q1-L1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4415992
                   583
BLAST score
                   1.0e-60
E value
                   114
Match length
                   98
% identity
NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]
                   204201
Seq. No.
                   LIB3083-050-Q1-L1-G7
Seq. ID
                   BLASTX
Method
                   g4490330
NCBI GI
                   413
BLAST score
                   1.0e-40
E value
                   105
Match length
                   79
% identity
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   204202
Seq. No.
                   LIB3083-050-Q1-L1-H1
Seq. ID
                   BLASTX
Method
```

27870

g1706958

% identity



```
3.0e-59
E value
Match length
                  113
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  204203
Seq. No.
                  LIB3083-050-Q1-L1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464840
                  451
BLAST score
                  4.0e-45
E value
                  89
Match length
                   97
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
NCBI Description
                   alpha-1 chain - fern (Anemia phyllitidis)
                   >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia
                   phyllitidis]
                   204204
Seq. No.
                   LIB3083-050-Q1-L1-H2
Seq. ID
                   BLASTX
Method
                   g4098331
NCBI GI
                   616
BLAST score
                   2.0e-64
E value
Match length
                   114
                   96
% identity
NCBI Description (U76896) beta-tubulin 5 [Triticum aestivum]
                   204205
Seq. No.
                   LIB3083-050-Q1-L1-H5
Seq. ID
                   BLASTX
Method
                   g2443755
NCBI GI
                   500
BLAST score
                   8.0e-51
E value
Match length
                   115
                   82
% identity
NCBI Description (AF020433) cyclophilin [Arabidopsis thaliana]
                   204206
Seq. No.
                   LIB3083-050-Q1-L1-H8
Seq. ID
                   BLASTX
Method
                   q2497538
NCBI GI
                   638
BLAST score
E value
                   6.0e-67
Match length
                   130
 % identity
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
NCBI Description
                   pyruvate kinase [Glycine max]
 Seq. No.
                   204207
 Seq. ID
                   LIB3083-050-Q1-L1-H9
                   BLASTX
 Method
                   g2213590
 NCBI GI
                   209
 BLAST score
                   1.0e-16
 E value
 Match length
                   86
                   45
```



```
(AC000348) T7N9.10 [Arabidopsis thaliana]
NCBI Description
                  204208
Seq. No.
                  LIB3083-051-Q1-L1-A1
Seq. ID
                  BLASTX
Method
                  q2129932
NCBI GI
BLAST score
                  604
                  6.0e-63
E value
                  111
Match length
% identity
                  myb-related transcription factor TMH1 - tomato
NCBI Description
                  >gi 1167486 emb_CAA64615 (X95297) transcription factor
                   [Lycopersicon esculentum]
                  204209
Seq. No.
                  LIB3083-051-Q1-L1-A10
Seq. ID
                  BLASTX
Method
                  q4417283
NCBI GI
BLAST score
                   223
                   3.0e-18
E value
                   117
Match length
                   40
% identity
NCBI Description (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                   204210
                   LIB3083-051-Q1-L1-A11
Seq. ID
                   BLASTX
Method
                   q3511285
NCBI GI
BLAST score
                   566
                   1.0e-58
E value
                   119
Match length
                   83
% identity
                   (AF081534) cellulose synthase [Populus alba \times Populus
NCBI Description
                   tremula]
Seq. No.
                   204211
                   LIB3083-051-Q1-L1-A12
Seq. ID
                   BLASTX
Method
                   q3548806
NCBI GI
BLAST score
                   370
                   1.0e-35
E value
                   122
Match length
% identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204212
Seq. No.
                   LIB3083-051-Q1-L1-A3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3608485
                   591
BLAST score
                   2.0e-61
E value
Match length
                   125
 % identity
                   (AF088915) proteasome beta subunit [Petunia x hybrida]
```

204213 Seq. No.

NCBI Description

LIB3083-051-Q1-L1-A4 Seq. ID



```
BLASTN
Method
NCBI GI
                  q2829205
                  376
BLAST score
E value
                  0.0e + 00
                  436
Match length
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  204214
Seq. No.
                  LIB3083-051-Q1-L1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g398845
BLAST score
                  704
                  1.0e-74
E value
                  147
Match length
                  90
% identity
NCBI Description (X74654) beta3 tubulin [Zea mays]
                  204215
Seq. No.
                  LIB3083-051-Q1-L1-A7
Seq. ID
                  BLASTN
Method
                  g1143223
NCBI GI
BLAST score
                  428
                  0.0e + 00
E value
Match length
                   448
                  29
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                   204216
                  LIB3083-051-Q1-L1-A8
Seq. ID
Method
                  BLASTX
                   g267070
NCBI GI
BLAST score
                   439
E value
                   2.0e-43
Match length
                   83
% identity
                   TUBULIN ALPHA-6 CHAIN >gi 282852 pir JQ1597 tubulin
NCBI Description
                   alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699)
                   TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_
                   (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis
                   thaliana]
                   204217
Seq. No.
                   LIB3083-051-Q1-L1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4559358
                   401
BLAST score
E value
                   4.0e-39
                   100
Match length
% identity
```

(AC006585) putative steroid binding protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 204218

LIB3083-051-Q1-L1-B1 Seq. ID

Method BLASTX

Method

NCBI GI

BLASTX

g2147484



```
NCBI GI
                   q71498
BLAST score
                   398
E value
                   7.0e-39
Match length
                   103
% identity
                   75
NCBI Description heat shock protein 17.7 - garden pea
Seq. No.
                   204219
Seq. ID
                   LIB3083-051-Q1-L1-B10
Method
                   BLASTX
NCBI GI
                   g1170851
BLAST score
                   260
E value
                   1.0e-22
Match length
                   119
% identity
                   47
NCBI Description
                   MANNOSYL-OLIGOSACCHARIDE ALPHA-1, 2-MANNOSIDASE
                   (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A)
                   >gi_1083410 pir A54408 mannosyl-oligosaccharide
                   1,2-alpha-mannosidase (EC 3.2.1.113) - mouse >gi_474280
                   (U04299) mannosyl-oligosaccharide alpha-1,2-mannosidase
                   [Mus musculus]
Seq. No.
                   204220
Seq. ID
                   LIB3083-051-Q1-L1-B11
Method
                   BLASTX
NCBI GI
                   g2829204
BLAST score
                   327
E value
                   1.0e-30
Match length
                   85
% identity
                   81
NCBI Description
                   (AF044204) lipid transfer protein precursor [Gossypium
                   hirsutum]
Seq. No.
                   204221
Seq. ID
                   LIB3083-051-Q1-L1-B2
Method
                   BLASTX
NCBI GI
                   g3114903
BLAST score
                   590
E value
                   3.0e-61
Match length
                   145
% identity
                   79
NCBI Description
                  (AJ005805) pcberl [Populus balsamifera subsp. trichocarpa]
Seq. No.
                   204222
Seq. ID
                  LIB3083-051-Q1-L1-B4
Method
                  BLASTX
NCBI GI
                  q3080414
BLAST score
                   621
E value
                  7.0e-65
Match length
                  141
% identity
NCBI Description
                  (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  204223
Seq. ID
                  LIB3083-051-Q1-L1-B6
```



```
BLAST score
                   358
                   5.0e-34
E value
                   92
Match length
                   70
 % identity
                   homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
NCBI Description
                   homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
                   204224
 Seq. No.
                   LIB3083-051-Q1-L1-B7
Seq. ID
Method
                   BLASTX
 NCBI GI
                   q3093294
 BLAST score
                   690
 E value
                   6.0e-73
                   147
 Match length
 % identity
                   (Y12782) putative villin [Arabidopsis thaliana]
 NCBI Description
                   204225
 Seq. No.
                   LIB3083-051-Q1-L1-B9
 Seq. ID
                   BLASTX
 Method
                   g2935416
 NCBI GI
                   380
 BLAST score
                   1.0e-36
 E value
 Match length
                   115
 % identity
                   (AF047896) isoflavone reductase homolog [Betula pendula]
 NCBI Description
                   204226
 Seq. No.
                   LIB3083-051-Q1-L1-C1
 Seq. ID
                   BLASTX
 Method
                   g2129473
 NCBI GI
                    259
 BLAST score
                    2.0e-22
 E value
 Match length
                    94
 % identity
                   arabinogalactan-like protein - loblolly pine >gi_607774
 NCBI Description
                    (U09556) arabinogalactan-like protein [Pinus taeda]
                    204227
 Seq. No.
                    LIB3083-051-Q1-L1-C10
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g525331
 BLAST score
                    41
                    5.0e-14
 E value
 Match length
                    57
                    93
 % identity
                    Pisum sativum Alaska alpha-tubulin (TubA1) gene, complete
 NCBI Description
 Seq. No.
                    204228
                    LIB3083-051-Q1-L1-C11
 Seq. ID
                    BLASTX
 Method
                    g2499710
 NCBI GI
                    484
 BLAST score
                    6.0e-49
 E value
                    103
 Match length
```

86

% identity



```
PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >qi 1438075 (L33686) phospholipase D [Ricinus communis]
                  204229
Seq. No.
                  LIB3083-051-Q1-L1-C2
Seq. ID
                  BLASTX
Method
                  q541951
NCBI GI
                  384
BLAST score
                  4.0e-37
E value
                  128
Match length
                  61
% identity
NCBI Description SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
                   [Glycine max]
                  204230
Seq. No.
                  LIB3083-051-Q1-L1-C3
Seq. ID
                  BLASTX
Method
                  q3080420
NCBI GI
                   462
BLAST score
                   3.0e-46
E value
                   148
Match length
% identity
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   204231
Seq. No.
                   LIB3083-051-Q1-L1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539292
BLAST score
                   459
                   7.0e-46
E value
                   97
Match length
                   87
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
                   204232
Seq. No.
                   LIB3083-051-Q1-L1-C6
Seq. ID
Method
                   BLASTX
                   q2501448
NCBI GI
                   392
BLAST score
                   4.0e-38
E value
                   92
Match length
% identity
                   UBIQUITIN-LIKE PROTEIN SMT3 >gi 1707372 emb CAA67923
NCBI Description
                   (X99609) ubiquitin-like protein [Arabidopsis thaliana]
 Seq. No.
                   204233
                   LIB3083-051-Q1-L1-C7
 Seq. ID
Method
                   BLASTN
                   q3449322
NCBI GI
 BLAST score
                   53
                   7.0e-21
E value
Match length
                   214
 % identity
                   84
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```





## MXC17, complete sequence [Arabidopsis thaliana]

Seq. No. 204234

Seq. ID LIB3083-051-Q1-L1-C8

Method BLASTX
NCBI GI g586076
BLAST score 421
E value 2.0e-41
Match length 108
% identity 75

NCBI Description TUBULIN BETA-1 CHAIN >gi\_486734\_pir\_\_S35142 tubulin beta

chain - white lupine >gi\_402636\_emb\_CAA49736\_ (X70184) Beta

tubulin 1 [Lupinus albus]

Seq. No. 204235

Seq. ID LIB3083-051-Q1-L1-C9

Method BLASTX
NCBI GI g3033377
BLAST score 152
E value 4.0e-10
Match length 98
% identity 40

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 204236

Seq. ID LIB3083-051-Q1-L1-D1

Method BLASTX
NCBI GI g2529677
BLAST score 539
E value 2.0e-55
Match length 125
% identity 85

NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis

thaliana]

Seq. No. 204237

Seq. ID LIB3083-051-Q1-L1-D10

Method BLASTX
NCBI GI g416758
BLAST score 442
E value 4.0e-44
Match length 105
% identity 72

NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)

carboxypeptidase Y-like protein [Arabidopsis thaliana]
>gi\_445120\_prf\_\_1908426A carboxypeptidase Y [Arabidopsis

thaliana]

Seq. No. 204238

Seq. ID LIB3083-051-Q1-L1-D11

Method BLASTX
NCBI GI g2541876
BLAST score 310
E value 1.0e-28
Match length 118
% identity 54



```
(D26015) CND41, chloroplast nucleoid DNA binding protein
 NCBI Description
                     [Nicotiana tabacum]
                    204239
 Seq. No.
                    LIB3083-051-Q1-L1-D12
 Seq. ID
                    BLASTX
 Method
                    q2190992
 NCBI GI
                     357
 BLAST score
                     5.0e-34
E value
                     104
 Match length
 % identity
                     (AF004358) glutathione S-transferase TSI-1 [Aegilops
 NCBI Description
                     tauschii]
                     204240
 Seq. No.
                     LIB3083-051-Q1-L1-D2
 Seq. ID
                     BLASTX
 Method
                     q586076
 NCBI GI
                     654
 BLAST score
                     8.0e-69
 E value
                     122
 Match length
                     98
 % identity
                     TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
 NCBI Description
                     tubulin 1 [Lupinus albus]
                     204241
 Seq. No.
                     LIB3083-051-Q1-L1-D4
 Seq. ID
                     BLASTX
 Method
                     g3522942
 NCBI GI
                     288
 BLAST score
                     7.0e-26
 E value
                     120
 Match length
                     52
 % identity
 NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]
                     204242
 Seq. No.
                     LIB3083-051-Q1-L1-D6
 Seq. ID
                     BLASTX
 Method
                     g2582971
 NCBI GI
 BLAST score
                     441
 E value
                     8.0e-44
                     144
 Match length
                     55
  % identity
                     (D83711) TKRP125 [Nicotiana tabacum]
  NCBI Description
                     204243
  Seq. No.
                     LIB3083-051-Q1-L1-D8
  Seq. ID
  Method
                     BLASTX
                     q3395432
  NCBI GI
  BLAST score
                      590
                      3.0e-61
  E value
                      144
  Match length
                      82
  % identity
  NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
```

204244

Seq. No.

Match length

99



```
Seq. ID
                  LIB3083-051-Q1-L1-D9
                  BLASTX
Method
                  g2431769
NCBI GI
                  234
BLAST score
                  1.0e-19
E value
                  57
Match length
% identity
                  81
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
                  204245
Seq. No.
                  LIB3083-051-Q1-L1-E10
Seq. ID
Method
                  BLASTX
                  q1377890
NCBI GI
BLAST score
                  154
                  3.0e-10
E value
Match length
                  31
                  97
% identity
NCBI Description (L77083) cdc2 gene product [Nicotiana tabacum]
                  204246
Seq. No.
                  LIB3083-051-Q1-L1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656029
BLAST score
                  39
                   1.0e-12
E value
Match length
                   58
                   91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQB2
                   204247
Seq. No.
                   LIB3083-051-Q1-L1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q81816
                   398
BLAST score
                   7.0e-39
E value
                   92
Match length
                   80
% identity
NCBI Description tubulin beta-1 chain - soybean
                   204248
Seq. No.
                   LIB3083-051-Q1-L1-E2
Seq. ID
Method
                   BLASTX
                   g398849
NCBI GI
                   673
BLAST score
                   5.0e-71
E value
                   126
Match length
                   97
% identity
NCBI Description (X74656) beta-5 tubulin [Zea mays]
                   204249
Seq. No.
                   LIB3083-051-Q1-L1-E3
Seq. ID
Method
                   BLASTX
                   g3935167
NCBI GI
BLAST score
                   475
                   9.0e-48
E value
```

Match length

% identity

117

99



```
% identity
NCBI Description
                   (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                   204250
Seq. ID
                   LIB3083-051-Q1-L1-E5
Method
                   BLASTX
NCBI GI
                   g3805765
BLAST score
                   192
E value
                   1.0e-14
Match length
                   60
% identity
                   63
NCBI Description
                   (AC005693) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   204251
Seq. ID
                   LIB3083-051-Q1-L1-E7
Method
                   BLASTX
NCBI GI
                   g2829893
BLAST score
                   434
E value
                   6.0e-43
Match length
                   103
% identity
                   84
NCBI Description
                  (AC002311) phosphoglucomutase [Arabidopsis thaliana]
Seq. No.
                   204252
Seq. ID
                   LIB3083-051-Q1-L1-E8
Method
                   BLASTX
NCBI GI
                   g417154
BLAST score
                   527
E value
                   7.0e-54
Match length
                   139
% identity
                   76
NCBI Description
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   204253
Seq. ID
                   LIB3083-051-Q1-L1-F10
Method
                   BLASTX
NCBI GI
                   g3915023
BLAST score
                   254
E value
                   4.0e-22
Match length
                   55
% identity
                   89
NCBI Description
                  SUCROSE-PHOSPHATE SYNTHASE 1
                   (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
                  >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate
                  synthase [Citrus unshiu]
Seq. No.
                  204254
Seq. ID
                  LIB3083-051-Q1-L1-F2
Method
                  BLASTX
NCBI GI
                  q464986
BLAST score
                  628
E value
                  1.0e-65
```



UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) 
>gi\_421857\_pir\_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana 
>gi\_297884\_emb\_CAA78714\_(Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] 
>gi\_600391\_emb\_CAA51201\_(X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] 
>gi\_4455355\_emb\_CAB36765.1\_(AL035524) ibiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. ID LIB3083-051-Q1-L1-F5
Method BLASTX
NCBI GI g3024501
BLAST score 357
E value 6.0e-34
Match length 89
% identity 76

NCBI Description RAS-RELATED PROTEIN RAB11C >gi\_1370146\_emb\_CAA98179\_

(Z73951) RAB11C [Lotus japonicus]

Seq. No. 204256

Seq. ID LIB3083-051-Q1-L1-F7

Method BLASTX
NCBI GI g464851
BLAST score 173
E value 2.0e-12
Match length 90
% identity 40

NCBI Description TUBULIN BETA-2 CHAIN >gi\_421784\_pir\_\_S32669 tubulin beta-2

chain - fern (Anemia phyllitidis) (fragment)

>gi\_296500\_emb\_CAA48930\_ (X69186) beta tubulin 2 [Anemia

phyllitidis]

Seq. No. 204257

Seq. ID LIB3083-051-Q1-L1-F8

Method BLASTX
NCBI GI g3377797
BLAST score 420
E value 3.0e-41
Match length 117
% identity 74

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 204258

Seq. ID LIB3083-051-Q1-L1-F9

Method BLASTX
NCBI GI g132825
BLAST score 168
E value 7.0e-12
Match length 77

NCBI Description



```
% identity
                    50S RIBOSOMAL PROTEIN CL25, CHLOROPLAST PRECURSOR
 NCBI Description
                    >gi 71308_pir__R5PM25 ribosomal protein PsCL25 precursor,
                    chloroplast - garden pea >gi_20877_emb_CAA32187_ (X14022)
                    PsCL25 ribosomal preprotein (AA -30 to 74) [Pisum sativum]
                    204259
 Seq. No.
                    LIB3083-051-Q1-L1-G1
 Seq. ID
                    BLASTX
 Method
                    q585876
NCBI GI
 BLAST score
                    191
                    2.0e-14
 E value
 Match length
                    41
                    93
 % identity
                    60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026
 NCBI Description
                     ribosomal protein L25 - common tobacco >gi 310935 (L18908)
                     60S ribosomal protein L25 [Nicotiana tabacum]
                     204260
 Seq. No.
                    LIB3083-051-Q1-L1-G11
  Seq. ID
                     BLASTX ·
 Method
                     g120673
 NCBI GI
                     524
  BLAST score
                     1.0e-53
  E value
  Match length
                     123
  % identity
                     GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
  NCBI Description
                     >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - garden petunia
                     >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde
                     3-phosphate dehydrogenase [Petunia x hybrida]
                     204261
  Seq. No.
                     LIB3083-051-Q1-L1-G12
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q1172555
  BLAST score
                     228
  E value
                     7.0e-19
                     76
  Match length
                     59
  % identity
                     34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
  NCBI Description
                     (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                     (POM 34) >gi 629720 pir__S46936 34K porin - potato
                     >gi_1076682_pir__A55364_porin (clone pPOM-34) - potato
                     mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA
                     porin [Solanum tuberosum]
                     204262
  Seq. No.
                     LIB3083-051-Q1-L1-G2
  Seq. ID
                     BLASTX
  Method
                     q4098331
  NCBI GI
  BLAST score
                     636
                     1.0e-66
  E value
                     120
  Match length
                     96
  % identity
```

(U76896) beta-tubulin 5 [Triticum aestivum]



```
204263
Seq. No.
                  LIB3083-051-Q1-L1-G3
Seq. ID
                  BLASTX
Method
                  q227774
NCBI GI
                  172
BLAST score
                  3.0e-12
E value
                  133
Match length
                  35
% identity
NCBI Description basic chitinase [Arabidopsis thaliana]
                  204264
Seq. No.
                  LIB3083-051-Q1-L1-G4
Seq. ID
                  BLASTX
Method
                  q3702333
NCBI GI
                   354
BLAST score
                  1.0e-33
E value
                   98
Match length
                   69
% identity
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
                   204265
Seq. No.
                   LIB3083-051-Q1-L1-G5
Seq. ID
                   BLASTX
Method
                   g2811278
NCBI GI
BLAST score
                   503
                   5.0e-51
E value
                   135
Match length
                   71
% identity
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   204266
Seq. No.
                   LIB3083-051-Q1-L1-G6
Seq. ID
                   BLASTX
Method
                   g3935157
NCBI GI
BLAST score
                   240
                   3.0e-20
E value
                   70
Match length
 % identity
                   (AC005106) T25N20.21 [Arabidopsis thaliana]
NCBI Description
                   204267
 Seq. No.
                   LIB3083-051-Q1-L1-G7
 Seq. ID
                   BLASTX
 Method
                   g2129473
 NCBI GI
                   295
 BLAST score
                   1.0e-26
 E value
                   105
 Match length
 % identity
                   arabinogalactan-like protein - loblolly pine >gi_607774
 NCBI Description
                    (U09556) arabinogalactan-like protein [Pinus taeda]
                   204268
 Seq. No.
                   LIB3083-051-Q1-L1-G8
 Seq. ID
                   BLASTX
 Method
                   g4098272
 NCBI GI
 BLAST score
                   187
```

4.0e-14

E value



```
Match length
% identity
                   92
                   (U76558) alpha-tubulin [Triticum aestivum]
NCBI Description
                   204269
Seq. No.
Seq. ID
                   LIB3083-051-Q1-L1-G9
Method
                   BLASTX
NCBI GI
                   q4455234
BLAST score
                   281
                   4.0e-25
E value
Match length
                   129
% identity
                   46
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                   204270
Seq. No.
Seq. ID
                   LIB3083-051-Q1-L1-H12
Method
                   BLASTX
NCBI GI
                   q3927825
                   433
BLAST score
                   6.0e-43
E value
Match length
                   115
                   76
% identity
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   204271
                   LIB3083-051-Q1-L1-H3
Seq. ID
Method
                   BLASTN
                   g1143223
NCBI GI
                   211
BLAST score
                   1.0e-115
E value
                   436
Match length
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                   204272
Seq. ID
                   LIB3083-051-Q1-L1-H4
Method
                   BLASTX
NCBI GI
                   g136057
BLAST score
                   551
E value
                   1.0e-56
Match length
                   141
% identity
                   74
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
Coptis japonica >gi_556171 (J04121) triosephosphate
                    isomerase [Coptis japonica]
                   204273
Seq. No.
                   LIB3083-051-Q1-L1-H5
Seq. ID
                   BLASTX
Method
                    q4426565
NCBI GI
                   141
BLAST score
E value
                   1.0e-08
                   113
Match length
```

27

NCBI Description (AF031483) unknown [Rattus norvegicus]

% identity

NCBI Description



```
204274
Seq. No.
                  LIB3083-051-Q1-L1-H6
Seq. ID
Method
                  BLASTX
                  g3290020
NCBI GI
                  541
BLAST score
                  2.0e-55
E value
                  121
Match length
                  88
% identity
                   (AF044172) cysteine synthase; CS-A; O-acetylserine (thiol)
NCBI Description
                  lyase; cytosolic isoform [Solanum tuberosum]
                  204275
Seq. No.
                  LIB3083-051-Q1-L1-H7
Seq. ID
Method
                  BLASTX
                   q2995405
NCBI GI
                   294
BLAST score
                   2.0e-26
E value
                   146
Match length
                   54
% identity
                  (Y12432) polyprotein [Ananas comosus]
NCBI Description
                   204276
Seq. No.
                   LIB3083-051-Q1-L1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2827141
                   228
BLAST score
                   7.0e-19
E value
                   106
Match length
                   53
% identity
                   (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   204277
Seq. No.
                   LIB3083-052-Q1-L1-A1
Seq. ID
Method
                   BLASTN
                   g2829205
NCBI GI
BLAST score
                   287
                   1.0e-160
E value
Match length
                   341
% identity
                   18
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
                   204278
Seq. No.
                   LIB3083-052-Q1-L1-A10
Seq. ID
Method
                   BLASTX
                   q2497743
NCBI GI
BLAST score
                   150
E value
                   8.0e-10
Match length
                   57
% identity
                   54
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
```

[Gossypium hirsutum]

>gi 999315 bbs 166991 (S78173) LTP=lipid transfer protein

[Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]

E value

5.0e-54



```
... Seq. No.
                    204279
 Seq. ID
                    LIB3083-052-Q1-L1-A2
 Method
                    BLASTX
 NCBI GI
                    g2244835°
                    282
 BLAST score
 E value
                    4.0e-25
                    74
 Match length
 % identity
                    68
 NCBI Description
                    (Z97337) protein kinase homolog [Arabidopsis thaliana]
 Seq. No.
                    204280
                    LIB3083-052-Q1-L1-A4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3738285
 BLAST score
                    443
                    4.0e-44
 E value
 Match length
                    118
 % identity
                    71
 NCBI Description
                    (AC005309) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    204281
 Seq. ID
                    LIB3083-052-Q1-L1-A6
 Method
                    BLASTX
 NCBI GI
                    g1890317
 BLAST score
                    547
                    3.0e-56
 E value
 Match length
                    145
 % identity
                    70
 NCBI Description
                    (Y11791) peroxidase ATP26a [Arabidopsis thaliana]
 Seq. No.
                    204282
 Seq. ID
                    LIB3083-052-Q1-L1-A7
 Method
                    BLASTX
 NCBI GI
                    g1915974
 BLAST score
                    478
 E value
                    1.0e-57
 Match length
                    140
                    84
 % identity
 NCBI Description
                    (U62329) fructokinase [Lycopersicon esculentum] >gi 2102693
                    (U64818) fructokinase [Lycopersicon esculentum]
                    204283
 Seq. No.
                    LIB3083-052-Q1-L1-B10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4204315
 BLAST score
                    310
 E value
                    2.0e-28
 Match length
                    117
 % identity
                    51
 NCBI Description
                    (AC003027) Unknown protein [Arabidopsis thaliana]
 Seq. No.
                    204284
 Seq. ID
                    LIB3083-052-Q1-L1-B11
 Method
                    BLASTX
 NCBI GI
                    q4204265
 BLAST score
                    527
```

Seq. ID



```
120
Match length
                  79
% identity
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
                  204285
Seq. No.
                  LIB3083-052-Q1-L1-B12
Seq. ID
                  BLASTX
Method
                  g1632831
NCBI GI
                  247
BLAST score
                  4.0e-39
E value
                  100
Match length
                  80
% identity
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                   204286
                   LIB3083-052-Q1-L1-B2
Seq. ID
                   BLASTX
Method
                   q1703375
NCBI GI
                   665
BLAST score
                   5.0e-70
E value
Match length
                   132
                   98
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                   DcARF1 [Daucus carota]
                   204287
Seq. No.
                   LIB3083-052-Q1-L1-B3
Seq. ID
                   BLASTX
Method
                   g3650030
NCBI GI
                   244
BLAST score
                   9.0e-21
E value
                   110
Match length
                   51
 % identity
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]
                   204288
 Seq. No.
                   LIB3083-052-Q1-L1-B4
 Seq. ID
                   BLASTX
 Method
                   g3150414
 NCBI GI
                   244
 BLAST score
                   1.0e-23
 E value
                   126
 Match length
                   46
 % identity
                   (AC004165) AtRanBP1b protein [Arabidopsis thaliana]
 NCBI Description
                   204289
 Seq. No.
                   LIB3083-052-Q1-L1-B5
 Seq. ID
                   BLASTX
 Method
                   q3757515
 NCBI GI
                   263
 BLAST score
 E value
                   7.0e-23
                   76
 Match length
 % identity
                   (AC005167) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    204290
 Seq. No.
```

27887

LIB3083-052-Q1-L1-B6



```
BLASTX
Method
                  q4469020
NCBI GI
BLAST score
                  416
                  8.0e-41
E value
                  115
Match length
% identity
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  204291
Seq. No.
                  LIB3083-052-Q1-L1-B7
Seq. ID
                  BLASTX
Method
                  g3559805
NCBI GI
BLAST score
                  235
                  1.0e-19
E value
Match length
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   204292
Seq. No.
                   LIB3083-052-Q1-L1-B8
Seq. ID
                   BLASTX
Method
                   g4510400
NCBI GI
BLAST score
                   662
                   1.0e-69
E value
Match length
                   139
                   87
% identity
                   (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   204293
Seq. No.
                   LIB3083-052-Q1-L1-B9
Seq. ID
                   BLASTX
Method
                   q2388689
NCBI GI
                   276
BLAST score
                   2.0e-24
E value
Match length
                   84
                   70
% identity
                   (AF016633) GH1 protein [Glycine max]
NCBI Description
                   204294
Seq. No.
                   LIB3083-052-Q1-L1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2497743
                   434
BLAST score
                   3.0e-43
E value
                   92
Match length
% identity
                   92
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
NCBI Description
                   >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein
                   [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                   [Gossypium hirsutum]
```

204295

BLASTX

LIB3083-052-Q1-L1-C5

Seq. No.

Seq. ID

Method



```
q3212866
NCBI GI
                  180
BLAST score
                  4.0e-13
E value
                  135
Match length
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  204296
Seq. No.
                  LIB3083-052-Q1-L1-C6
Seq. ID
                  BLASTX
Method
                  g1326163
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  63
Match length
% identity
                  79
NCBI Description (U54704) stress related protein PvSRP [Phaseolus vulgaris]
                  204297
Seq. No.
                  LIB3083-052-Q1-L1-D10
Seq. ID
                  BLASTX
Method
                  g2065531
NCBI GI
                  233
BLAST score
                  9.0e-20
E value
                  89
Match length
                  54
% identity
NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
                  204298
Seq. No.
                  LIB3083-052-Q1-L1-D3
Seq. ID
                  BLASTX
Method
                  g464444
NCBI GI
                  697
BLAST score
                  9.0e-74
E value
                  148
Match length
                  89
% identity
                  PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome -
                  Arabidopsis thaliana >gi 166830 (M98495) proteasome
                   [Arabidopsis thaliana]
                  204299
Seq. No.
                  LIB3083-052-Q1-L1-D4
Seq. ID
                  BLASTX
Method
                  g2995953
NCBI GI
                   315
BLAST score
E value
                   5.0e-29
                  105
Match length
                   61
% identity
NCBI Description (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
Seq. No.
                   204300
                   LIB3083-052-Q1-L1-D7
Seq. ID
                   BLASTX
Method
                   q1076580
NCBI GI
                   331
BLAST score
E value
                   7.0e-31
```

117

Match length



% identity alcohol dehydrogenase homolog ADH3b - tomato NCBI Description >gi 913446 bbs 160508 (S75487) alcohol dehydrogenase ADH {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 390 aa] [Lycopersicon esculentum] 204301 Seq. No. Seq. ID LIB3083-052-Q1-L1-D8 BLASTX Method g4098331 NCBI GI 503 BLAST score 1.0e-65 E value 142 Match length 87 % identity (U76896) beta-tubulin 5 [Triticum aestivum] NCBI Description 204302 Seq. No. Seq. ID LIB3083-052-Q1-L1-D9 BLASTX Method q2739046 NCBI GI BLAST score 410 E value 3.0e-40Match length 125 % identity 61 (AF024652) polyphosphoinositide binding protein Ssh2p NCBI Description [Glycine max] 204303 Seq. No. LIB3083-052-Q1-L1-E1 Seq. ID Method BLASTX g1076627 NCBI GI 415 BLAST score 1.0e-44 E value 100 Match length % identity 95 inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco NCBI Description >gi 790479 emb\_CAA58701\_ (X83730) inorganic pyrophosphatase [Nicotiana tabacum] 204304 Seq. No. LIB3083-052-Q1-L1-E10 Seq. ID Method BLASTX NCBI GI g1730630 204 BLAST score E value 4.0e-16 Match length 106 41 % identity HYPOTHETICAL 82.6 KD PROTEIN B0361.8 IN CHROMOSOME III NCBI Description >gi 458956 (U00031) similar to cytoplasmic domain of synaptobrevin [Caenorhabditis elegans]

Seq. No. 204305

Seq. ID LIB3083-052-Q1-L1-E11

Method BLASTX
NCBI GI g1914683
BLAST score 167
E value 2.0e-12

27890

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```
Match length
                  66
% identity
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                  204306
Seq. No.
                  LIB3083-052-Q1-L1-E12
Seq. ID
                  BLASTX
Method
                  g464621
NCBI GI
                  315
BLAST score
                  3.0e-29
E value
                  108
Match length
% identity
                  59
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir_ S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                  204307
Seq. No.
                  LIB3083-052-Q1-L1-E3
Seq. ID
Method
                  BLASTX
                  g2511598
NCBI GI
BLAST score
                   309
E value
                   3.0e-28
Match length
                   80
% identity
                   (Y13696) multicatalytic endopeptidase complex, proteasome
NCBI Description
                   component, beta subunit [Arabidopsis thaliana]
Seq. No.
                   204308
                   LIB3083-052-Q1-L1-E4
Seq. ID
Method
                   BLASTX
                   q398994
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
Match length
                   47
                   83
% identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
NCBI Description
                   (ETHYLENE-FORMING ENZYME) (EFE) >gi 166313 (M97961) tomato
                   and apple ACC oxidase homologue [Actinidia deliciosa]
                   204309
Seq. No.
                   LIB3083-052-Q1-L1-E5
Seq. ID
                   BLASTX
Method
                   g1707642
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
                   45
Match length
                   73
 % identity
                   (Y07748) TMK [Oryza sativa]
 NCBI Description
                   204310
 Seq. No.
 Seq. ID
                   LIB3083-052-Q1-L1-E7
                   BLASTX
 Method
                   g4006878
 NCBI GI
```

471

124

2.0e-47

BLAST score

Match length

E value

Seq. ID



```
% identity
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
                  204311
Seq. No.
                  LIB3083-052-Q1-L1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2347208
                  409
BLAST score
E value
                  5.0e-40
                  133
Match length
% identity
NCBI Description (AC002338) APG protein isolog [Arabidopsis thaliana]
                  204312
Seq. No.
                  LIB3083-052-Q1-L1-F11
Seq. ID
                  BLASTN
Method
                  q1000085
NCBI GI
                  54
BLAST score
                  1.0e-21
E value
                  102
Match length
                  94
% identity
NCBI Description Gossypium hirsutum clone CKE6-4A E6 gene, complete cds
                  204313
Seq. No.
                  LIB3083-052-Q1-L1-F12
Seq. ID
                  BLASTX
Method
                  g3668082
NCBI GI
                  167
BLAST score
                   8.0e-12
E value
                   65
Match length
                   62
% identity
NCBI Description (AC004667) putative DAL1 protein [Arabidopsis thaliana]
                   204314
Seq. No.
                   LIB3083-052-Q1-L1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4539383
                   509
BLAST score
                   9.0e-52
E value
                   144
Match length
% identity
                   63
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   204315
Seq. No.
                   LIB3083-052-Q1-L1-F5
Seq. ID
                   BLASTX
Method
                   q3334113
NCBI GI
BLAST score
                   466
E value
                   1.0e-46
Match length
                   89
                   100
% identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015)
                   acyl-CoA-binding protein [Gossypium hirsutum]
                   204316
 Seq. No.
```

27892

LIB3083-052-Q1-L1-F7

E value,

Match length

83



```
BLASTX
Method
                  q464849
NCBI GI
                   730
BLAST score
                  1.0e-77
E value
                  145
Match length
                   99
% identity
                  TUBULIN ALPHA CHAIN >gi_486847_pir__$36232 tubulin alpha
NCBI Description
                   chain - almond >gi 20413 emb CAA47635_ (X67162)
                   alpha-tubulin [Prunus dulcis]
Seq. No.
                   204317
Seq. ID
                   LIB3083-052-Q1-L1-F8
Method
                   BLASTX
NCBI GI
                   q1778378
BLAST score
                   242
                   2.0e-20
E value
                   83
Match length
% identity
                   (U81289) NAP1Ps [Pisum sativum]
NCBI Description
                   204318
Seq. No.
                   LIB3083-052-Q1-L1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539324
                   323
BLAST score
                   3.0e-30
E value
                   97
Match length
                   72
% identity
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                   204319
Seq. No.
                   LIB3083-052-Q1-L1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3763940
BLAST score
                   188
E value
                   2.0e-14
Match length
                   68
                   49
% identity
                   (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   204320
Seq. No.
                   LIB3083-052-Q1-L1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4415996
BLAST score
                   361
                   1.0e-34
E value
                   96
Match length
                   77
% identity
                   (AF059290) beta-tubulin 4 [Eleusine indica]
NCBI Description
                   204321
Seq. No.
                   LIB3083-052-Q1-L1-G2
Seq. ID
                   BLASTX
Method
                   g2065531
NCBI GI
                   281
BLAST score
                   2.0e-25
```



```
% identity
NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
                  204322
Seq. No.
                  LIB3083-052-Q1-L1-G4
Seq. ID
Method
                  BLASTX
                  g2961357
NCBI GI
                  186
BLAST score
                  6.0e-14
E value
Match length
                  127
% identity
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]
Seq. No.
                  204323
                  LIB3083-052-Q1-L1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3328221
BLAST score
                  191
E value
                  7.0e-16
Match length
                  48
% identity
NCBI Description (AF076920) thioredoxin peroxidase [Secale cereale]
Seq. No.
                  204324
                  LIB3083-052-Q1-L1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3236237
BLAST score
                  480
E value
                  2.0e-48
Match length
                  132
% identity
                  (AC004684) putative ribotol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   204325
                  LIB3083-052-Q1-L1-H11
Seq. ID
Method
                  BLASTX
                   q4539397
NCBI GI
BLAST score
                   252
                   5.0e-45
E value
                   106
Match length
                  78
% identity
                   (AL035526) cellulose synthase-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   204326
                  LIB3083-052-Q1-L1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3549666
                   357
BLAST score
                   6.0e-34
E value
Match length
                   87
                   78
% identity
                  (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
```

204327

LIB3083-052-Q1-L1-H4

Seq. No.

Seq. ID



```
BLASTX
Method
                  q4263771
NCBI GI
                   148
BLAST score
                   2.0e-09
E value
                   147
Match length
                   29
% identity
                  (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                   precursor [Arabidopsis thaliana]
Seq. No.
                   204328
                   LIB3083-052-Q1-L1-H6
Seq. ID
Method
                   BLASTX
                   g2982259
NCBI GI
BLAST score
                   511
                   5.0e-52
E value
Match length
                   121
% identity
                   79
                   (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                   mariana]
                   204329
Seq. No.
Seq. ID
                   LIB3083-052-Q1-L1-H7
Method
                   BLASTX
NCBI GI
                   g4262250
BLAST score
                   385
E value
                   3.0e-37
Match length
                   142
                   54
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
                   204330
Seq. No.
                   LIB3083-053-Q1-L1-A10
Seq. ID
Method
                   BLASTX
                   g2739046
NCBI GI
BLAST score
                   295
                   2.0e-30
E value
                   112
Match length
                   62
% identity
                   (AF024652) polyphosphoinositide binding protein Ssh2p
NCBI Description
                   [Glycine max]
                   204331
Seq. No.
                   LIB3083-053-Q1-L1-A11
Seq. ID
Method
                   BLASTX
                   g1703375
NCBI GI
                   593
BLAST score
                   1.0e-61
E value
Match length
                   115
                   100
% identity
                   ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj_BAA08259_ (D45420)
NCBI Description
                   DcARF1 [Daucus carota]
                   204332
Seq. No.
Seq. ID
                   LIB3083-053-Q1-L1-A12
                   BLASTX
Method
```

g2078350

163

NCBI GI BLAST score



E value 3.0e-11 Match length 96 43 % identity (U95923) transaldolase [Solanum tuberosum] NCBI Description 204333 Seq. No. LIB3083-053-Q1-L1-A2 Seq. ID Method BLASTX g3522929 NCBI GI 586 BLAST score E value 7.0e-61 Match length 125 % identity (AC002535) putative dTDP-glucose 4-6-dehydratase NCBI Description [Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] 204334 Seq. No. LIB3083-053-Q1-L1-A3 Seq. ID BLASTX Method g1076545 NCBI GI 435 BLAST score 3.0e-43 E value Match length 113 % identity guanine nucleotide regulatory protein - fava bean NCBI Description >gi 547478\_emb\_CAA85733\_ (Z37503) guanine nucleotide regulatory protein [Vicia faba] >gi\_1098297\_prf\_\_2115367E small GTP-binding protein [Vicia faba] Seq. No. 204335 LIB3083-053-Q1-L1-A4 Seq. ID BLASTX Method NCBI GI q2633727 150 BLAST score 1.0e-09 E value Match length 99 38 % identity (Z99111) ykrT [Bacillus subtilis] NCBI Description 204336 Seq. No. LIB3083-053-Q1-L1-A8 Seq. ID Method BLASTX NCBI GI g4539327 BLAST score 469 4.0e-47 E value 114 Match length 81 % identity (AL035679) putative proton pump [Arabidopsis thaliana] NCBI Description Seq. No. 204337 LIB3083-053-Q1-L1-B1 Seq. ID

Method BLASTX
NCBI GI g1658197
BLAST score 515
E value 2.0e-52
Match length 133



```
% identity
                   (U74630) calreticulin [Ricinus communis] >gi_1763297
NCBI Description
                   (U74631) calreticulin [Ricinus communis]
Seq. No.
                  LIB3083-053-Q1-L1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  310
                  1.0e-174
E value
Match length
                  317
% identity
                  20
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  204339
Seq. No.
                  LIB3083-053-Q1-L1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539292
BLAST score
                   254
                   6.0e-22
E value
Match length
                   70
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
                   204340
Seq. No.
Seq. ID
                   LIB3083-053-Q1-L1-B12
Method
                   BLASTX
NCBI GI
                   g4539394
BLAST score
                   311
                   1.0e-28
E value
Match length
                   138
% identity
NCBI Description (AL035526) putative protein [Arabidopsis thaliana]
                   204341
Seq. No.
                   LIB3083-053-Q1-L1-B3
Seq. ID
Method
                   BLASTN
                   g1143223
NCBI GI
                   383
BLAST score
                   0.0e + 00
E value
                   406
Match length
                   57
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   204342
Seq. No.
Seq. ID
                   LIB3083-053-Q1-L1-B4
                   BLASTX
Method
                   g4490305
NCBI GI
                   360
BLAST score
```

2.0e-34 E value Match length 125 57 % identity

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 204343

Method

NCBI GI

BLAST score

BLASTX

398

g1169534



```
Seq. ID
                   LIB3083-053-Q1-L1-B6
Method
                   BLASTX
NCBI GI
                   g3121848
BLAST score
                   707
E value
                   5.0e-75
Match length
                   138
% identity
                   64
NCBI Description
                   CALMODULIN >gi_1835521 (U83402) calmodulin [Capsicum
                   annuum]
Seq. No.
                   204344
                   LIB3083-053-Q1-L1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3183321
BLAST score
                   327
E value
                   2.0e-30
Match length
                   96
% identity
                   66
NCBI Description
                   HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I
                   >gi_2330820_emb_CAB11050_ (Z98530) hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   204345
Seq. ID
                   LIB3083-053-Q1-L1-B8
Method
                   BLASTX
NCBI GI
                   g4098331
BLAST score
                   698
E value
                   5.0e-74
Match length
                   129
% identity
                   98
NCBI Description
                   (U76896) beta-tubulin 5 [Triticum aestivum]
Seq. No.
                   204346
Seq. ID
                   LIB3083-053-Q1-L1-B9
Method
                   BLASTX
NCBI GI
                   g2832625
BLAST score
                   144
E value
                   5.0e-09
Match length
                   40
% identity
                   62
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  204347
Seq. ID
                  LIB3083-053-Q1-L1-C1
Method
                  BLASTX
NCBI GI
                  q4006886
BLAST score
                  180
E value
                  2.0e-13
Match length
                  68
% identity
                  65
NCBI Description
                  (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                  204348
Seq. ID
                  LIB3083-053-Q1-L1-C10
```



```
9.0e-39
E value
Match length
                  83
% identity
                  94
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203
                  phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                  >qi 433609 emb CAA82232 (Z28386) enolase [Ricinus
                  communis]
                  204349
Seq. No.
Seq. ID
                  LIB3083-053-Q1-L1-C3
Method
                  BLASTX
NCBI GI
                  g602076
BLAST score
                  556
                  2.0e-57
E value
                  113
Match length
                  25
% identity
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                  204350
Seq. No.
                  LIB3083-053-Q1-L1-C5
Seq. ID
Method
                  BLASTX
                  g2894378
NCBI GI
BLAST score
                  183
E value
                  9.0e-14
                  69
Match length
% identity
                  52
                  (Y14573) putative ribophorin I homologue [Hordeum vulgare]
NCBI Description
                  204351
Seq. No.
                  LIB3083-053-Q1-L1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337207
BLAST score
                  357
                  6.0e-34
E value
                  126
Match length
% identity
                  (AC006403) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  204352
                  LIB3083-053-Q1-L1-C7
Seq. ID
Method
                  BLASTX
                  q1705678
NCBI GI
BLAST score
                   643
                  1.0e-67
E value
                  124
Match length
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                  PROTEIN HOMOLOG) (VCP) >qi 862480 (U20213)
                  valosin-containing protein [Glycine max]
```

Seq. No. 204353 Seq. ID LIB3083-053-Q1-L1-C8

Method BLASTX
NCBI GI g4468990
BLAST score 148

```
1.0e-09
E value
                  35
Match length
                  86
% identity
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  204354
                  LIB3083-053-Q1-L1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850587
BLAST score
                  453
E value
                  3.0e-45
Match length
                  134
% identity
                  72
                  (AC005278) Strong similarity to gi 2244780 hypothetical
NCBI Description
                  protein from Arabidopsis thaliana chromosome 4 contig
                  gb Z97335. [Arabidopsis thaliana]
Seq. No.
                  204355
                  LIB3083-053-Q1-L1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g547683
BLAST score
                  186
E value
                   4.0e-14
Match length
                   50
                   78
% identity
NCBI Description
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601 prf_1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
                   204356
Seq. No.
```

HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat

LIB3083-053-Q1-L1-D12 Seq. ID

Method BLASTX g3617837 NCBI GI BLAST score 610 1.0e-63 E value 121 Match length 93 % identity

(AF035820) gibberellin action negative regulator SPY NCBI Description

[Hordeum vulgare]

204357 Seq. No.

Seq. ID LIB3083-053-Q1-L1-D4

Method BLASTX g3153902 NCBI GI BLAST score 410 3.0e-40 E value 104 Match length 77 % identity

(AF066076) 14-3-3-like protein [Helianthus annuus] NCBI Description

204358 Seq. No.

Seq. ID LIB3083-053-Q1-L1-D5

Method BLASTX q4388730 NCBI GI BLAST score 288 E value 8.0e-29



```
Match length
% identity
                  (AC006413) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  204359
Seq. No.
                  LIB3083-053-Q1-L1-D8
Seq. ID
                  BLASTX
Method
                  g1703115
NCBI GI
                  555
BLAST score
                  4.0e-57
E value
                  102
Match length
                  100
% identity
                  ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
NCBI Description
                  thaliana >gi_1145695 (\overline{U39}480) actin [Arabidopsis thaliana]
                  >gi 3236244 (AC004684) actin 3 protein [Arabidopsis
                   thaliana]
                  204360
Seq. No.
                  LIB3083-053-Q1-L1-E1
Seq. ID
                  BLASTX
Method
                  g345829
NCBI GI
                   281
BLAST score
                   5.0e-25
E value
                   83
Match length
                   61
% identity
NCBI Description ubiquitin carrier protein E2 - human
                   204361
Seq. No.
                   LIB3083-053-Q1-L1-E12
Seq. ID
                   BLASTX
Method
                   g136739
NCBI GI
                   609
BLAST score
                   2.0e-63
E value
                   132
Match length
% identity
                   85
                   UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                   PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                   potato >qi 218001 dbj BAA00570 (D00667) UDP-glucose
                   pyrophosphorylase precursor [Solanum tuberosum]
                   204362
Seq. No.
                   LIB3083-053-Q1-L1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2995405
                   297
BLAST score
                   6.0e-27
E value
                   135
Match length
 % identity
```

Seq. No. 204363

NCBI Description

Seq. ID LIB3083-053-Q1-L1-E4

Method BLASTX
NCBI GI g1518388
BLAST score 276
E value 1.0e-24

(Y12432) polyprotein [Ananas comosus]



```
Match length
                  59
% identity
                  (X91172) korean-radish isoperoxidase [Raphanus sativus]
NCBI Description
                  204364
Seq. No.
                  LIB3083-053-Q1-L1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  371
                  9.0e-36
E value
Match length
                  90
% identity
                   81
                  40S RIBOSOMAL PROTEIN S11 >gi_82722 pir S16577 ribosomal
NCBI Description
                   protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                   ribosomal protein S11 [Zea mays]
                   204365
Seq. No.
                  LIB3083-053-Q1-L1-E7
Seq. ID
                  BLASTX
Method
                   g1293835
NCBI GI
BLAST score
                   248
                   4.0e-21
E value
                   110
Match length
                   47
% identity
                  (U56965) C15H9.5 gene product [Caenorhabditis elegans]
NCBI Description
                   204366
Seq. No.
                   LIB3083-053-Q1-L1-E9
Seq. ID
Method
                   BLASTX
                   q3243234
NCBI GI
                   433
BLAST score
E value
                   5.0e-43
                   108
Match length
% identity
                   (AF071477) isoflavone reductase related protein [Pyrus
NCBI Description
                   communis]
                   204367
Seq. No.
                   LIB3083-053-Q1-L1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2055230
BLAST score
                   327
                   1.0e-30
E value
                   115
Match length
% identity
                   (AB000130) SRC2 [Glycine max]
NCBI Description
                   204368
Seq. No.
Seq. ID
                   LIB3083-053-Q1-L1-F3
Method
                   BLASTX
                   g1076627
NCBI GI
BLAST score
                   302
                   1.0e-27
E value
Match length
                   82
                   72
% identity
                   inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco
NCBI Description
                   >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase
```

Method

BLASTX



## [Nicotiana tabacum]

```
Seq. No.
                  204369
                  LIB3083-053-Q1-L1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4218121
BLAST score
                  196
E value
                  4.0e-15
                  43
Match length
                  77
% identity
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]
                  204370
Seq. No.
                  LIB3083-053-Q1-L1-F7
Seq. ID
Method
                  BLASTX
                  g3790102
NCBI GI
                  314
BLAST score
                  3.0e-29
E value
                  91
Match length
                  62
% identity
                  (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                  alpha subunit [Citrus X paradisi]
                  204371
Seq. No.
                  LIB3083-053-Q1-L1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2924520
                  417
BLAST score
                  5.0e-41
E value
Match length
                  108
                   81
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   204372
                  LIB3083-053-Q1-L1-G2
Seq. ID
Method
                   BLASTX
                   g2245087
NCBI GI
                   183
BLAST score
E value
                   1.0e-13
                   88
Match length
                   43
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204373
                   LIB3083-053-Q1-L1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3608485
BLAST score
                   689
                   7.0e-73
E value
Match length
                   141
                   94
% identity
NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]
Seq. No.
                   204374
                   LIB3083-053-Q1-L1-G6
Seq. ID
```



```
NCBI GI
                  g3024020
BLAST score
                  615
E value
                  3.0e-64
Match length
                  121
                  95
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
                  204375
Seq. No.
                  LIB3083-053-Q1-L1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351206
BLAST score
                  543
E value
                  7.0e-56
Match length
                  121
% identity
                  85
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                  4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_629663 pir S44169 trans-cinnamate 4-monooxygenase (EC
                  1.14.13.11) cytochrome P450 73 - Madagascar periwinkle
                  >gi_2129922_pir__S68204 trans-cinnamate 4-monooxygenase (EC
                  1.14.13.11) - Madagascar periwinkle
                  >gi_473229_emb_CAA83552_ (Z32563) cinnamate 4-hydroxylase
                  (CYP73) [Catharanthus roseus]
Seq. No.
                  204376
Seq. ID
                  LIB3083-053-Q1-L1-H2
Method
                  BLASTX
NCBI GI
                  g2982268
BLAST score
                  207
E value
                  1.0e-16
                  40
Match length
                  97
% identity
NCBI Description
                  (AF051217) probable 40S ribosomal protein S15 [Picea
                  mariana]
Seq. No.
                  204377
Seq. ID
                  LIB3083-053-Q1-L1-H8
Method
                  BLASTX
NCBI GI
                  q4467157
BLAST score
                  220
E value
                  5.0e-18
Match length
                  105
% identity
NCBI Description
                  (AL035540) disease resistance response like protein
                  [Arabidopsis thaliana]
Seq. No.
                  204378
Seq. ID
                  LIB3083-054-Q1-L1-A11
Method
                  BLASTX
NCBI GI
                  g2369714
```

NCBI GI g2369714
BLAST score 517
E value 7.0e-53
Match length 108
% identity 91

NCBI Description (297178) elongation factor 2 [Beta vulgaris]

```
Seq. No.
                    204379
Seq. ID
                    LIB3083-054-Q1-L1-B12
Method
                    BLASTX
NCBI GI
                    q2864609
                    248
BLAST score
E value
                    3.0e-21
                    126
Match length
% identity
                    (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                    >gi_4049337_emb_CAA22562_ (AL034567) putative protein
                    [Arabidopsis thaliana]
                    204380
Seq. No.
                    LIB3083-054-Q1-L1-C12
Seq. ID
                    BLASTX
Method
                    q586076
NCBI GI
BLAST score
                    665
                    5.0e-70
E value
                    126
Match length
% identity
NCBI Description TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                    tubulin 1 [Lupinus albus]
Seq. No.
                    204381
                    LIB3083-054-Q1-L1-D10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q586076
                    617
BLAST score
                    2.0e-64
E value
                    122
Match length
% identity
                    TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
NCBI Description
                    tubulin 1 [Lupinus albus]
Seq. No.
                    204382
Seq. ID
                    LIB3083-054-Q1-L1-D12
Method
                    BLASTX
NCBI GI
                    q4415992
BLAST score
                    698
                    6.0e-74
E value
Match length
                    134
% identity
                    99
NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]
Seq. No.
                    204383
                    LIB3083-054-Q1-L1-D9
Seq. ID
Method
                    BLASTX
                    q417745
NCBI GI
                    677
BLAST score
                    2.0e-71
E value
                    138
Match length
% identity
                    95
                    ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                    HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)
```



## S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

```
204384
Seq. No.
                  LIB3083-054-Q1-L1-E11
Seq. ID
                  BLASTX
Method
                  g4512673
NCBI GI
BLAST score
                  527
                  7.0e-54
E value
Match length
                  140
                  79
% identity
                  (AC006931) putative phosphoprotein phosphatase [Arabidopsis
NCBI Description
                  thaliana]
                  204385
Seq. No.
                  LIB3083-054-Q1-L1-E12
Seq. ID
                  BLASTX
Method
                  g1785791
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
                  53
Match length
% identity
                  55
                  (Y08502) orf204 [Arabidopsis thaliana]
NCBI Description
                  204386
Seq. No.
                  LIB3083-054-Q1-L1-F12
Seq. ID
                  BLASTX
Method
                  g3337352
NCBI GI
                  179
BLAST score
                   3.0e-13
E value
                  78
Match length
                   49
% identity
                   (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
                   204387
Seq. No.
                   LIB3083-054-Q1-L1-F9
Seq. ID
                   BLASTX
Method
                   g3283893
NCBI GI
                   251
BLAST score
                   2.0e-21
E value
Match length
                   124
                   40
% identity
                  (AF070626) unknown [Homo sapiens]
NCBI Description
                   204388
Seq. No.
                   LIB3083-054-Q1-L1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464849
BLAST score
                   628
E value
                   1.0e-65
Match length
                   142
% identity
                   87
                   TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 20413 emb_CAA47635 (X67162)
                   alpha-tubulin [Prunus dulcis]
```

Seq. No. 204389



```
LIB3083-054-Q1-L1-G9
Seq. ID
                  BLASTX
Method
                   g2129495
NCBI GI
                   683
BLAST score
                   3.0e-72
E value
Match length
                   142
% identity
                   89
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi 1000090
                   (\overline{U}3\overline{0}508) E6 [Gossypium barbadense]
Seq. No.
                   204390
                   LIB3083-054-Q1-L1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4103342
                   494
BLAST score
                   5.0e-50
E value
Match length
                   113
                   87
% identity
                   (AF022377) agamous-like putative transcription factor
NCBI Description
                   [Cucumis sativus]
                   204391
Seq. No.
Seq. ID
                   LIB3083-055-Q1-L1-A11
                   BLASTX
Method
                   q1706956
NCBI GI
                   217
BLAST score
                   1.0e-17
E value
Match length
                   46
                   91
% identity
                   (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204392
Seq. No.
                   LIB3083-055-Q1-L1-B7
Seq. ID
Method
                   BLASTX
                   q3334405
NCBI GI
                   534
BLAST score
                   7.0e-55
E value
Match length
                   111
                   98
% identity
                   VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                   >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
                   204393
Seq. No.
                   LIB3083-055-Q1-L1-C4
Seq. ID
                   BLASTX
Method
                   q3860277
NCBI GI
BLAST score
                   538
                   4.0e-55
E value
                   115
Match length
                   91
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
```

ribosomal protein L10A [Arabidopsis thaliana]

thaliana] >gi\_4314394\_gb AAD15604\_ (AC006232) putative



```
LIB3083-055-Q1-L1-C6
Seq. ID
                  BLASTN
Method
                  g3327922
NCBI GI
BLAST score
                  33
                  6.0e-09
E value
                  77
Match length
                  86
% identity
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  204395
Seq. No.
                  LIB3083-055-Q1-L1-C8
Seq. ID
Method
                  BLASTX
                   q3860308
NCBI GI
                   150
BLAST score
                   1.0e-09
E value
Match length
                   53
% identity
                   62
                  (AJ012681) hypothetical protein [Cicer arietinum]
NCBI Description
                   204396
Seq. No.
Seq. ID
                   LIB3083-055-Q1-L1-D11
Method
                   BLASTX
NCBI GI
                   g1170603
BLAST score
                   185
                   8.0e-14
E value
Match length
                   97
                   41
% identity
                   PROBABLE SERINE/THREONINE-PROTEIN C2F7.03C
NCBI Description
                   >gi 2130372 pir S58147 hypothetical protein SPAC2F7.03c -
                   fission yeast (Schizosaccharomyces pombe)
                   >gi 1052786 emb CAA90490 (Z50142) protein kinase
                   [Schizosaccharomyces pombe]
Seq. No.
                   204397
                   LIB3083-055-Q1-L1-D12
Seq. ID
                   BLASTN
Method
                   q2980787
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   75
Match length
% identity
                   88
                   Arabidopsis thaliana DNA chromosome 4, Pl clone M7J2
NCBI Description
                   (ESSAII project)
                   204398
Seq. No.
Seq. ID
                   LIB3083-055-Q1-L1-D2
                   BLASTX
Method
                   g3641298
NCBI GI
BLAST score
                   152
                   2.0e-14
E value
                   76
```

61 % identity (AF087135) F1FO-type ATPase subunit d [Homo sapiens] NCBI Description

Match length

>gi\_4454676\_gb\_AAD20956\_ (AF070650) F1F0-type ATP synthase

subunit d [Homo sapiens]



```
204399
Seq. No.
                  LIB3083-055-Q1-L1-D5
Seq. ID
                  BLASTX
Method
                  g4512653
NCBI GI
                  263
BLAST score
                  6.0e-23
E value
                  68
Match length
                  76
% identity
                  (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204400
Seq. No.
                  LIB3083-055-Q1-L1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829899
BLAST score
                  276
E value
                  2.0e-24
Match length
                  127
% identity
                   43
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp AJ001449_2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   204401
                  LIB3083-055-Q1-L1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g188625
BLAST score
                   36
E value
                   9.0e-11
                   203
Match length
% identity
                   84
                  Human moesin mRNA, complete cds.
NCBI Description
                   >gi 4505256_ref_NM_002444.1_MSN_ Homo sapiens moesin (MSN)
                   mRNA
Seq. No.
                   204402
Seq. ID
                   LIB3083-055-Q1-L1-F4
                   BLASTX
Method
                   q3395440
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
                   109
Match length
                   42
% identity
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204403
                   LIB3083-055-Q1-L1-F5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169712
BLAST score
                   41
                   9.0e-14
E value
Match length
                   122
                   89
% identity
NCBI Description Ricinus communis metallothionein (RCMIT) mRNA, complete cds
                   204404
Seq. No.
Seq. ID
                   LIB3083-055-Q1-L1-F6
```

27909

BLASTX

Method

```
q1737490
NCBI GI
BLAST score
                  156
E value
                  2.0e-10
Match length
                  65
                  46
% identity
NCBI Description
                  (U81006) p76 [Homo sapiens]
Seq. No.
                  204405
                  LIB3083-055-Q1-L1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129473
BLAST score
                  255
E value
                  5.0e-22
Match length
                  94
                  52
% identity
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                  204406
Seq. No.
                  LIB3083-055-Q1-L1-G4
Seq. ID
                  BLASTX
Method
                  g4539525
NCBI GI
BLAST score
                  343
                  2.0e-32
E value
Match length
                  108
                   55
% identity
NCBI Description (AJ012370) NAALADase II protein [Homo sapiens]
                  204407
Seq. No.
                  LIB3083-055-Q1-L1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2689631
                   679
BLAST score
E value
                   1.0e-71
Match length
                   134
                   99
% identity
                  (AF022389) ADP-ribosylation factor [Vigna unguiculata]
NCBI Description
                   204408
Seq. No.
Seq. ID
                   LIB3083-055-Q1-L1-G6
Method
                   BLASTX
NCBI GI
                   g3834307
BLAST score
                   263
                   5.0e-23
E value
Match length
                   70
% identity
                   71
NCBI Description
```

(AC005679) Strong similarity to gene T10I14.120 gi 2832679 putative protein from Arabidopsis thaliana BAC gb\_AL021712.

ESTs gb N65887 and gb N65627 come from this gene.

[Arabidopsis thaliana]

204409 Seq. No.

LIB3083-055-Q1-L1-G7 Seq. ID

Method BLASTX NCBI GI g4567283 BLAST score 255 4.0e-22 E value

BLAST score

E value

214

3.0e-17

```
Match length
% identity
                  76
                  (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204410
Seq. No.
                  LIB3083-055-Q1-L1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1354849
BLAST score
                  450
                  6.0e-45
E value
                  121
Match length
                  69
% identity
                  (U57350) epoxide hydrolase [Nicotiana tabacum]
NCBI Description
                  204411
Seq. No.
                  LIB3083-055-Q1-L1-H3
Seq. ID
                  BLASTX
Method
                  g627566
NCBI GI
                  154
BLAST score
                  3.0e-10
E value
                  58
Match length
                  52
% identity
                  phosphate carrier protein, form B - human
NCBI Description
                  >gi_38262_emb_CAA42641_ (X60036) phosphate carrier protein
                   [Homo sapiens] >gi_4505775_ref_NP_002626.1_pPHC_ phosphate
                  carrier, mitochondrial
                  204412
Seq. No.
                  LIB3083-055-Q1-L1-H4
Seq. ID
Method
                  BLASTX
                  g627566
NCBI GI
BLAST score
                   233
E value
                   2.0e-19
                   87
Match length
% identity
                   57
                  phosphate carrier protein, form B - human
NCBI Description
                   >gi_38262_emb_CAA42641_ (X60036) phosphate carrier protein
                   [Homo sapiens] >gi_4505775_ref_NP_002626.1_pPHC_ phosphate
                   carrier, mitochondrial
                   204413
Seq. No.
                   LIB3083-055-Q1-L1-H5
Seq. ID
                   BLASTX
Method
                   g541951
NCBI GI
BLAST score
                   224
E value
                   2.0e-18
Match length
                   99
                   48
% identity
                  SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
NCBI Description
                   [Glycine max]
                   204414
Seq. No.
Seq. ID
                   LIB3083-055-Q1-L1-H7
Method
                   BLASTX
NCBI GI
                   g2865523
```



```
Match length
                   68
                   29
% identity
                  (AF044584) cold regulated LTCOR18 [Lavatera thuringiaca]
NCBI Description
                  204415
Seq. No.
                  LIB3083-056-Q1-L1-A1
Seq. ID
                  BLASTX
Method
                   g2462746
NCBI GI
BLAST score
                   543
                   1.0e-55
E value
                   136
Match length
                   74
% identity
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   204416
Seq. No.
                   LIB3083-056-Q1-L1-A3
Seq. ID
Method
                   BLASTX
                   q3402722
NCBI GI
                   525
BLAST score
E value
                   1.0e-53
                   141
Match length
                   70
% identity
                   (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204417
                   LIB3083-056-Q1-L1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q806310
                   171
BLAST score
                   4.0e-12
E value
                   144
Match length
                   16
% identity
                   (J02746) proline-rich protein [Glycine max]
NCBI Description
                   204418
Seq. No.
                   LIB3083-056-Q1-L1-A5
Seq. ID
                   BLASTX
Method
                   g2462746
NCBI GI
BLAST score
                   634
                   2.0e-66
E value
                   146
Match length
                   80
% identity
                   (ACO02292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   204419
Seq. No.
                   LIB3083-056-Q1-L1-A7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3193284
BLAST score
                   373
                   8.0e-36
E value
Match length
                   136
                   52
% identity
                  (AF069298) No definition line found [Arabidopsis thaliana]
```

NCBI Description

```
LIB3083-056-Q1-L1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3033381
BLAST score
                   581
                   3.0e-60
E value
                   137
Match length
% identity
                   (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis
NCBI Description
                   thaliana]
                   204421
Seq. No.
                   LIB3083-056-Q1-L1-B11
Seq. ID
Method
                   BLASTX
                   g2654358
NCBI GI
                   389
BLAST score
                   1.0e-37
E value
Match length
                   147
                   52
% identity
                   (Y15522) MNUDC protein [Mus musculus]
NCBI Description
                   >gi 2808636 emb CAA57201_ (X81443) Sig 92 [Mus musculus]
                   204422
Seq. No.
                   LIB3083-056-Q1-L1-B4
Seq. ID
Method
                   BLASTX
                   g267069
NCBI GI
BLAST score
                   521
E value
                   3.0e-53
Match length
                   102
                   94
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   204423
Seq. ID
                   LIB3083-056-Q1-L1-B5
Method
                   BLASTN
                   q2829203
NCBI GI
BLAST score
                   56
E value
                   1.0e-22
                   124
Match length
                   86
% identity
                   Gossypium hirsutum cultivar Siokra 1-2 lipid transfer
NCBI Description
                   protein precursor (LTP) mRNA, complete cds
                   204424
Seq. No.
                   LIB3083-056-Q1-L1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3868758
                   435
BLAST score
E value
                   5.0e-43
                   95
Match length
% identity
```

NCBI Description

Seq. ID LIB3083-056-Q1-L1-B7

(D89802) elongation factor 1B gamma [Oryza sativa]



Method BLASTX
NCBI GI g131770
BLAST score 296
E value 6.0e-27
Match length 98
% identity 54

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880 pir R3DO24

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi\_7353\_emb\_CAA29844\_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 204426

Seq. ID LIB3083-056-Q1-L1-B8

Method BLASTX
NCBI GI g4468990
BLAST score 462
E value 3.0e-46
Match length 155
% identity 63

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 204427

Seq. ID LIB3083-056-Q1-L1-B9

Method BLASTX
NCBI GI g3641837
BLAST score 301
E value 1.0e-31
Match length 103
% identity 71

NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein

[Arabidopsis thaliana]

Seq. No. 204428

Seq. ID LIB3083-056-Q1-L1-C10

Method BLASTN
NCBI GI g1143223
BLAST score 180
E value 1.0e-96
Match length 330
% identity 57

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 204429

Seq. ID LIB3083-056-Q1-L1-C11

Method BLASTX
NCBI GI g2244738
BLAST score 635
E value 1.0e-66
Match length 136
% identity 92

NCBI Description (D88416) endo-1,3-beta-glucanase [Gossypium hirsutum]

Seq. No. 204430

Seq. ID LIB3083-056-Q1-L1-C12

Method BLASTX NCBI GI g3395431

```
BLAST score
                  282
E value
                  3.0e-25
Match length
                  108
% identity
                  47
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  204431
Seq. ID
                  LIB3083-056-Q1-L1-C2
Method
                  BLASTX
NCBI GI
                  g81452
BLAST score
                  213
E value
                  4.0e-17
Match length
                  44
% identity
                  93
NCBI Description
                 tubulin beta chain - red goosefoot (fragment)
                  >gi 82057 pir S06045 tubulin beta chain - carrot
                  (fragment) >gi 829259 emb CAA34673 (X16700) tubulin like
                  protein fragment (AA 1-77) [Chenopodium rubrum]
                  >gi 829261 emb CAA34609 (X16608) tubulin like protein
                  fragment (AA 1-77) [Daucus carota]
                  204432
Seq. No.
                  LIB3083-056-Q1-L1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282962
BLAST score
                  141
E value
                  6.0e-09
Match length
                  47
% identity
                  62
NCBI Description flavanone 3 beta-hydroxylase - garden petunia (fragment)
Seq. No.
                  204433
Seq. ID
                  LIB3083-056-Q1-L1-C6
Method
                  BLASTX
NCBI GI
                  g2271477
BLAST score
                  177
                  9.0e-13
E value
Match length
                  38
                  87
% identity
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]
Seq. No.
                  204434
                  LIB3083-056-Q1-L1-C7
Seq. ID
Method
                  BLASTX
                  g1477428
NCBI GI
BLAST score
                  691
E value
                  4.0e-73
Match length
                  149
```

% identity 89

NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 204435

Seq. ID LIB3083-056-Q1-L1-C9

Method BLASTX NCBI GI q3892059 BLAST score 199 2.0e-15 E value



```
Match length
% identity
NCBI Description
                   (AC002330) predicted protein of unknown function
                   [Arabidopsis thaliana]
Seq. No.
                   204436
Seq. ID
                   LIB3083-056-Q1-L1-D10
Method
                   BLASTX
NCBI GI
                   q3915089
BLAST score
                   273
E value
                   1.0e-24
Match length
                   73
% identity
                   74
NCBI Description
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
                   4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_2144269_pir__JC5129 trans-cinnamate 4-monooxygenase (EC
                   1.14.13.11) A - Populus kitakamiensis
                  >gi_1139561_dbj BAA11579 (D82815) cinnamic acid
                   4-hydroxylase [Populus kitakamiensis]
                  >gi_1777370_dbj_BAA11576_ (D82812) cinnamic acid
                   4-hydroxylase [Populus kitakamiensis]
Seq. No.
                  204437
Seq. ID
                  LIB3083-056-Q1-L1-D12
Method
                  BLASTX
NCBI GI
                  q3341681
BLAST score
                  224
E value
                  2.0e-18
Match length
                  51
% identity
                  84
NCBI Description
                  (AC003672) small GTP-binding protein [Arabidopsis thaliana]
                  >gi_741994_prf__2008312A GTP-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  204438
Seq. ID
                  LIB3083-056-Q1-L1-D5
Method
                  BLASTX
NCBI GI
                  g3860247
BLAST score
                  244
E value
                  6.0e-21
Match length
                  102
% identity
                  55
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  204439
                  LIB3083-056-Q1-L1-D6
Seq. ID
Method
                  BLASTX
```

NCBI GI q3935145 BLAST score 299 E value 4.0e-27 Match length 85 % identity 65

(AC005106) T25N20.9 [Arabidopsis thaliana] NCBI Description

Seq. No.

204440

Seq. ID

LIB3083-056-Q1-L1-E11

Method

BLASTX



```
NCBI GI
                   g131773
BLAST score
                   446
E value
                  2.0e-44
Match length
                  112
% identity
                  81
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
                  >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                  maize
Seq. No.
                  204441
Seq. ID
                  LIB3083-056-Q1-L1-E3
Method
                  BLASTN
NCBI GI
                  g2829203
BLAST score
                  38
                  5.0e-12
E value
Match length
                  217
% identity
                  84
NCBI Description
                  Gossypium hirsutum cultivar Siokra 1-2 lipid transfer
                  protein precursor (LTP) mRNA, complete cds
Seq. No.
                  204442
Seq. ID
                  LIB3083-056-Q1-L1-E5
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  162
E value
                  4.0e-86
Match length
                  222
% identity
                  30
NCBI Description
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
                  precursor (PRP) mRNA, complete cds
Seq. No.
                  204443
Seq. ID
                  LIB3083-056-Q1-L1-E6
Method
                  BLASTX
NCBI GI
                  g2289002
BLAST score
                  170
E value
                  4.0e-12
Match length
                  100
% identity
                  42
NCBI Description
                  (AC002335) unknown protein [Arabidopsis thaliana]
Seq. No.
                  204444
Seq. ID
                  LIB3083-056-Q1-L1-F10
Method
                  BLASTX
NCBI GI
                  q541951
BLAST score
                  170
E value
                  1.0e-19
Match length
                  90
% identity
NCBI Description
                  SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
                  [Glycine max]
```

Seq. ID LIB3083-056-Q1-L1-F2

Method BLASTX NCBI GI g4432859 BLAST score 225



```
2.0e-18
E value
Match length
                  145
                  43
% identity
NCBI Description
                  (AC006300) unknown protein [Arabidopsis thaliana]
                  204446
Seq. No.
Seq. ID
                  LIB3083-056-Q1-L1-F4
Method
                  BLASTX
NCBI GI
                  g1352078
BLAST score
                  228
                  2.0e-19
E value
                  47
Match length
                  74
% identity
                  BETA-GALACTOSIDASE PRECURSOR (LACTASE)
NCBI Description
                  (EXO-(1-->4)-BETA-D-GALACTANASE) >gi 507278 (L29451)
                  b-galactosidase-related protein; putative [Malus domestica]
                  204447
Seq. No.
Seq. ID
                  LIB3083-056-Q1-L1-F6
Method
                  BLASTX
NCBI GI
                  g3023956
                  194
BLAST score
                  9.0e-15
E value
                  152
Match length
% identity
                  VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi 607003
NCBI Description
                  (L28125) beta transducin-like protein [Podospora anserina]
                  204448
Seq. No.
Seq. ID
                  LIB3083-056-Q1-L1-F8
                  BLASTX
Method
                  g267069
NCBI GI
BLAST score
                  525
                  1.0e-53
E value
                  111
Match length
                  88
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  204449
Seq. No.
Seq. ID
                  LIB3083-056-Q1-L1-F9
Method
                  BLASTX
NCBI GI
                  q2920666
BLAST score
                  248
                  3.0e-21
E value
Match length
                  67
% identity
```

NCBI Description (AF048978) 2,4-D inducible glutathione S-transferase

[Glycine max]

Seq. No. 204450

Seq. ID LIB3083-056-Q1-L1-G10

Method BLASTX
NCBI GI g2129578
BLAST score 550



1.0e-56 E value 123 Match length % identity 84

dTDP-glucose 4-6-dehydratases homolog - Arabidopsis NCBI Description thaliana >gi 928932 emb CAA89205 (Z49239) homolog of

dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >qi 1585435 prf 2124427B diamide resistance gene

[Arabidopsis thaliana]

204451 Seq. No.

LIB3083-056-Q1-L1-G2 Seq. ID

Method BLASTX NCBI GI q3036816 BLAST score 221 E value 5.0e-18 91 Match length % identity

(AL022373) myosin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 204452

LIB3083-056-Q1-L1-G4 Seq. ID

Method BLASTX NCBI GI g4193382 BLAST score 370 E value 2.0e-35 Match length 86 % identity

(AF083336) ribosomal protein S27 [Arabidopsis thaliana] NCBI Description

>gi\_4193384 (AF083337) ribosomal protein S27 [Arabidopsis

thaliana]

204453 Seq. No.

Seq. ID LIB3083-056-Q1-L1-G6

BLASTX Method NCBI GI q951453 BLAST score 444 E value 3.0e-44 Match length 127 67 % identity

(M95746) initiation factor (iso)4f p82 subunit [Triticum NCBI Description

aestivum]

Seq. No. 204454

Seq. ID LIB3083-056-Q1-L1-G9

Method BLASTX NCBI GI g140739 BLAST score 161 6.0e-11 E value Match length 120

% identity 33

HYPOTHETICAL 31.0 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION NCBI Description

(ORF 2) >gi\_78519\_pir\_\_JQ0613 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli >gi 216632 dbj BAA14238 (D90212) ORF2 [Escherichia coli] >gi\_606065 (U18997) ORF\_f299 [Escherichia coli] >gi 1789513

(AE000394) putative dehydrogenase [Escherichia coli]

```
204455
Seq. No.
Seq. ID
                  LIB3083-056-Q1-L1-H1
Method
                  BLASTX
NCBI GI
                  g4544412
BLAST score
                  368
E value
                  4.0e-35
Match length
                  149
                  44
% identity
NCBI Description
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  204456
Seq. ID
                  LIB3083-056-Q1-L1-H12
Method
                  BLASTX
NCBI GI
                  q3242709
BLAST score
                  247
                  2.0e-36
E value
Match length
                  119
% identity
                  65
                   (AC003040) putative guanine nucleotide-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  204457
                  LIB3083-056-Q1-L1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3327868
BLAST score
                  165
E value
                  1.0e-11
Match length
                  106
% identity
                  38
                  (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
NCBI Description
                  thaliana]
                  204458
Seq. No.
Seq. ID
                  LIB3083-056-Q1-L1-H5
Method
                  BLASTX
NCBI GI
                  g2501850
BLAST score
                  313
                  6.0e-29
E value
                  77
Match length
                  79
% identity
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
Seq. No.
                  204459
Seq. ID
                  LIB3083-056-Q1-L1-H6
Method
                  BLASTX
NCBI GI
                  g4098128
```

Method BLASTX
NCBI GI g4098128
BLAST score 701
E value 3.0e-74
Match length 148
% identity 93

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 204460

Seq. ID LIB3083-056-Q1-L1-H7

Method BLASTX NCBI GI g1174592 BLAST score 735



E value 3.0e-78 Match length 146 % identity 95

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 204461

Seq. ID LIB3083-056-Q1-L1-H8

Method BLASTX
NCBI GI g1171866
BLAST score 448
E value 1.0e-44
Match length 128
% identity 68

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR

(COMPLEX I-20KD) (CI-20KD) >gi\_629601\_pir\_\_S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi\_562282 emb\_CAA57725\_ (X82274) PSST subunit of

NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 204462

Seq. ID LIB3083-057-Q1-L1-A10

Method BLASTN
NCBI GI g3063438
BLAST score 34
E value 2.0e-09
Match length 74
% identity 86

NCBI Description Complete sequence of Arabidopsis F22013, complete sequence

[Arabidopsis thaliana]

Seq. No. 204463

Seq. ID LIB3083-057-Q1-L1-A11

Method BLASTN
NCBI GI g1706957
BLAST score 34
E value 2.0e-09
Match length 90
% identity 92

NCBI Description Gossypium hirsutum cellulose synthase (celA2) mRNA, partial

cds

Seq. No. 204464

Seq. ID LIB3083-057-Q1-L1-A12

Method BLASTX
NCBI GI g1350983
BLAST score 292
E value 2.0e-26
Match length 72
% identity 82

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

Seq. No. 204465

Seq. ID LIB3083-057-Q1-L1-B11

Method BLASTX NCBI GI g729623



```
453
BLAST score
                  3.0e-45
E value
                  109
Match length
                  83
% identity
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP
NCBI Description
                  78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG
                  5) (BIP 5) >gi_100340_pir__S21880 heat shock protein BiP
                  homolog blp5 - common tobacco >gi_19813_emb_CAA42660
                  (X60058) luminal binding protein (BiP) [Nicotiana tabacum]
                  204466
Seq. No.
                  LIB3083-057-Q1-L1-B12
Seq. ID
                  BLASTX
Method
                  q3367515
NCBI GI
                  558
BLAST score
                  2.0e-57
E value
                  148
Match length
                  74
% identity
                  (AC004392) Similar to
NCBI Description
                  glucose-6-phosphate/phosphate-translocator (GPT)
                  gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
Seq. No.
                  204467
                  LIB3083-057-Q1-L1-C10
Seq. ID
                  BLASTX
Method
                  q1518540
NCBI GI
                  728
BLAST score
                  2.0e-77
E value
                  155
Match length
                  93
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  204468
Seq. No.
Seq. ID
                  LIB3083-057-Q1-L1-C11
                  BLASTX
Method
                  q3694872
NCBI GI
BLAST score
                  566
                  2.0e-58
E value
                  131
Match length
                  82
% identity
                  (AF092547) profilin [Ricinus communis]
NCBI Description
                  204469
Seq. No.
Seq. ID
                  LIB3083-057-Q1-L1-C9
                  BLASTX
Method
                  q464849
NCBI GI
BLAST score
                   525
                  1.0e-53
E value
                  125
Match length
                  85
% identity
                  TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                   chain - almond >gi_20413_emb_CAA47635_ (X67162)
```

alpha-tubulin [Prunus dulcis]

Seq. No. 204470

Seq. ID LIB3083-057-Q1-L1-D10

Method BLASTX

Seq. ID Method

NCBI GI

```
q3927831
NCBI GI
BLAST score
                  594
E value
                  9.0e-62
                  131
Match length
% identity
                  67
NCBI Description
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                  thalianal
                           204471
Seq. No.
                  LIB3083-057-QI-L1-D12
Seq. ID
                  BLASTN
Method
                  q4104241
NCBI GI
                  202
BLAST score
                  1.0e-110
E value
                  214
Match length
                  99
% identity
                  Gossypium hirsutum palmitoyl-acyl carrier protein
NCBI Description
                  thioesterase (FatB1) mRNA, partial cds
Seq. No.
                  204472
Seq. ID
                  LIB3083-057-Q1-L1-D9
                  BLASTX
Method
NCBI GI
                  q417154
BLAST score
                  714
                  3.0e-77
E value
Match length
                  157
                  96
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100685 pir_S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  204473
Seq. No.
Seq. ID
                  LIB3083-057-Q1-L1-E12
                  BLASTX
Method
NCBI GI
                   g1743009
BLAST score
                  147
                  7.0e-10
E value
Match length
                   55
                   53
% identity
                  (Y10036) SNF1-related protein kinase [Cucumis sativus]
NCBI Description
Seq. No.
                  204474
Seq. ID
                  LIB3083-057-Q1-L1-F10
Method
                  BLASTN
NCBI GI
                   q4580454
BLAST score
                   84
E value
                   2.0e-39
Match length
                   312
% identity
                   82
                  Arabidopsis thaliana chromosome II BAC T2G17 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   204475
```

27923

LIB3083-057-Q1-L1-F12

BLASTX

q2738248

```
BLAST score
                   596
E value
                   6.0e-62
Match length
                   141
% identity
                   86
NCBI Description
```

(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No. 204476 LIB3083-057-Q1-L1-F9 Seq. ID Method BLASTX NCBI GI g902584 BLAST score 786 4.0e-84

E value Match length 162 % identity 15

NCBI Description (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea

mays]

204477 Seq. No. Seq. ID LIB3083-057-Q1-L1-G10 Method BLASTX NCBI GI g3142297 BLAST score 451

6.0e-45 E value Match length 147 % identity 60

NCBI Description (AC002411) Contains similarity to serine/threonine protein

phosphatase gb\_X83099 from S. cerevisiae. [Arabidopsis

thaliana]

Seq. No. 204478

Seq. ID LIB3083-057-Q1-L1-G11

Method BLASTX NCBI GI q559684 BLAST score 626 E value 2.0e-65 Match length 129 % identity 90

NCBI Description (L36097) aquaporin [Mesembryanthemum crystallinum]

Seq. No. 204479

Seq. ID LIB3083-057-Q1-L1-G12

Method BLASTX NCBI GI g3927825 BLAST score 643 E value 2.0e-67 Match length 133 % identity 92

(AC005727) putative dTDP-glucose 4-6-dehydratase NCBI Description

[Arabidopsis thaliana]

Seq. No. 204480

Seq. ID LIB3083-057-Q1-L1-G9

Method BLASTX NCBI GI g2760320 BLAST score 177 E value 9.0e-13

Match length 38 % identity

NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.

204481 Seq. ID LIB3083-057-Q1-L1-H10

Method BLASTX NCBI GI g3892055 BLAST score 369 E value 2.0e-35 147 Match length 41

% identity NCBI Description (AC002330) putative transport protein [Arabidopsis

thaliana]

Seq. No. 204482

Seq. ID LIB3083-057-Q1-L1-H11

Method BLASTN NCBI GI g1143223 BLAST score 314 E value 1.0e-176 497 Match length 38 % identity

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 204483

Seq. ID LIB3083-057-Q1-L1-H12

Method BLASTX g485742 NCBI GI BLAST score 681 E value 6.0e-72 Match length 145 96 % identity

NCBI Description (L32791) pyrophosphatase [Beta vulgaris]

Seq. No. 204484

Seq. ID LIB3083-057-Q1-L1-H9

Method BLASTX NCBI GI q135406 BLAST score 651 E value 2.0e-68 Match length 137 % identity

NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin

> alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi\_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 204485

Seq. ID LIB3083-058-Q1-L1-B3

Method BLASTX NCBI GI g3695388 BLAST score 275 E value 2.0e-24 Match length 90 54 % identity

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

```
204486
Seq. No.
Seq. ID
                  LIB3083-058-Q1-L1-B8
Method
                  BLASTX
NCBI GI
                  q4567286
BLAST score
                  437
E value
                  2.0e-43
Match length
                  118
% identity
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                  thaliana]
                  204487
Seq. No.
Seq. ID
                  LIB3083-058-Q1-L1-B9
Method
                  BLASTX
NCBI GI
                  g4572676
                  300
BLAST score
                  3.0e-27
E value
Match length
                  110
                  51
% identity
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204488
Seq. No.
                  LIB3083-058-Q1-L1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2494113
BLAST score
                  645
                  9.0e-68
E value
                  128
Match length
                  90
% identity
NCBI Description
                  (AC002376) Strong similarity to Musa pectate lyase
                   (qb X92943). ESTs qb AA042458, qb ATTS4502, qb N38552 come
                  from this gene. [Arabidopsis thaliana]
                  204489
Seq. No.
Seq. ID
                  LIB3083-058-Q1-L1-E1
                  BLASTX
Method
                  q728880
NCBI GI
                  192
BLAST score
                  8.0e-15
E value
Match length
                  72
                  54
% identity
                  N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
NCBI Description
                  >qi 517485 emb CAA54691 (X77588) ARD1 N-acetyl transferase
                  homologue [Homo sapiens] >qi 1302661 (U52112) ARD1 N-acetyl
                  transferase related protein [Homo sapiens]
                  204490
Seq. No.
Seq. ID
                  LIB3083-058-Q1-L1-F7
Method
                  BLASTX
NCBI GI
                  g2281115
BLAST score
                  162
E value
                  4.0e-11
Match length
                  37
% identity
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
```

27926

thaliana]

```
204491
Seq. No.
Seq. ID
                  LIB3083-058-Q1-L1-F9
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  502
                  6.0e-51
E value
Match length
                  126
                  74
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                  204492
Seq. No.
                  LIB3083-059-Q1-L1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334113
BLAST score
                  240
                  2.0e-26
E value
                  92
Match length
                  66
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
NCBI Description
                  acyl-CoA-binding protein [Gossypium hirsutum]
                  204493
Seq. No.
                  LIB3083-059-Q1-L1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3985958
BLAST score
                  53
                  6.0e-21
E value
                  212
Match length
                  86
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
                  204494
Seq. No.
                  LIB3083-059-Q1-L1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3511285
BLAST score
                  336
                  1.0e-31
E value
Match length
                  101
% identity
                  (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
                  tremula]
Seq. No.
                  204495
Seq. ID
                  LIB3083-059-Q1-L1-B10
Method
                  BLASTX
NCBI GI
                  g4544399
BLAST score
                  379
                  7.0e-37
E value
Match length
                  91
% identity
                  76
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  204496
Seq. No.
Seq. ID
                  LIB3083-059-Q1-L1-B12
```



```
BLASTX
Method
NCBI GI
                  g2555159
BLAST score
                   252
                   9.0e-22
E value
                   74
Match length
% identity
                   65
                  (AF025302) putative aldolase [Arabidopsis thaliana]
NCBI Description
                   204497
Seq. No.
Seq. ID
                  LIB3083-059-Q1-L1-B7
                  BLASTX
Method
NCBI GI
                   g3286691
BLAST score
                   356
                   7.0e - 34
E value
                   94
Match length
                   66
% identity
                   (AJ007450) auxilin-like protein [Arabidopsis thaliana]
NCBI Description
                   204498
Seq. No.
                   LIB3083-059-Q1-L1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4115337
BLAST score
                   488
                   2.0e-49
E value
                   105
Match length
% identity
                   16
                  (L81141) ubiquitin [Pisum sativum]
NCBI Description
                   204499
Seq. No.
Seq. ID
                   LIB3083-059-Q1-L1-C8
                   BLASTX
Method
NCBI GI
                   q1854386
BLAST score
                   488
E value
                   2.0e-49
                   125
Match length
                   73
% identity
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                   vinifera]
                   204500
Seq. No.
Seq. ID
                   LIB3083-059-Q1-L1-C9
Method
                   BLASTX
NCBI GI
                   g2500354
BLAST score
                   547
E value
                   2.0e-56
                   109
Match length
                   93
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   204501
Seq. No.
Seq. ID
                   LIB3083-059-Q1-L1-D6
Method
                   BLASTX
```

NCBI GI g2388575
BLAST score 185
E value 6.0e-14
Match length 106

Seq. ID

204507

LIB3083-059-Q1-L1-F10

```
% identity
                  (AC000098) YUP8H12.18 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204502
                  LIB3083-059-Q1-L1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3264769
BLAST score
                   554
E value
                   4.0e-57
Match length
                   126
% identity
                   44
                  (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                   armeniaca]
                  204503
Seq. No.
Seq. ID
                  LIB3083-059-Q1-L1-D8
Method
                  BLASTX
NCBI GI
                   g4406780
BLAST score
                   527
                   6.0e-54
E value
Match length
                  125
% identity
                   82
NCBI Description
                  (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                   204504
Seq. ID
                  LIB3083-059-Q1-L1-E4
Method
                  BLASTX
NCBI GI
                  g3005931
BLAST score
                  218
E value
                   5.0e-18
                  86
Match length
% identity
                   47
NCBI Description (AJ005016) ABC transporter [Homo sapiens]
                  204505
Seq. No.
                  LIB3083-059-Q1-L1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g459712
BLAST score
                  46
E value
                  9.0e-17
Match length
                  74
                  91
% identity
NCBI Description
                  Chicken c-beta-5-tubulin gene, exon 4
Seq. No.
                  204506
Seq. ID
                  LIB3083-059-Q1-L1-E9
Method
                  BLASTX
NCBI GI
                  g4139172
BLAST score
                  490
E value
                  1.0e-49
Match length
                  103
% identity
                  85
NCBI Description (AF092952) beta 1 tubulin [Cyanophora paradoxa]
```



```
Method
                  BLASTX
NCBI GI
                  q70642
BLAST score
                  465
                  8.0e-47
E value
Match length
                  100
                  19
% identity
                  ubiquitin precursor - Arabidopsis thaliana
NCBI Description
                  >gi 17678 emb CAA31331 (X12853) polyubiquitin (AA 1 - 382)
                  [Arabidopsis thaliana] >gi 987519 (U33014) polyubiquitin
                  [Arabidopsis thaliana] >gi 226499 prf 1515347A
                  poly-ubiquitin [Arabidopsis thaliana]
                  204508
Seq. No.
Seq. ID
                  LIB3083-059-Q1-L1-F9
Method
                  BLASTX
NCBI GI
                  g4263695
BLAST score
                  157
                  1.0e-10
E value
Match length
                  67
                  52
% identity
NCBI Description
                  (AC006223) putative myosin II heavy chain [Arabidopsis
```

Seq. ID LIB3083-059-Q1-L1-G10

thaliana]

Method BLASTX
NCBI GI g1777386
BLAST score 243
E value 8.0e-21
Match length 98
% identity 47

NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No. 204510

Seq. ID LIB3083-059-Q1-L1-H11

Method BLASTN
NCBI GI g3702724
BLAST score 66
E value 8.0e-29
Match length 206
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K17N15, complete sequence [Arabidopsis thaliana]

Seq. No. 204511

Seq. ID LIB3083-059-Q1-L1-H12

Method BLASTX
NCBI GI g1848212
BLAST score 504
E value 3.0e-51
Match length 100
% identity 48

NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana

tabacum]

Seq. No. 204512

Seq. ID LIB3083-059-Q1-L1-H9



```
Method
                  g267069
NCBI GI
BLAST score
                  664
                  6.0e-70
E value
                  124
Match length
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  204513
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-A1
Method
                  BLASTN
                  g1370189
NCBI GI
                  65
BLAST score
                  3.0e-28
E value
                  113
Match length
                  89
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB8A
Seq. No.
                  204514
Seq. ID
                  LIB3083-060-Q1-L1-A11
Method
                  BLASTX
                  q3264611
NCBI GI
BLAST score
                  446
                  2.0e-44
E value
                  93
Match length
                  89
% identity
                  (AF061511) seven in absentia homolog [Zea mays]
NCBI Description
Seq. No.
                  204515
Seq. ID
                  LIB3083-060-Q1-L1-A2
                  BLASTN
Method
NCBI GI
                  q1143223
BLAST score
                  49
                  7.0e-19
E value
                  89
Match length
                  89
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                  204516
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-A4
Method
                  BLASTX
NCBI GI
                  q3024126
BLAST score
                   409
E value
                  2.0e-40
Match length
                   94
                   85
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
```

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 1655576 emb CAA95856 (Z71271) S-adenosyl-L-methionine

synthetase 1 [Catharanthus roseus]

204517 Seq. No.

LIB3083-060-Q1-L1-A6 Seq. ID

Method BLASTX

```
q1346523
NCBI GI
                  195
BLAST score
                  2.0e-15
E value
Match length
                  66
% identity
                  61
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
                  >gi_1084428_pir__S49491 methionine adenosyltransferase (EC
                  2.5.1.6) - garden petunia >gi_559506_emb_CAA57696_ (X82214)
                  methionine adenosyltransferase [Petunia x hybrida]
Seq. No.
                  204518
                  LIB3083-060-Q1-L1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q17677
BLAST score
                  43
E value
                  3.0e-15
Match length
                  75
                  35
% identity
NCBI Description Arabidopsis thaliana UBQ4 gene for polyubiquitin
                  204519
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-A9
Method
                  BLASTX
NCBI GI
                  g3395432
BLAST score
                  532
                  2.0e-54
E value
Match length
                  133
% identity
                  80
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204520
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-B1
                  BLASTX
Method
NCBI GI
                  g3366661
BLAST score
                  372
                  5.0e-36
E value
                  86
Match length
% identity
                  87
                  (AF038875) proliferating cell nuclear antigen [Nicotiana
NCBI Description
                  tabacum] >gi 3514105 (AF085197) proliferating cell nuclear
                  antigen [Nicotiana tabacum]
                  204521
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-B11
                  BLASTX
Method
                  g586076
NCBI GI
BLAST score
                  344
                  2.0e-32
E value
                  107
Match length
                   64
% identity
                  TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
```

Seq. ID LIB3083-060-Q1-L1-B3

tubulin 1 [Lupinus albus]



```
Method BLASTX
NCBI GI g2832628
BLAST score 359
E value 2.0e-34
Match length 90
% identity 77
NCBI Description (AL021713)
```

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 204523 Seq. ID LIB3083-060-Q1-L1-B7

Method BLASTX
NCBI GI g1854386
BLAST score 240
E value 1.0e-20
Match length 57

Match length 57 % identity 77

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No. 204524

Seq. ID LIB3083-060-Q1-L1-B8

Method BLASTX
NCBI GI g3759177
BLAST score 147
E value 2.0e-09
Match length 43
% identity 65

NCBI Description (AB018408) 3-phosphoserine phosphatase [Arabidopsis

thaliana] >gi\_3759179\_dbj\_BAA33807\_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No. 204525

Seq. ID LIB3083-060-Q1-L1-B9

Method BLASTX
NCBI GI g1170767
BLAST score 264
E value 5.0e-23
Match length 83
% identity 63

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN)

>gi\_626074\_pir\_\_S45176 transcription factor SUG1 homolog -

fission yeast (Schizosaccharomyces pombe) >gi 406051

(U02280) Let1 [Schizosaccharomyces pombe]

>gi 4106689 emb CAA22628 (AL035065) 26s protease

regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No. 204526

Seq. ID LIB3083-060-Q1-L1-C1

Method BLASTX
NCBI GI g1854386
BLAST score 386
E value 1.0e-37
Match length 94
% identity 76

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

```
204527
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-C11
                  BLASTX
Method
                  g2493130
NCBI GI
BLAST score
                  496
E value
                  2.0e-50
                  107
Match length
% identity
                  91
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi 459200 (U07053) vacuolar H+-ATPase subunit B
                  [Gossypium hirsutum]
                  204528
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-C3
Method
                  BLASTX
NCBI GI
                  q3834310
BLAST score
                  283
                  2.0e-25
E value
Match length
                  57
% identity
                  96
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                  gb D83004 from Homo sapiens. ESTs gb T88233, gb Z24464,
                  gb N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  204529
Seq. ID
                  LIB3083-060-Q1-L1-C9
Method
                  BLASTX
                  g4406789
NCBI GI
                  402
BLAST score
                  2.0e-39
E value
                  101
Match length
% identity
                   (AC006532) putative glutamate decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  204530
Seq. ID
                  LIB3083-060-Q1-L1-D10
Method
                  BLASTX
                  g1143511
NCBI GI
BLAST score
                   447
                  8.0e-45
E value
Match length
                  94
                  87
% identity
                   (Z47076) Ser/Thr protein phosphatase homologous to PPX
NCBI Description
                   [Malus domestica] >gi 1586034 prf 2202340A Ser/Thr protein
                  phosphatase [Malus domestica]
Seq. No.
                   204531
Seq. ID
                  LIB3083-060-Q1-L1-D4
```

BLASTN Method NCBI GI g1143223 BLAST score 215 1.0e-117 E value Match length 296 94 % identity

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

NCBI GI BLAST score

E value

```
Seq. No.
                  204532
Seq. ID
                  LIB3083-060-Q1-L1-D6
Method
                  BLASTN
NCBI GI
                  g1143223
BLAST score
                  109
                  2.0e-54
E value
                  251
Match length
% identity
                  32
                  Gossypium barbadense FbLate-2 gene, complete cds
NCBI Description
                  204533
Seq. No.
                  LIB3083-060-Q1-L1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464840
BLAST score
                  488
                  2.0e-49
E value
Match length
                  120
% identity
                  84
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
                  alpha-1 chain - fern (Anemia phyllitidis)
                  >gi 296494 emb CAA48927 (X69183) alpha tubulin [Anemia
                  phyllitidis]
Seq. No.
                  204534
                  LIB3083-060-Q1-L1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q134218
                  253
BLAST score
E value
                  2.0e-22
Match length
                  62
                  76
% identity
                  PROACTIVATOR POLYPEPTIDE PRECURSOR [CONTAINS: SAPOSIN A
NCBI Description
                  (PROTEIN A); SAPOSIN B (SPHINGOLIPID ACTIVATOR PROTEIN 1)
                  (SAP-1) (DISPERSIN) (SULFATIDE/GM1 ACTIVATOR); SAPOSIN C
                  (CO-BETA-GLUCOSIDASE) (A1 ACTIVATOR) (GLUCOSYLCERAM...
                  >gi 183231 (J03077) co-beta glucosidase precursor [Homo
                  sapiens] >gi 337756 (J03015) sphingolipid activator
                  precursor [Homo sapiens] >gi_337762 (M32221) prosaposin
                  [Homo sapiens]
Seq. No.
                  204535
Seq. ID
                  LIB3083-060-Q1-L1-E2
Method
                  BLASTX
NCBI GI
                  q1616785
BLAST score
                  399
E value
                  7.0e-39
Match length
                  133
% identity
NCBI Description
                  (U71121) pyruvate decarboxylase [Arabidopsis thaliana]
                  204536
Seq. No.
                  LIB3083-060-Q1-L1-E4
Seq. ID
Method
                  BLASTX
```

27935

g2191141

1.0e-35



```
Match length
                  63
% identity
                  (AF007269) A IG002N01.21 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  204537
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-F1
Method
                  BLASTX
NCBI GI
                  g1839188
BLAST score
                  496
E value
                  3.0e-50
Match length
                  134
                  72
% identity
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  204538
Seq. ID
                  LIB3083-060-Q1-L1-F3
Method
                  BLASTX
NCBI GI
                  g2213871
BLAST score
                  227
                  7.0e-19
E value
Match length
                  103
% identity
                  50
                  (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                  crystallinum]
                  204539
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-F7
Method
                  BLASTX
                  g2213871
NCBI GI
                  193
BLAST score
                  8.0e-15
E value
Match length
                  90
                  47
% identity
                  (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  204540
Seq. ID
                  LIB3083-060-Q1-L1-G10
Method
                  BLASTX
NCBI GI
                  g2760317
BLAST score
                  261
E value
                  5.0e-23
Match length
                  92
                   63
% identity
NCBI Description
                  (AC002130) F1N21.1 [Arabidopsis thaliana]
Seq. No.
                  204541
                  LIB3083-060-Q1-L1-G11
```

Seq. ID

BLASTX Method g3885329 NCBI GI BLAST score 395 E value 1.0e-38 92 Match length 82 % identity

(AC005623) alien-like protein [Arabidopsis thaliana] NCBI Description



```
204542
Seq. No.
                  LIB3083-060-Q1-L1-G3
Seq. ID
                  BLASTX
Method
                  g4098319
NCBI GI
                  474
BLAST score
                  7.0e-48
E value
Match length
                  109
                  83
% identity
NCBI Description (U76744) beta-tubulin 1 [Triticum aestivum]
                  204543
Seq. No.
                  LIB3083-060-Q1-L1-G5
Seq. ID
                  BLASTX
Method
                  g3395440
NCBI GI
BLAST score
                  179
                  3.0e-13
E value
                  63
Match length
                  48
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                  204544
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-G7
Method
                  BLASTX
                  g135460
NCBI GI
BLAST score
                  286
                  9.0e-26
E value
                  79
Match length
                  72
% identity
                  TUBULIN BETA-2 CHAIN >gi 100933 pir_S14702 tubulin beta-2
NCBI Description
                  chain - maize >gi 22184 emb CAA37061 (X52879) beta 2
                  tubulin (AA 1-444) [Zea mays]
Seq. No.
                  204545
                  LIB3083-060-Q1-L1-H1
Seq. ID
                  BLASTX
Method
                  q4455244
NCBI GI
BLAST score
                  171
                  2.0e-12
E value
                  90
Match length
                  46
% identity
                  (AL035523) MtN3-like protein [Arabidopsis thaliana]
NCBI Description
                  204546
Seq. No.
Seq. ID
                  LIB3083-060-Q1-L1-H4
                  BLASTX
Method
                  g3335355
NCBI GI
BLAST score
                  496
                  2.0e-50
E value
Match length
                  106
                  24
% identity
                  (AC004512) Match to polyubiquitin DNA gb L05401 from A.
NCBI Description
                  thaliana. Contains insertion of mitochondrial NADH
                  dehydrogenase gb X82618 and gb X98301. May be a pseudogene
                  with an expressed insert. EST gb AA586248 comes from this
```

region. [Arabi



LIB3083-060-Q1-L1-H5 Seq. ID BLASTX Method NCBI GI g1709253 193 BLAST score 5.0e-15 E value 72 Match length 47 % identity SERINE/THREONINE-PROTEIN KINASE NEK3 (NIMA-RELATED PROTEIN NCBI Description KINASE 3) (HSPK 36) >gi 479173\_emb\_CAA82310\_ (Z29067) protein kinase [Homo sapiens] 204548 Seq. No. LIB3083-060-Q1-L1-H7 Seq. ID BLASTN Method g1143223 NCBI GI BLAST score 62 2.0e-26 E value 199 Match length 86 % identity NCBI Description Gossypium barbadense FbLate-2 gene, complete cds Seq. No. 204549 Seq. ID LIB3083-060-Q1-L1-H9 Method BLASTX q464849 NCBI GI 250 BLAST score 5.0e-22 E value Match length 59 % identity 85 TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha NCBI Description chain - almond >gi 20413 emb CAA47635 (X67162) alpha-tubulin [Prunus dulcis] 204550 Seq. No. LIB3083-061-Q1-L1-A10 Seq. ID BLASTX Method q2384671 NCBI GI 307 BLAST score 2.0e-28 E value 86 Match length 73 % identity (AF012657) putative potassium transporter AtKT2p NCBI Description [Arabidopsis thaliana] 204551 Seq. No. LIB3083-061-Q1-L1-A12 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g1854386
BLAST score 467
E value 7.0e-47
Match length 113
% identity 80

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No. 204552

Seq. ID LIB3083-061-Q1-L1-B9



```
Method
                  BLASTX
NCBI GI
                  g135406
BLAST score
                  449
                  6.0e-45
E value
Match length
                  105
                  85
% identity
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >qi 166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
                  204553
Seq. No.
                  LIB3083-061-Q1-L1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4103342
BLAST score
                  454
                  2.0e-45
E value
Match length
                  111
                  80
% identity
NCBI Description
                  (AF022377) agamous-like putative transcription factor
                  [Cucumis sativus]
                  204554
Seq. No.
Seq. ID
                  LIB3083-061-Q1-L1-D11
                  BLASTX
Method
NCBI GI
                  g3334320
BLAST score
                  646
                  7.0e-68
E value
                  132
Match length
                  94
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
                  204555
Seq. No.
                  LIB3083-061-Q1-L1-D12
Seq. ID
Method
                  BLASTX
                  q2384671
NCBI GI
BLAST score
                  441
                  8.0e-44
E value
Match length
                  131
% identity
                  (AF012657) putative potassium transporter AtKT2p
NCBI Description
                   [Arabidopsis thaliana]
                  204556
Seq. No.
                  LIB3083-061-Q1-L1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                  151
                  8.0e-10
E value
Match length
                  84
% identity
                  44
```

NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 204557

LIB3083-061-Q1-L1-E10 Seq. ID

Method BLASTX



```
NCBI GI g4406774
BLAST score 455
E value 1.0e-45
Match length 108
% identity 78
NCBI Description (AC00683
5' parti
Seq. No. 204558
Seq. ID LIB3083-
```

(AC006836) putative nonsense-mediated mRNA decay protein,

5' partial [Arabidopsis thaliana]

Seq. ID LIB3083-061-Q1-L1-F11
Method BLASTX
NCBI GI g2129770
BLAST score 161
E value 4.0e-11

E value 4.0 Match length 49 % identity 61

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi\_1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 204559

Seq. ID LIB3083-061-Q1-L1-F9

Method BLASTX
NCBI GI g2129770
BLAST score 484
E value 8.0e-49
Match length 127
% identity 69

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -

Arabidopsis thaliana >gi\_1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 204560

Seq. ID LIB3083-061-Q1-L1-G12

Method BLASTX
NCBI GI g2281102
BLAST score 219
E value 5.0e-18
Match length 98
% identity 50

NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No. 204561

Seq. ID LIB3083-061-Q1-L1-H12

Method BLASTX
NCBI GI g3421090
BLAST score 336
E value 7.0e-32
Match length 86
% identity 77

NCBI Description (AF043525) 20S proteasome subunit PAE2 [Arabidopsis

thaliana]

```
Seq. No.
                   204562
Seq. ID
                  LIB3083-061-Q1-L1-H9
Method
                  BLASTX
NCBI GI
                   q2959370
BLAST score
                   267
E value
                   2.0e-23
                   132
Match length
                   37
% identity
NCBI Description
                  (AL022117) hypothetical protein [Schizosaccharomyces pombe]
                   204563
Seq. No.
                  LIB3083-062-Q1-L1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2118017
BLAST score
                   321
                   5.0e-30
E value
                   89
Match length
% identity
                   62
NCBI Description
                  non-S-RNase (EC 3.1.-.-) - Japanese pear
                   >gi_1526417_dbj_BAA08475_ (D49529) ribonuclease [Pyrus
                  pyrifolia]
                   204564
Seq. No.
                   LIB3083-062-Q1-L1-B10
Seq. ID
Method
                   BLASTX
                   q3980413
NCBI GI
                   391
BLAST score
                   6.0e-38
E value
                   124
Match length
% identity
                   12
NCBI Description
                   (AC004561) pumilio-like protein [Arabidopsis thaliana]
                   204565
Seq. No.
                   LIB3083-062-Q1-L1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4371292
BLAST score
                   335
                   1.0e-31
E value
Match length
                   94
                   67
% identity
NCBI Description
                   (AC006260) unknown protein [Arabidopsis thaliana]
Seq. No.
                   204566
                   LIB3083-062-Q1-L1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1181589
BLAST score
                   197
                   3.0e-15
E value
Match length
                   85
% identity
                   44
NCBI Description
                   (D83070) high mobility group protein [Canavalia gladiata]
                   >gi 1483173 dbj BAA13133 (D86594) high mobility group
```

protein [Canavalia gladiata]

204567 Seq. No.

LIB3083-062-Q1-L1-D11 Seq. ID

Method BLASTX

```
NCBI GI
                   q4103342
BLAST score
                   618
E value
                   1.0e-64
Match length
                   136
% identity
NCBI Description
                   (AF022377) agamous-like putative transcription factor
                   [Cucumis sativus]
                   204568
Seq. No.
                   LIB3083-062-Q1-L1-D12
Seq. ID
                   BLASTX
Method
                   g862640
NCBI GI
BLAST score
                   244
                   3.0e-21
E value
Match length
                   75
                   67
% identity
NCBI Description
```

(U20182) MADS-box protein AGL11 [Arabidopsis thaliana] >gi\_4538999\_emb\_CAB39620.1\_ (AL049481) MADS-box protein

AGL11 [Arabidopsis thaliana]

Seq. No. 204569 LIB3083-062-Q1-L1-D9 Seq. ID BLASTX Method g1181589 NCBI GI 177 BLAST score

4.0e-13 E value 56 Match length 61 % identity

(D83070) high mobility group protein [Canavalia gladiata] NCBI Description

>gi\_1483173\_dbj\_BAA13133\_ (D86594) high mobility group

protein [Canavalia gladiata]

204570 Seq. No.

Seq. ID LIB3083-062-Q1-L1-E10

BLASTX Method NCBI GI q2131352 BLAST score 218 1.0e-17 E value Match length 120 38 % identity

hypothetical protein YDL166c - yeast (Saccharomyces NCBI Description

cerevisiae) >gi\_1061273\_emb\_CAA91580\_ (Z67750) putative

protein [Saccharomyces cerevisiae]

>gi\_1431264\_emb\_CAA98740\_ (Z74214) ORF YDL166c

[Saccharomyces cerevisiae]

Seq. No. 204571

LIB3083-062-Q1-L1-E11 Seq. ID

Method BLASTX q1174592 NCBI GI BLAST score 587 E value 4.0e-61 Match length 110 99 % identity

NCBI Description TUBULIN ALPHA-1 CHAIN >qi 2119270 pir S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

```
204572
Seq. No.
Seq. ID
                  LIB3083-062-Q1-L1-E12
                  BLASTX
Method
                  q123534
NCBI GI
BLAST score
                   277
                   1.0e-24
E value
                   72
Match length
                   72
% identity
                  17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3)
NCBI Description
                   >gi 71493 pir HHSY17 heat shock protein 17 - soybean
                   >gi 18656 emb CAA25578 (X01104) heat shock protein 6871
                   (aa 1-153) [Glycine max] >gi 224205_prf__1012218B protein
                   6871, heat shock [Glycine max]
                   204573
Seq. No.
                   LIB3083-062-Q1-L1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2252863
BLAST score
                   619
                   1.0e-64
E value
                   138
Match length
                   84
% identity
                   (AF013294) similar to nucleolin protein [Arabidopsis
NCBI Description
                   thaliana]
                   204574
Seq. No.
                   LIB3083-062-Q1-L1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2058456
BLAST score
                   536
                   4.0e-55
E value
                   108
Match length
                   95
% identity
NCBI Description
                   (U66408) GTP-binding protein [Arabidopsis thaliana]
                   >qi 2345150 gb AAB67830 (AF014822) developmentally
                   regulated GTP binding protein [Arabidopsis thaliana]
                   204575
Seq. No.
                   LIB3083-062-Q1-L1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1550660
BLAST score
                   357
                   5.0e-34
E value
Match length
                   115
                   57
% identity
                   (Z80226) ptrBa [Mycobacterium tuberculosis]
NCBI Description
Seq. No.
                   204576
                   LIB3083-062-Q1-L1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244732
                   399
BLAST score
                   4.0e-39
E value
                   77
Match length
                   100
% identity
                  (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
NCBI Description
```

```
204577
Seq. No.
Seq. ID
                  LIB3083-062-Q1-L1-G9
Method
                  BLASTX
                  g3913518
NCBI GI
                  302
BLAST score
                  1.0e-27
E value
                  103
Match length
% identity
                  63
                  3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
NCBI Description
                  (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                  (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate
                  nucleotidase [Arabidopsis thaliana]
                  204578
Seq. No.
Seq. ID
                  LIB3083-062-Q1-L1-H10
                  BLASTX
Method
                  g3236240
NCBI GI
                  576
BLAST score
                  1.0e-59
E value
Match length
                  125
% identity
                  82
                  (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204579
Seq. No.
                  LIB3083-063-Q1-L1-A1
Seq. ID
                  BLASTX
Method
                  g2306917
NCBI GI
BLAST score
                  461
                  2.0e-46
E value
                  99
Match length
                  90
% identity
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                  thaliana]
                  204580
Seq. No.
Seq. ID
                  LIB3083-063-Q1-L1-A10
                  BLASTX
Method
                  g2829204
NCBI GI
BLAST score
                  319
                  1.0e-29
E value
Match length
                  82
% identity
                   (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
                  204581
Seq. No.
Seq. ID
                  LIB3083-063-Q1-L1-A11
                  BLASTX
Method
                  q425194
NCBI GI
BLAST score
                   522
E value
                   1.0e-53
Match length
                   107
                   94
% identity
                  (L26243) heat shock protein [Spinacia oleracea] >gi_2660772
NCBI Description
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
```

oleracea]

```
Seq. No.
                  204582
                  LIB3083-063-Q1-L1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2497743
BLAST score
                  177
                  6.0e-13
E value
                  57
Match length
% identity
                  61
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
NCBI Description
                  >gi 999315 bbs 166991 (S78173) LTP=lipid transfer protein
                  [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                  [Gossypium hirsutum]
                  204583
Seq. No.
                  LIB3083-063-Q1-L1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g124224
BLAST score
                  558
E value
                  1.0e-57
Match length
                  108
                  96
% identity
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 100345 pir S21060 translation initiation factor eIF-5A
                   - common tobacco >gi 19887 emb CAA45105 (X63543)
                  eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
                  204584
Seq. No.
Seq. ID
                  LIB3083-063-Q1-L1-A6
Method
                  BLASTX
NCBI GI
                  q1477428
BLAST score
                  453
                  2.0e-45
E value
Match length
                  109
                  83
% identity
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
Seq. No.
                  204585
                  LIB3083-063-Q1-L1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                   492
E value
                   6.0e-50
Match length
                  100
                   10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                   204586
                  LIB3083-063-Q1-L1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2244772
BLAST score
                   451
                   4.0e-45
E value
Match length
                  120
```

(Z97335) transport protein [Arabidopsis thaliana]

72

% identity

NCBI Description

```
Seq. No.
   Seq. ID
                     LIB3083-063-Q1-L1-B1
                     BLASTX
   Method
   NCBI GI
                      g4263795
   BLAST score
                      328
                      1.0e-30
   E value
                      91
   Match length
                      66
   % identity
                      (AC006068) putative glucosyltransferase [Arabidopsis

    NCBI Description

                      thaliana]
                      204588
   Seq. No.
   Seq. ID
                      LIB3083-063-Q1-L1-B11
   Method
                      BLASTX
                      g2576411
   NCBI GI
                      182
   BLAST score
   E value
                      1.0e-23
   Match length
                      88
                      78
   % identity
                      (AF012833) similar to dynamin-like protein encoded by
   NCBI Description
                      GenBank Accession Number X99669 [Arabidopsis thaliana]
   Seq. No.
                      204589
   Seq. ID
                      LIB3083-063-Q1-L1-B12
   Method
                      BLASTX
   NCBI GI
                      g4160280
   BLAST score
                      539
   E value
                      3.0e-55
   Match length
                      120
                      78
   % identity
                     (AJ006224) purple acid phosphatase [Ipomoea batatas]
   NCBI Description
                      204590
   Seq. No.
   Seq. ID
                      LIB3083-063-Q1-L1-B4
   Method
                      BLASTX
   NCBI GI
                      g730220
   BLAST score
                      166
   E value
                      1.0e-11
                      56
   Match length
                      55
   % identity
                      OXALYL-COA DECARBOXYLASE >gi_1086099_pir__A55219 oxalyl-CoA
   NCBI Description
                      decarboxylase (EC 4.1.1.8) - Oxalobacter formigenes
```

>gi 150447 (M77128) oxalyl-CoA decarboxylase [Oxalobacter

formigenes]

204591 Seq. No.

Seq. ID LIB3083-063-Q1-L1-B8

Method BLASTX NCBI GI g4006877 BLAST score 272 5.0e-24E value Match length 60 % identity 42

NCBI Description (Z99707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No. 204592

LIB3083-063-Q1-L1-B9 Seq. ID

```
BLASTX
Method
NCBI GI
                  g3915031
BLAST score
                  449
E value
                  7.0e-45
Match length
                  86
% identity
                  100
NCBI Description
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >qi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
Seq. No.
                  204593
Seq. ID
                  LIB3083-063-Q1-L1-C12
Method
                  BLASTX
NCBI GI
                  g2642428
BLAST score
                  156
                  1.0e-10
E value
Match length
                  80
% identity
                  47
NCBI Description
                  (AC002391) unknown protein, 3' partial [Arabidopsis
                  thaliana]
                  204594
Seq. No.
                  LIB3083-063-Q1-L1-C3
Seq. ID
Method
                  BLASTX
                  g2982453
NCBI GI
BLAST score
                  396
                  1.0e-38
E value
                  90
Match length
% identity
                  84
NCBI Description
                  (AL022223) fructose-bisphosphate aldolase-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  204595
Seq. ID
                  LIB3083-063-Q1-L1-C4
Method
                  BLASTX
NCBI GI
                  g120669
BLAST score
                  483
                  8.0e-49
E value
Match length
                  119
% identity
                  78
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >qi 19566 emb CAA42905 (X60347) qlyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
```

Seq. No. 204596

Seq. ID LIB3083-063-Q1-L1-C5

Method BLASTX
NCBI GI g2213595
BLAST score 332
E value 3.0e-31
Match length 98
% identity 63

NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]



```
204597
Seq. No.
                  LIB3083-063-Q1-L1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2267567
                  394
BLAST score
                  2.0e-38
E value
Match length
                  85
                  87
% identity
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
                  204598
Seq. No.
Seq. ID
                  LIB3083-063-Q1-L1-C8
                  BLASTN
Method
NCBI GI
                  g451543
                  285
BLAST score
                  1.0e-159
E value
                   303
Match length
                   73
% identity
                  Gossypium barbadense Sea Island proline-rich cell wall
NCBI Description
                  protein gene complete cds. >gi 1598725_gb_I18370_I18370
                   Sequence 25 from patent US
                   204599
Seq. No.
Seq. ID
                  LIB3083-063-Q1-L1-C9
                  BLASTN
Method
                   g2264306
NCBI GI
                   37
BLAST score
                   2.0e-11
E value
Match length
                   161
                   81
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBK5, complete sequence [Arabidopsis thaliana]
                   204600
Seq. No.
Seq. ID
                   LIB3083-063-Q1-L1-D1
                   BLASTX
Method
NCBI GI
                   g3953478
BLAST score
                   225
                   2.0e-18
E value
Match length
                   132
                   44
% identity
                   (AC002328) F2202.23 [Arabidopsis thaliana]
NCBI Description
```

204601 Seq. No.

Seq. ID LIB3083-063-Q1-L1-D4

Method BLASTX q1174592 NCBI GI BLAST score 512 3.0e-52 E value Match length 96 % identity

TUBULIN ALPHA-1 CHAIN >qi 2119270 pir S60233 alpha-tubulin NCBI Description

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]



```
204602
Seq. No.
                   LIB3083-063-Q1-L1-D5
Seq. ID
Method
                   BLASTX
                   g2129499
NCBI GI
BLAST score
                   489
                   1.0e-49
E value
Match length
                   106
                   87
% identity
                   fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                   >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                   204603
Seq. No.
Seq. ID
                   LIB3083-063-Q1-L1-E1
                   BLASTX
Method
NCBI GI
                   g3123908
                   374
BLAST score
                   5.0e-36
E value
                   126
Match length
                   35
% identity
NCBI Description
                   (AF038392) pre-mRNA splicing factor [Homo sapiens]
                   204604
Seq. No.
Seq. ID
                   LIB3083-063-Q1-L1-E11
                   BLASTX
Method
NCBI GI
                   g629838
BLAST score
                   582
                   2.0e-60
E value
Match length
                   113
                   96
% identity
                   tubulin beta-4 chain - maize >gi 416145 (L10635) beta-4
NCBI Description
                   tubulin [Zea mays]
                   204605
Seq. No.
                   LIB3083-063-Q1-L1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q544358
                   216
BLAST score
                   1.0e-17
E value
                   92
Match length
% identity
                   47
                   FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECURSOR
NCBI Description
                   (FVT-1) >gi_481027_pir__S37652 FVT1 protein - human >gi_296186_emb_CAA45197_ (X63657) FVT1 gene is disrupted in
                   a t(2;18) chromosomal translocation involving Ig
                   gene in a follicular lymphoma [Homo sapiens]
                   >qi 4503817 ref NP 002026.1 pFVT1 follicular lymphoma
                   variant translocation
Seq. No.
                   204606
Seq. ID
                   LIB3083-063-Q1-L1-E5
Method
                   BLASTX
NCBI GI
                   g3157910
BLAST score
                   351
E value
                   2.0e-33
Match length
                   105
% identity
                   66
                   (AF003551) lysine-ketoglutarate reductase/saccharopine
NCBI Description
```



## dehydrogenase bifunctional enzyme [Zea mays]

```
204607
Seq. No.
                  LIB3083-063-Q1-L1-E6
Seq. ID
                  BLASTX
Method
                  g3142289
NCBI GI
                  398
BLAST score
                  4.0e-39
E value
                  88
Match length
% identity
                  84
                  (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                  gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
                  204608
Seq. No.
                  LIB3083-063-Q1-L1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695388
BLAST score
                  241
                  2.0e-20
E value
Match length
                  86
% identity
                  51
                  (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
                  204609
Seq. No.
                  LIB3083-063-Q1-L1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499946
BLAST score
                  544
                   6.0e-56
E value
Match length
                  121
                   85
% identity
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana
                   tabacum]
                   204610
Seq. No.
Seq. ID
                   LIB3083-063-Q1-L1-E9
                   BLASTN
Method
                   g435038
NCBI GI
                   229
BLAST score
                   1.0e-126
E value
Match length
                   241
                   99
% identity
                  Gossypium hirsutum proline-rich cell wall protein mRNA,
NCBI Description
                   complete cds
                   204611
Seq. No.
Seq. ID
                   LIB3083-063-Q1-L1-F10
                   BLASTX
Method
NCBI GI
                   g1935918
BLAST score
                   498
                   1.0e-50
E value
                   110
Match length
% identity
                   (U93559) putative serine/threonine protein kinase [Brassica
NCBI Description
```

27950

rapa]

BLAST score

% identity

E value Match length 319 2.0e-29

95

71

NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG

```
204612
Seq. No.
Seq. ID
                  LIB3083-063-Q1-L1-F11
Method
                  BLASTX
NCBI GI
                  g3915031
BLAST score
                  488
                  2.0e-49
E value
                  107
Match length
                  90
% identity
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                   (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
                  204613
Seq. No.
                  LIB3083-063-Q1-L1-F12
Seq. ID
                  BLASTX
Method
                  g1174592
NCBI GI
BLAST score
                   583
                   1.0e-60
E value
Match length
                  112
                  96
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   204614
Seq. No.
                   LIB3083-063-Q1-L1-F2
Seq. ID
                   BLASTX
Method
                   g4454464
NCBI GI
BLAST score
                   373
E value
                   6.0e-36
                   104
Match length
                   66
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204615
Seq. No.
Seq. ID
                   LIB3083-063-Q1-L1-F3
Method
                   BLASTX
                   q3249084
NCBI GI
BLAST score
                   338
                   7.0e-32
E value
Match length
                   107
                   21
% identity
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
NCBI Description
                   gb_X92750 from Mus musculus. ESTs gb_AA712687 and
                   gb Z37223 come from this gene [Arabidopsis thaliana]
                   204616
Seq. No.
                   LIB3083-063-Q1-L1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2500347
```



>gi\_3878691\_emb\_CAA90127\_ (Z49911) similar to ribosomal
protein (L7AE family); cDNA EST EMBL:D73957 comes from this
gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST
EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393
comes from this gene; cD

Seq. No. 204617 Seq. ID LIB3083-063-Q1-L1-G10 Method BLASTX g121631 NCBI GI 285 BLAST score 1.0e-25 E value 73 Match length 73 % identity

NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR

>gi 72323 pir KNNT2S glycine-rich protein 2 - wood tobacco

>gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana

sylvestris]

Seq. No. 204618

Seq. ID LIB3083-063-Q1-L1-G11

Method BLASTX
NCBI GI g462013
BLAST score 530
E value 2.0e-54
Match length 119
% identity 88

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_542022\_pir\_\_S39558 HSP90 homolog - Madagascar
periwinkle >gi\_348696 (L14594) heat shock protein 90

[Catharanthus roseus]

Seq. No. 204619

Seq. ID LIB3083-063-Q1-L1-G12

Method BLASTX
NCBI GI g2853219
BLAST score 302
E value 5.0e-28
Match length 70
% identity 76

NCBI Description (AJ000923) glutathione transferase [Carica papaya]

Seq. No. 204620

Seq. ID LIB3083-063-Q1-L1-G2

Method BLASTX
NCBI GI g3236238
BLAST score 472
E value 2.0e-47
Match length 135
% identity 69

NCBI Description (AC004684) putative ARF1 GTPase activating protein

[Arabidopsis thaliana] >gi 4519792 dbj BAA75744.1\_

(AB017876) Asp1 [Arabidopsis thaliana]

Seq. No. 204621

Seq. ID LIB3083-063-Q1-L1-G3

Method BLASTX

```
q3935167
NCBI GI
                  530
BLAST score
                  3.0e-54
E value
                  121
Match length
                  86
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
                  204622
Seq. No.
Seq. ID
                  LIB3083-063-Q1-L1-G4
                  BLASTX
Method
                  g2130073
NCBI GI
                  478
BLAST score
                  3.0e-48
E value
                  109
Match length
                  87
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970 dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
                  204623
Seq. No.
                  LIB3083-063-Q1-L1-G5
Seq. ID
                  BLASTX
Method
                   g2160185
NCBI GI
                   383
BLAST score
                   4.0e-37
E value
                   116
Match length
                   62
% identity
                  (ACO00132) Similar to S. pombe ISP4 (gb_D83992).
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   204624
Seq. ID
                   LIB3083-063-Q1-L1-G8
                   BLASTX
Method
NCBI GI
                   q3608171
BLAST score
                   425
                   5.0e-42
E value
                   113
Match length
                   75
% identity
                  (D86306) proton-translocating inorganic pyrophosphatase
NCBI Description
                   [Cucurbita moschata]
                   204625
Seq. No.
Seq. ID
                   LIB3083-063-Q1-L1-H10
                   BLASTX
Method
                   q1083221
NCBI GI
BLAST score
                   163
                   3.0e-11
E value
```

112 Match length % identity 37

apolipoprotein D - mouse >gi\_575657\_emb\_CAA57974\_ (X82648) NCBI Description

apolipoprotein D [Mus musculus]

204626 Seq. No.

LIB3083-063-Q1-L1-H11 Seq. ID

Method BLASTX NCBI GI g4455206

```
311
BLAST score
                   1.0e-28
E value
                   83
Match length
                   70
% identity
                   (AL035440) putative beta-1, 3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   204627
Seq. No.
                  LIB3083-063-Q1-L1-H2
Seq. ID
Method
                  BLASTX
                   q1351856
NCBI GI
                   276
BLAST score
                   5.0e-28
E value
                   93
Match length
                   70
% identity
```

ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) NCBI Description (ACONITASE) >gi\_868003\_dbj\_BAA06108\_ (D29629) aconitase

[Cucurbita sp.]

204628 Seq. No. LIB3083-063-Q1-L1-H4 Seq. ID Method BLASTX NCBI GI q4415992 BLAST score 631 3.0e-66 E value

119 Match length % identity 100

NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]

204629 Seq. No. LIB3083-063-Q1-L1-H8 Seq. ID Method BLASTX NCBI GI g114181

BLAST score 358 3.0e-34 E value 108 Match length 66 % identity

3-DEHYDROQUINATE SYNTHASE >gi 68385 pir SYECQ NCBI Description

3-dehydroquinate synthase (EC 4.6.1.3) - Escherichia coli >gi 40968 emb CAA27495 (X03867) 3-dehydroquinate synthase (aa 1-362) [Escherichia coli] >gi 41225\_emb\_CAA79666 (Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett. 200:11-17(1986) [Escherichia coli] >gi\_606323 (U18997) 3-dehydroquinate synthase [Escherichia coli] >gi\_1789791 (AE000414) 3-dehydroquinate synthase [Escherichia coli]

204630 Seq. No.

Seq. ID LIB3083-064-Q1-L1-A10

Method BLASTX g2154715 NCBI GI 537 BLAST score 4.0e-55 E value Match length 118 % identity 88

(Y09418) CDPK-related protein kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 204631



```
LIB3083-064-Q1-L1-A11
Seq. ID
                  BLASTX
Method
                  g3202040
NCBI GI
                  463
BLAST score
                  2.0e-46
E value
                  152
Match length
% identity
                  (AF069323) permease 1 [Mesembryanthemum crystallinum]
NCBI Description
                  204632
Seq. No.
                  LIB3083-064-Q1-L1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172874
                  145
BLAST score
                   3.0e-09
E value
                   80
Match length
% identity
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                   >gi 479589 pir S34823 dehydration-induced protein RD22 -
                   Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                   [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
                   [Arabidopsis thaliana]
Seq. No.
                   204633
                   LIB3083-064-Q1-L1-B2
Seq. ID
                   BLASTX
Method
                   q2982249
NCBI GI
                   146
BLAST score
                   2.0e-09
E value
                   29
Match length
                   86
% identity
                   (AF051207) probable 60S ribosomal protein L15 [Picea
NCBI Description
                   mariana]
                   204634
Seq. No.
                   LIB3083-064-Q1-L1-B5
Seq. ID
Method
                   BLASTX
                   q586076
NCBI GI
BLAST score
                   612
                   6.0e-64
E value
                   113
Match length
                   98
% identity
                   TUBULIN BETA-1 CHAIN >gi_486734 pir S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                   tubulin 1 [Lupinus albus]
Seq. No.
                   204635
                   LIB3083-064-Q1-L1-B8
Seq. ID
                   BLASTX
Method
                   q4539292
NCBI GI
                   473
BLAST score
                   1.0e-47
E value
                   104
Match length
                   85
 % identity
                   (ALO49480) putative ribosomal protein S10 [Arabidopsis
 NCBI Description
```

thaliana]

```
204636
Seq. No.
Seq. ID
                  LIB3083-064-Q1-L1-B9
                  BLASTX
Method
                  g2995990
NCBI GI
                  274
BLAST score
                  2.0e-24
E value
                  101
Match length
                  55
% identity
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                  204637
Seq. No.
                  LIB3083-064-Q1-L1-C1
Seq. ID
Method
                  BLASTX
                  g2739387
NCBI GI
BLAST score
                  231
                  3.0e-19
E value
                  122
Match length
                  39
% identity
                  (AC002505) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  204638
                  LIB3083-064-Q1-L1-C12
Seq. ID
Method
                  BLASTX
                  g2213628
NCBI GI
BLAST score
                  214
E value
                  3.0e-17
Match length
                  116
% identity
                   46
                  (AC000103) F21J9.20 [Arabidopsis thaliana]
NCBI Description
                  204639
Seq. No.
                  LIB3083-064-Q1-L1-C3
Seq. ID
                  BLASTX
Method
                  g320960
NCBI GI
                                                                BLAST score
                   265
                   3.0e-30
E value
                   119
Match length
                   52
% identity
                  tubulin alpha-II chain - Plasmodium falciparum >gi 160108
NCBI Description
                   (M34390) alpha-tubulin II [Plasmodium falciparum]
                   204640
Seq. No.
Seq. ID
                   LIB3083-064-Q1-L1-C4
                   BLASTX
Method
                   g4263695
NCBI GI
BLAST score
                   187
                   4.0e-14
E value
                   116
Match length
% identity
                   (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                   thaliana]
```

204641

BLASTX

LIB3083-064-Q1-L1-C8

Seq. No. Seq. ID

Method

15%

Match length

99



```
NCBI GI
                  q2673912
BLAST score
                  303
                  1.0e-27
E value
Match length
                  94
                  61
% identity
                  (AC002561) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204642
Seq. No.
Seq. ID
                  LIB3083-064-Q1-L1-C9
Method
                  BLASTX
NCBI GI
                  q1352440
BLAST score
                  417
E value
                  6.0e-41
                  89
Match length
                  78
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                  (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)
                  (EIF-4F P26 SUBUNIT) >gi_1002915 (U34597) p26 [Oryza
                  sativa]
Seq. No.
                  204643
                  LIB3083-064-Q1-L1-D1
Seq. ID
                  BLASTX
Method
                  q1292710
NCBI GI
                  597
BLAST score
                  3.0e-62
E value
Match length
                  118
                  62
% identity
                  (X97558) calmodulin-1 [Capsicum annuum]
NCBI Description
                  204644
Seq. No.
                  LIB3083-064-Q1-L1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455129
BLAST score
                  306
                  6.0e-28
E value
                  90
Match length
% identity
                  63
                  (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
NCBI Description
                  204645
Seq. No.
                  LIB3083-064-Q1-L1-D3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q473216
                  36
BLAST score
                  8.0e-11
E value
Match length
                  44
                  95
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                  204646
Seq. No.
Seq. ID
                  LIB3083-064-Q1-L1-D5
                  BLASTX
Method
NCBI GI
                  q3004564
BLAST score
                  312
E value
                   9.0e-29
```

7.



```
% identity
                  (AC003673) putative receptor Ser/Thr protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  204647
Seq. No.
Seq. ID
                  LIB3083-064-Q1-L1-D8
                  BLASTX
Method
                  g2218152
NCBI GI
                  631
BLAST score
                  4.0e-66
E value
                  123
Match length
% identity
                  93
                  (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                  unguiculata]
                  204648
Seq. No.
                  LIB3083-064-Q1-L1-D9
Seq. ID
Method
                  BLASTN
                  g451543
NCBI GI
BLAST score
                  81
                  1.0e-37
E value
Match length
                  289
% identity
                  82
                  Gossypium barbadense Sea Island proline-rich cell wall
NCBI Description
                  protein gene complete cds. >gi_1598725_gb_I18370_I18370
                  Sequence 25 from patent US
Seq. No.
                  204649
                  LIB3083-064-Q1-L1-E11
Seq. ID
Method
                  BLASTX
                  g3212877
NCBI GI
                   570
BLAST score
E value
                  7.0e-59
                  143
Match length
% identity
                  74
                  (AC004005) Lea-like protein [Arabidopsis thaliana]
NCBI Description
                   204650
Seq. No.
                  LIB3083-064-Q1-L1-E3
Seq. ID
                  BLASTX
Method
                   g4262186
NCBI GI
BLAST score
                   500
E value
                   8.0e-51
                   120
Match length
                   78
% identity
                   (AC005508) Highly similar to cullin 3 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   204651
Seq. ID
                   LIB3083-064-Q1-L1-E4
                   BLASTX
Method
                   g2129552
NCBI GI
BLAST score
                   382
```

6.0e-37 E value 90 Match length 81 % identity

NCBI Description calcium-dependent protein kinase 19 - Arabidopsis thaliana

NCBI Description

Seq. No.

204657



## (fragment)

```
204652
Seq. No.
                   LIB3083-064-Q1-L1-E6
Seq. ID
                   BLASTX
Method
                   g3068705
NCBI GI
BLAST score
                   192
                   1.0e-14
E value
                   92
Match length
                   45
% identity
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204653
                   LIB3083-064-Q1-L1-E7
Seq. ID
                   BLASTX
Method
                   q4512667
NCBI GI
                   596
BLAST score
                   4.0e-62
E value
Match length
                   122
                   89
% identity
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                   204654
Seq. No.
Seq. ID
                   LIB3083-064-Q1-L1-E8
                   BLASTX
Method
                   q1771162
NCBI GI
BLAST score
                   494
                   4.0e-50
E value
Match length
                   124
% identity
                   (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                   >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
                   204655
Seq. No.
                   LIB3083-064-Q1-L1-F1
Seq. ID
Method
                   BLASTX
                   g586076
NCBI GI
BLAST score
                   584
                   1.0e-60
E value
                   107
Match length
                   98
% identity
                   TUBULIN BETA-1 CHAIN >gi_486734 pir S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                   tubulin 1 [Lupinus albus]
Seq. No.
                   204656
                   LIB3083-064-Q1-L1-F10
Seq. ID
                   {\tt BLASTX}
Method
                   g2982303
NCBI GI
                   296
BLAST score
                   3.0e-27
E value
                   77
Match length
                   75
 % identity
```

27959

(AF051236) hypothetical protein [Picea mariana]



LIB3083-064-Q1-L1-F2 Seq. ID Method BLASTX g3204103 NCBI GI 314 BLAST score 4.0e-29 E value 108 Match length % identity (AJ006761) hypothetical protein [Cicer arietinum] NCBI Description 204658 Seq. No. LIB3083-064-Q1-L1-F4 Seq. ID Method BLASTX NCBI GI q4539002 BLAST score 228 7.0e-19 E value 125 Match length 45 % identity (AL049481) putative protein [Arabidopsis thaliana] NCBI Description 204659 Seq. No. LIB3083-064-Q1-L1-F6 Seq. ID BLASTX Method q4512659 NCBI GI BLAST score 345 1.0e-32 E value 123 Match length 57 % identity (AC006931) putative protein kinase [Arabidopsis thaliana] NCBI Description >gi\_4544465\_gb\_AAD22372.1\_AC006580\_4 (AC006580) putative protein kinase [Arabidopsis thaliana] 204660 Seq. No. LIB3083-064-Q1-L1-F7 Seq. ID Method BLASTX q3420057 NCBI GI BLAST score 429 E value 2.0e-42 121 Match length % identity (AC004680) putative ABC transporter [Arabidopsis thaliana] NCBI Description 204661 Seq. No. LIB3083-064-Q1-L1-F8 Seq. ID Method BLASTX q4510373 NCBI GI 259 BLAST score E value 1.0e-22 Match length 103 % identity 53 (AC007017) putative harpin-induced protein [Arabidopsis NCBI Description thaliana] 204662 Seq. No. LIB3083-064-Q1-L1-G11 Seq. ID Method BLASTX

27960

g4325370

161

NCBI GI BLAST score

NCBI Description



```
7.0e-15
E value
                   59
Match length
                   73
% identity
                   (AF128396) similar to human phosphotyrosyl phosphatase
NCBI Description
                   activator PTPA (GB:X73478) [Arabidopsis thaliana]
Seq. No.
                   204663
                  LIB3083-064-Q1-L1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885334
                   370
BLAST score
E value
                   2.0e-37
Match length
                   117
                   74
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
                   204664
Seq. No.
                   LIB3083-064-Q1-L1-G7
Seq. ID
Method
                   BLASTX
                   q3878134
NCBI GI
                   219
BLAST score
E value
                   7.0e-18
Match length
                   75
                   49
% identity
                   (Z68218) K01H12.1 [Caenorhabditis elegans]
NCBI Description
                   204665
Seq. No.
                   LIB3083-064-Q1-L1-G9
Seq. ID
Method
                   BLASTX
                   g4325370
NCBI GI
                   265
BLAST score
E value
                   4.0e-23
Match length
                   63
                   79
% identity
                   (AF128396) similar to human phosphotyrosyl phosphatase
NCBI Description
                   activator PTPA (GB:X73478) [Arabidopsis thaliana]
                   204666
Seq. No.
                   LIB3083-064-Q1-L1-H1
Seq. ID
                   BLASTX
Method
                   g4510381
NCBI GI
                   373
BLAST score
                   5.0e-36
E value
                   91
Match length
                   82
% identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204667
Seq. No.
                   LIB3083-064-Q1-L1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1644427
                   398
BLAST score
                   7.0e-39
E value
Match length
                   108
                   75
% identity
```

27961

(U74610) glyoxalase II [Arabidopsis thaliana]



```
204668
Seq. No.
                  LIB3083-064-Q1-L1-H4
Seq. ID
                  BLASTX
Method
                  q2129473
NCBI GI
BLAST score
                  184
                  9.0e-14
E value
Match length
                  72
                  50
% identity
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                  204669
Seq. No.
                  LIB3083-064-Q1-L1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539452
                  267
BLAST score
                  9.0e-24
E value
                   68
Match length
                   71
% identity
                  (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                   204670
Seq. No.
                  LIB3083-064-Q1-L1-H6
Seq. ID
                   BLASTX
Method
                   g1477428
NCBI GI
                   232
BLAST score
                   7.0e-20
E value
                   47
Match length
                   94
% identity
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
                   204671
Seq. No.
                   LIB3083-064-Q1-L1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1706956
                   517
BLAST score
                   7.0e-53
E value
Match length
                   105
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204672
Seq. No.
                   LIB3083-065-Q1-L1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3413511
BLAST score
                   499
                   1.0e-50
E value
Match length
                   110
 % identity
                   (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
                   oleracea]
                   204673
 Seq. No.
                   LIB3083-065-Q1-L1-A9
 Seq. ID
```

BLASTX

Method



```
g1732511
NCBI GI
                  484
BLAST score
                  7.0e-49
E value
                  105
Match length
                  85
% identity
                  (U62742) Ran binding protein 1 homolog [Arabidopsis
NCBI Description
                  thaliana]
                  204674
Seq. No.
                  LIB3083-065-Q1-L1-B1
Seq. ID
                  BLASTX
Method
                  g4140398
NCBI GI
                  296
BLAST score
                  9.0e-27
E value
                  87
Match length
% identity
                   63
NCBI Description (AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]
                   204675
Seq. No.
                   LIB3083-065-Q1-L1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4580471
BLAST score
                   427
E value
                   3.0e-42
Match length
                   115
                   66
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204676
Seq. No.
                   LIB3083-065-Q1-L1-B12
Seq. ID
                   BLASTX
Method
                   q3334346
NCBI GI
BLAST score
                   269
                   7.0e-24
E value
                   63
Match length
                   83
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
NCBI Description
                   >gi_2852445_dbj_BAA24697_ (AB003378) SUI1 homolog [Salix
                   bakko]
                   204677
Seq. No.
                   LIB3083-065-Q1-L1-B2
Seq. ID
                   BLASTX
Method
                   g3882081
NCBI GI
BLAST score
                   669
                   2.0e-70
E value
                   139
Match length
                   38
% identity
                  (AJ012552) polyubiquitin [Vicia faba]
NCBI Description
                   204678
Seq. No.
Seq. ID
                   LIB3083-065-Q1-L1-B3
                   BLASTX
Method
                   g3142294
NCBI GI
BLAST score
                   565
```

2.0e-58

116

. E value

Match length



```
% identity
                  (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                  gb U37354 from S. pombe. ESTs gb T41979, gb N37284 and
                  gb N37529 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  204679
                  LIB3083-065-Q1-L1-B4
Seq. ID
Method
                  BLASTX
                  g3650032
NCBI GI
BLAST score
                  237
                  7.0e-20
E value
Match length
                  49
% identity
                  73
                  (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                  [Arabidopsis thaliana]
                  204680
Seq. No.
Seq. ID
                  LIB3083-065-Q1-L1-B5
Method
                  BLASTX
NCBI GI
                  g135496
BLAST score
                  232
E value
                  2.0e-19
Match length
                  44
% identity
                  98
                  TUBULIN BETA CHAIN >gi 85377_pir__S02327 tubulin beta chain
NCBI Description
                  - sea urchin (Strongylocentrotus purpuratus) (fragment)
                  >gi 1335670 emb CAA30385 (X07502) beta-tubulin (AA
                  156-447) [Strongylocentrotus purpuratus]
Seq. No.
                  204681
Seq. ID
                  LIB3083-065-Q1-L1-B6
Method
                  BLASTX
NCBI GI
                  g4417283
                  233
BLAST score
                  2.0e-19
E value
                  104
Match length
% identity
                  42
                  (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                  204682
Seq. No.
Seq. ID
                  LIB3083-065-Q1-L1-B7
                  BLASTX
Method
                  g2895866
NCBI GI
BLAST score
                  202
                  8.0e-16
E value
                  36
Match length
% identity
                   (AF045770) methylmalonate semi-aldehyde dehydrogenase
NCBI Description
```

[Oryza sativa]

Seq. No. 204683

Seq. ID LIB3083-065-Q1-L1-C10

Method BLASTX
NCBI GI g549986
BLAST score 498
E value 2.0e-50
Match length 115

```
% identity
                  (U13149) possible apospory-associated protein [Pennisetum
NCBI Description
                  ciliare]
                  204684
Seq. No.
Seq. ID
                  LIB3083-065-Q1-L1-C4
                  BLASTX
Method
NCBI GI
                  g4314378
BLAST score
                  159
                  9.0e-11
E value
                  47
Match length
                  57
% identity
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                  204685
Seq. No.
Seq. ID
                  LIB3083-065-Q1-L1-C5
Method
                  BLASTX
                  g1076334
NCBI GI
BLAST score
                  140
                  1.0e-08
E value
                  95
Match length
% identity
                   41
NCBI Description
                  hypothetical protein HYP1 - Arabidopsis thaliana
                  >qi 499168 emb CAA56145 (X79707) HYP1 [Arabidopsis
                   thaliana]
                   204686
Seq. No.
Seq. ID
                  LIB3083-065-Q1-L1-C6
                  BLASTX
Method
NCBI GI
                  g4090257
BLAST score
                   416
E value
                   7.0e-41
Match length
                   83
                   93
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   204687
Seq. No.
                  LIB3083-065-Q1-L1-D1
Seq. ID
                   BLASTX
Method
                   g2879811
NCBI GI
                   502
BLAST score
E value
                   6.0e-51
                   101
Match length
                   94
% identity
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
                   204688
Seq. No.
Seq. ID
                   LIB3083-065-Q1-L1-D10
Method
                   BLASTX
                   g398849
NCBI GI
                   440
BLAST score
E value
                   7.0e-44
                   93
Match length
```

(X74656) beta-5 tubulin [Zea mays]

87

204689

% identity

Seq. No.

NCBI Description

Seq. ID



```
LIB3083-065-Q1-L1-D11
Seq. ID
Method
                    BLASTX
                    q4008159
NCBI GI
                    462
BLAST score
                    3.0e-46
E value
Match length
                    102
% identity
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
                    204690
Seq. No.
                    LIB3083-065-Q1-L1-D12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3212870
                    175
BLAST score
                    1.0e-12
E value
                     50
Match length
                     70
% identity
                    (AC004005) putative N-myristoyltransferase [Arabidopsis
NCBI Description
                     thaliana]
                     204691
Seq. No.
                     LIB3083-065-Q1-L1-D3
Seq. ID
                     BLASTX
Method
NCBI GI
                     q2493495
                     237
BLAST score
                     7.0e-20
E value
                     62
Match length
                     71
% identity
                     SERINE CARBOXYPEPTIDASE-LIKE >gi 2129878_pir__S72370
NCBI Description
                     carboxypeptidase - garden pea (fragment)
                     \label{eq:carboxypeptidase} $$ \Rightarrow i 1089904 = mb CAA92216 (Z68130) $$ carboxypeptidase [Pisum sativum] $$ \Rightarrow i 1587217 = prf 2206338A Ser carboxypeptidase $$ $$
                     [Pisum sativum]
                     204692
Seq. No.
                     LIB3083-065-Q1-L1-D4
Seq. ID
Method
                     BLASTX
                     q3885336
NCBI GI
                     263
BLAST score
E value
                     6.0e-23
                     136
Match length
 % identity
                     (AC005623) receptor-like protein kinase [Arabidopsis
NCBI Description
                     thaliana]
                     204693
 Seq. No.
                     LIB3083-065-Q1-L1-D7
 Seq. ID
 Method
                     BLASTX
                     g2342719
 NCBI GI
 BLAST score
                     220
_E value
                     7.0e-18
                     136
 Match length
 % identity
                    (AC002341) SF16 protein isolog [Arabidopsis thaliana]
 NCBI Description
                     204694
 Seq. No.
```

27966

LIB3083-065-Q1-L1-D8



Method BLASTX g3834307 NCBI GI 298 BLAST score 5.0e-27 E value 87 Match length 68 % identity (AC005679) Strong similarity to gene T10I14.120 gi\_2832679 NCBI Description putative protein from Arabidopsis thaliana BAC gb AL021712. ESTs gb N65887 and gb N65627 come from this gene. [Arabidopsis thaliana] Seq. No. 204695 LIB3083-065-Q1-L1-E1

Seq. ID LIB3083-065-Q1-L1-E1
Method BLASTX
NCBI GI g2500047
BLAST score 580
E value 4.0e-60
Match length 125
% identity 84

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi\_534916\_emb\_CAA85362\_ (Z36894) soluble inorganic pyrophosphatase [Solanum

tuberosum]

Seq. No. 204696 Seq. ID LIB3083-065-Q1-L1-E11

Method BLASTX
NCBI GI g3377797
BLAST score 245
E value 2.0e-21
Match length 56
% identity 86

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA

H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

-R90691 [Ara

Seq. No. 204697

Seq. ID LIB3083-065-Q1-L1-E12

Method BLASTX
NCBI GI g2887459
BLAST score 612
E value 6.0e-64
Match length 126
% identity 98

NCBI Description (AB010922) actin [Cucumis sativus]

Seq. No. 204698

Seq. ID LIB3083-065-Q1-L1-E2

Method BLASTX
NCBI GI g4508079
BLAST score 158
E value 1.0e-10
Match length 35
% identity 69

NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

```
204699
Seq. No.
Seq. ID
                  LIB3083-065-Q1-L1-E3
Method
                  BLASTX
NCBI GI
                  g1813329
BLAST score
                  150
E value
                  1.0e-09
                  78
Match length
                  47
% identity
NCBI Description
                  (AB000637) HMG-1 [Canavalia gladiata]
Seq. No.
                  204700
                  LIB3083-065-Q1-L1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2146739
BLAST score
                  581
E value
                  3.0e-60
Match length
                  136
% identity
                  hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.
                  204701
Seq. ID
                  LIB3083-065-Q1-L1-E6
Method
                  BLASTX
NCBI GI
                  q4193382
BLAST score
                   409
E value
                   5.0e-40
Match length
                  81
% identity
                   90
                   (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                  >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                   thaliana]
                   204702
Seq. No.
                  LIB3083-065-Q1-L1-E8
Seq. ID
                  BLASTX
Method
                   q1076529
NCBI GI
BLAST score
                   265
                   1.0e-47
E value
                   137
Match length
                   70
% identity
                  heat shock protein HSP71.2 - garden pea >gi_562006 (U08848)
NCBI Description
                   PsHSP71.2 [Pisum sativum] >gi_1771479_emb_CAA67867_
                   (X99515) heat shock protein hsp70 [Pisum sativum]
                   204703
Seq. No.
Seq. ID
                   LIB3083-065-Q1-L1-F10
Method
                   BLASTN
                   g2829205
NCBI GI
BLAST score
                   301
                   1.0e-169
E value
Match length
                   349
                   75
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
```



```
204704
Seq. No.
                  LIB3083-065-Q1-L1-F11
Seq. ID
                  BLASTX
Method
                  g2267567
NCBI GI
                  405
BLAST score
E value
                  1.0e-39
Match length
                  89
                  87
% identity
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
                   204705
Seq. No.
                   LIB3083-065-Q1-L1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4309759
BLAST score
                   327
E value
                   2.0e-30
                   107
Match length
                   62
% identity
                   (AC006217) unknown protein with Src homology 3 (SH3) domain
NCBI Description
                   profile (PDOC50002) [Arabidopsis thaliana]
Seq. No.
                   204706
                   LIB3083-065-Q1-L1-F2
Seq. ID
                   BLASTX
Method
                   q586076
NCBI GI
BLAST score
                   600
E value
                   2.0e-62
Match length
                   120
% identity
                   TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                   tubulin 1 [Lupinus albus]
                   204707
Seq. No.
                   LIB3083-065-Q1-L1-F4
Seq. ID
                   BLASTX
Method
                   g2244734
NCBI GI
                   346
BLAST score
                   4.0e-33
E value
                   76
Match length
                   91
% identity
                   (D88414) actin [Gossypium hirsutum]
NCBI Description
                   204708
Seq. No.
                   LIB3083-065-Q1-L1-F6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1518539
                   58
BLAST score
                   7.0e-24
E value
                   142
Match length
                   85
% identity
                   Glycine max UDP-glucose dehydrogenase mRNA, complete cds
NCBI Description
```

204709

LIB3083-065-Q1-L1-F8

Seq. No.

Seq. ID

BLAST score

E value

205 1.0e-111



```
BLASTX
Method
                  g2827699
NCBI GI
                  141
BLAST score
                   9.0e-09
E value
                   139
Match length
                   35
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   204710
Seq. No.
                   LIB3083-065-Q1-L1-F9
Seq. ID
                   BLASTX
Method
                   g4115377
NCBI GI
                   301
BLAST score
                   1.0e-27
E value
Match length
                   87
                   69
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204711
Seq. No.
                   LIB3083-065-Q1-L1-G1
Seq. ID
                   BLASTX
Method
                   g862640
NCBI GI
                   496
BLAST score
                   3.0e-50
E value
                   107
Match length
                   91
% identity
                   (U20182) MADS-box protein AGL11 [Arabidopsis thaliana]
NCBI Description
                   >gi_4538999_emb_CAB39620.1_ (AL049481) MADS-box protein
                   AGL11 [Arabidopsis thaliana]
                   204712
Seq. No.
                   LIB3083-065-Q1-L1-G10
Seq. ID
                   BLASTX
Method
                   g4309767
NCBI GI
BLAST score
                   142
                   9.0e-09
E value
                   73
Match length
                   48
% identity
                   (AC006217) putative Athila retroelement ORF1 protein
NCBI Description
                    [Arabidopsis thaliana]
                   204713
 Seq. No.
                   LIB3083-065-Q1-L1-G11
 Seq. ID
                   BLASTN
Method
NCBI GI
                   g1143223
                   96
BLAST score
                   1.0e-46
 E value
                    209
Match length
 % identity
                   Gossypium barbadense FbLate-2 gene, complete cds
 NCBI Description
                    204714
 Seq. No.
                    LIB3083-065-Q1-L1-G12
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g11800
```



275 Match length 96 % identity Tobacco chloroplast spacer region between the 16S and 23S NCBI Description rRNAs. Also contains two transfer RNAs specific for Ile and Ala which are interrupted by introns Seq. No. 204715 LIB3083-065-Q1-L1-G2 Seq. ID Method BLASTX NCBI GI q2811025 BLAST score 526 E value 9.0e-54 Match length 141 67 % identity ASPARTIC PROTEINASE PRECURSOR >gi\_1944181\_dbj\_BAA19607\_ NCBI Description (AB002695) aspartic endopeptidase [Cucurbita pepo] Seq. No. 204716 LIB3083-065-Q1-L1-G4 Seq. ID Method BLASTX g2842480 NCBI GI 517 BLAST score E value 9.0e-53 Match length 129 % identity (ALO21749) ADP, ATP carrier-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 204717 LIB3083-065-Q1-L1-G7 Seq. ID Method BLASTX NCBI GI g2642448 BLAST score 271 6.0e-24 E value Match length 128 % identity 15 (AC002391) hypothetical protein [Arabidopsis thaliana] NCBI Description >qi 3169187 (AC004401) hypothetical protein [Arabidopsis thaliana] 204718 Seq. No. LIB3083-065-Q1-L1-H1 Seq. ID BLASTX Method NCBI GI g2501850 678 BLAST score 1.0e-71 E value 136 Match length % identity 93 (AF012823) GDP dissociation inhibitor [Nicotiana tabacum] NCBI Description

Seq. ID LIB3083-065-Q1-L1-H2

204719

Method BLASTX
NCBI GI g3927825
BLAST score 396
E value 2.0e-38
Match length 107

Seq. No.



```
% identity
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   204720
Seq. No.
                   LIB3083-065-Q1-L1-H5
Seq. ID
Method
                   BLASTX
                   g3559805
NCBI GI
                   486
BLAST score
E value
                   4.0e-49
Match length
                   139
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   204721
Seq. No.
                   LIB3083-065-Q1-L1-H7
Seq. ID
                   BLASTX
Method
                   q2244734
NCBI GI
                   683
BLAST score
                   3.0e-72
E value
                   135
Match length
                   99
% identity
                   (D88414) actin [Gossypium hirsutum]
NCBI Description
                   204722
Seq. No.
                   LIB3083-065-Q1-L1-H8
Seq. ID
                   BLASTX
Method
                   q1702983
NCBI GI
                   332
BLAST score
                   5.0e-31
E value
                   111
Match length
                   57
% identity
                   AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855_pir__S11850
NCBI Description
                   hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria
                   x ananassa] >gi 927034 (L44142) auxin-repressed protein
                   [Fragaria ananassa]
                   204723
Seq. No.
                   LIB3083-065-Q1-L1-H9
Seq. ID
                   BLASTX
Method
                   g629651
NCBI GI
                   509
BLAST score
E value
                    9.0e-52
                    135
Match length
% identity
                    69
                   cysteine proteinase - spring vetch >gi_2129904_pir__S51817
NCBI Description
                    cysteine proteinase (EC 3.4.22.-) precursor - spring vetch
                    >qi 535473 emb CAA53377 (X75749) cysteine protease [Vicia
                    sativa]
```

Seq. No. 204724

Seq. ID LIB3083-066-Q1-L1-A1

Method BLASTX NCBI GI g82263 BLAST score 306

27972

÷.



```
4.0e-28
E value
                  80
Match length
                  76
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)3II) - potato
                  204725
Seq. No.
                  LIB3083-066-Q1-L1-A10
Seq. ID
                  BLASTX
Method
                   g2500354
NCBI GI
                   637
BLAST score
E value
                   7.0e-67
                   124
Match length
                   95
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   204726
                   LIB3083-066-Q1-L1-A3
Seq. ID
Method
                   BLASTX
                   q4115918
NCBI GI
BLAST score
                   186
E value
                   6.0e-14
Match length
                   45
                   80
% identity
                   (AF118222) similar to nascent polypeptide associated
NCBI Description
                   complex alpha chain [Arabidopsis thaliana]
                   204727
Seq. No.
                   LIB3083-066-Q1-L1-A5
Seq. ID
                   BLASTX
Method
                   g4204259
NCBI GI
BLAST score
                   219
                   9.0e-18
E value
                   98
Match length
                   46
% identity
                   (AC005223) 18074 [Arabidopsis thaliana]
NCBI Description
                   204728
Seq. No.
                   LIB3083-066-Q1-L1-A8
Seq. ID
                   BLASTX
Method
                   g116923
NCBI GI
                   368
BLAST score
                   2.0e-35
E value
                   95
Match length
                   69
 % identity
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi 111414 pir S13520 beta-COP protein - rat
                   >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                   norvegicus]
                   204729
 Seq. No.
                   LIB3083-066-Q1-L1-A9
 Seq. ID
```

BLASTX

166 1.0e-11

g232033

Method

NCBI GI BLAST score

E value



```
52
Match length
                  63
% identity
                  ELONGATION FACTOR 1 BETA' >gi 479830 pir__S35501
NCBI Description
                  translation elongation factor eEF-1 beta chain - wheat
                  >gi 218341 dbj BAA02436_ (D13147) elongation factor 1 beta'
                  [Triticum aestivum]
                  204730
Seq. No.
                  LIB3083-066-Q1-L1-B1
Seq. ID
Method
                  BLASTX
                  g1843527
NCBI GI
BLAST score
                  443
                  4.0e-44
E value
                  115
Match length
                  77
% identity
                  (U73747) annexin [Gossypium hirsutum]
NCBI Description
Seq. No.
                  204731
                  LIB3083-066-Q1-L1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829899
                  297
BLAST score
E value
                   7.0e-27
Match length
                   123
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp_AJ001449_2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
                   204732
Seq. No.
                   LIB3083-066-Q1-L1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g974294
                   331
BLAST score
E value
                   5.0e-31
Match length
                   109
% identity
                   60
                   (U31309) LP6 [Pinus taeda]
NCBI Description
                   204733
Seq. No.
                   LIB3083-066-Q1-L1-B5
Seq. ID
                   BLASTX
Method
                   g416758
NCBI GI
                   268
BLAST score
                   1.0e-23
E value
                   105
Match length
% identity
                   51
                   SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
NCBI Description
                   carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
```

Seq. No. 204734

Seq. ID LIB3083-066-Q1-L1-B6

Method BLASTN NCBI GI g167322 BLAST score 256



1.0e-142 E value 283 Match length 97 % identity Gossypium hirsutum ORF with two tentative start codons, NCBI Description complete cds. >gi\_1598702\_gb\_I18347\_I18347 Sequence 2 from patent US 5495070 >gi 1601688 gb 121334 I21334 Sequence 2 from patent US 5521078 >gi\_2082615\_gb\_I40323\_I40323 Sequence 2 from patent US  $\overline{5}620882$ >gi\_2086583\_gb\_I36758\_I36758 Sequence 2 from patent US 5608148 >gi 2087591 gb I35740 I35740 Sequence 2 from patent US 204735 Seq. No. LIB3083-066-Q1-L1-B8 Seq. ID Method BLASTX NCBI GI q1171866 BLAST score 297 E value 6.0e-27 Match length 116 54 % identity NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR NCBI Description (COMPLEX I-20KD) (CI-20KD) >gi\_629601\_pir\_\_S48826 NADH dehydrogenase (ubiquinone)  $(EC_{1.6.5.3})$  chain PSST - wild cabbage >gi 562282 emb CAA57725 (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea] 204736 Seq. No. LIB3083-066-Q1-L1-C1 Seq. ID BLASTX Method NCBI GI g2511693 BLAST score 401 4.0e-39 E value Match length 139 57 % identity (Z99954) cysteine proteinase precursor [Phaseolus vulgaris] NCBI Description 204737 Seq. No. LIB3083-066-Q1-L1-C4 Seq. ID Method BLASTX g2996096 NCBI GI BLAST score 675 3.0e-71 E value 132 Match length 97 % identity (AF030517) translation elongation factor-1 alpha; EF-1 NCBI Description alpha [Oryza sativa] 204738 Seq. No. LIB3083-066-Q1-L1-C5 Seq. ID BLASTX Method g1197461 NCBI GI

Method BLASTX
NCBI GI g1197461
BLAST score 740
E value 7.0e-79
Match length 141
% identity 96

NCBI Description (X78819) casein kinase I [Arabidopsis thaliana]



```
204739
Seq. No.
                  LIB3083-066-Q1-L1-C6
Seq. ID
                  BLASTX
Method
                  g2865523
NCBI GI
                  205
BLAST score
                  4.0e-16
E value
Match length
                  68
% identity
                  (AF044584) cold regulated LTCOR18 [Lavatera thuringiaca] ...
NCBI Description
Seq. No.
Seq. ID
                  LIB3083-066-Q1-L1-C7
Method
                  BLASTX
                  g2384671
NCBI GI
                   340
BLAST score
                   6.0e-32
E value
                   70
Match length
                   94
% identity
                   (AF012657) putative potassium transporter AtKT2p
NCBI Description
                   [Arabidopsis thaliana]
                   204741
Seq. No.
                   LIB3083-066-Q1-L1-D11
Seq. ID
Method
                   BLASTX
                   q2244734
NCBI GI
BLAST score
                   662
                   9.0e-70
E value
                   132
Match length
% identity
                   98
                  (D88414) actin [Gossypium hirsutum]
NCBI Description
                   204742
Seq. No.
                   LIB3083-066-Q1-L1-D2
Seq. ID
Method
                   BLASTX
                   g643469
NCBI GI
BLAST score
                   298
                   3.0e-27
E value
                   102
Match length
% identity
                   (U19886) unknown [Lycopersicon esculentum]
NCBI Description
                   204743
Seq. No.
                   LIB3083-066-Q1-L1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129770
                   575
BLAST score
                   2.0e-59
E value
Match length
                   121
% identity
                   81
                   xyloglucan endotransglycosylase-related protein XTR-2 -
NCBI Description
                   Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
                   >gi 2154611 dbj BAA20290 (D63510) endoxyloglucan
                   transferase related protein [Arabidopsis thaliana]
```

Seq. ID LIB3083-066-Q1-L1-D6



```
BLASTX
Method
                  g3024126
NCBI GI
                  741
BLAST score
E value
                   6.0e-79
                  144
Match length
                   96
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
                   204745
Seq. No.
                  LIB3083-066-Q1-L1-D7
Seq. ID
                  BLASTX
Method
                   g4539301
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
                   105
Match length
% identity
                   43
                   (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                   thaliana]
                   204746
Seq. No.
                   LIB3083-066-Q1-L1-E10
Seq. ID
                   BLASTX
Method
                   q116343
NCBI GI
BLAST score
                   266
                   2.0e-23
E value
                   119
Match length
                   42
% identity
NCBI Description BASIC ENDOCHITINASE PRECURSOR
Seq. No.
                   204747
Seq. ID
                   LIB3083-066-Q1-L1-E11
                   BLASTX
Method
                   q4006858
NCBI GI
BLAST score
                   352
                   2.0e-33
E value
                   118
Match length
                   55
% identity
                   (Z99707) cold acclimation protein homolog [Arabidopsis
NCBI Description
                   thaliana]
                   204748
Seq. No.
Seq. ID
                   LIB3083-066-Q1-L1-E12
Method
                   BLASTX
                   g1477428
NCBI GI
BLAST score
                   222
                   3.0e-18
E value
                   49
Match length
                   86
% identity
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
```

Seq. ID LIB3083-066-Q1-L1-E3

Method BLASTX NCBI GI g2129499



```
BLAST score
                  363
E value
                  2.0e-51
                  124
Match length
                  73
% identity
                  fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  204750
Seq. No.
                  LIB3083-066-Q1-L1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1174498
BLAST score
                  389
E value
                  9.0e-38
Match length
                  93
% identity
                  SYNAPTOBREVIN-RELATED PROTEIN >gi 600710 (M90418) formerly
NCBI Description
                  called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                  204751 -
Seq. No.
                  LIB3083-066-Q1-L1-E8
Seq. ID
Method
                  BLASTX
                  q1749752
NCBI GI
BLAST score
                  284
                  2.0e-25
E value
Match length
                  125
                   42
% identity
                   (D89272) similar to Saccharomyces cerevisiae T-complex
NCBI Description
                  protein 1, theta subunit, SWISS-PROT Accession Number P47079
                   [Schizosaccharomyces pombe]
Seq. No.
                   204752
                   LIB3083-066-Q1-L1-F11
Seq. ID
Method
                   BLASTX
                   q1658197
NCBI GI
BLAST score
                   614
E value
                   5.0e-64
                   143
Match length
% identity
                   (U74630) calreticulin [Ricinus communis] >gi_1763297
NCBI Description
                   (U74631) calreticulin [Ricinus communis]
                   204753
Seq. No.
                   LIB3083-066-Q1-L1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3287688
BLAST score
                   353
                   2.0e-33
E value
Match length
                   86
                   80
% identity
                   (AC003979) Contains similarity to ycf37 gene product
NCBI Description
                   gb_1001425 from Synechocystis sp. genome gb_D63999. ESTs
                   gb_T43026, gb_R64902, gb_Z18169 and gb_N37374 come from
```

Seq. ID LIB3083-066-Q1-L1-F3

this gene. [Arabidopsis thaliana]

BLAST score

E value

167 8.0e-12



```
Method
                   BLASTX
                   g1706958
NCBI GI
                   496
BLAST score
                   2.0e-50
E value
Match length
                   95
                   99
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204755
Seq. No.
Seq. ID
                   LIB3083-066-Q1-L1-F4
Method
                   BLASTX
NCBI GI
                   g4508073
BLAST score
                   422
E value
                   1.0e-41
                   142
Match length
                   58
% identity
                  (AC005882) 43220 [Arabidopsis thaliana]
NCBI Description
                   204756
Seq. No.
                   LIB3083-066-Q1-L1-F6
Seq. ID
Method
                   BLASTX
                   q3894191
NCBI GI
BLAST score
                   274
E value
                   3.0e-24
                   89
Match length
                   58
% identity
                  (AC005662) unknown protein [Arabidopsis thaliana]
NCBI Description
                   204757
Seq. No.
                   LIB3083-066-Q1-L1-F7
Seq. ID
Method
                   BLASTX
                   g836950
NCBI GI
BLAST score
                   166
                   8.0e-12
E value
Match length
                   126
% identity
                   11
                   (U20810) CIP1 [Arabidopsis thaliana]
NCBI Description
                   >qi 1096881 prf 2112355A CIP1 protein [Arabidopsis
                   thaliana]
                   204758
Seq. No.
                   LIB3083-066-Q1-L1-F8
Seq. ID
                   BLASTX
Method
                   g2811025
NCBI GI
                   372
BLAST score
                   7.0e-36
E value
                   107
Match length
                   67
% identity
                   ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607
NCBI Description
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
                   204759
Seq. No.
                   LIB3083-066-Q1-L1-F9
Seq. ID
                   BLASTX
Method
                   g3914467
NCBI GI
```



```
Match length
                  48
% identity
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >qi 1864003 dbj BAA19252_ (AB001422) 21D7 [Nicotiana
                  tabacum]
                  204760
Seq. No.
                  LIB3083-066-Q1-L1-G1
Seq. ID
Method
                  BLASTX
                  g2129950
NCBI GI
BLAST score
                  471
                  2.0e-47
E value
Match length
                  109
% identity
                   84
                  inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) -
NCBI Description
                   common tobacco
                   204761
Seq. No.
                   LIB3083-066-Q1-L1-G11
Seq. ID
                   BLASTX
Method
                   g3096939
NCBI GI
                   268
BLAST score
                   1.0e-23
E value
                   58
Match length
% identity
                   79
                   (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                   204762
Seq. No.
                   LIB3083-066-Q1-L1-G12
Seq. ID
                   BLASTN
Method
                   q3241920
NCBI GI
BLAST score
                   52
                   2.0e-20
E value
Match length
                   235
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAE1, complete sequence [Arabidopsis thaliana]
                   204763
Seq. No.
                   LIB3083-066-Q1-L1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2791276
BLAST score
                   293
E value
                   2.0e-26
Match length
                   81
                   73
 % identity
                   (Z95327) Cleavage Stimulation Factor (CF-1, Polyadenylation
NCBI Description
                   Factor) 64 kD subunit [Homo sapiens]
                   204764
 Seq. No.
                   LIB3083-066-Q1-L1-G3
 Seq. ID
                   BLASTX
 Method
                   g1706956
 NCBI GI
                   248
 BLAST score
```

27980

2.0e-37

108

98

E value

Match length

% identity

Method

NCBI GI

BLASTX

g3935181



```
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
                  204765
Seq. No.
                  LIB3083-066-Q1-L1-G4
Seq. ID
                  BLASTX
Method
                   g3540208
NCBI GI
BLAST score
                   356
                   6.0e-34
E value
                   124
Match length
                   58
% identity
                  (AC004260) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   204766
Seq. No.
                   LIB3083-066-Q1-L1-G5
Seq. ID
                   BLASTX
Method
                   g4493917
NCBI GI
                   142
BLAST score
                   8.0e-09
E value
                   81
Match length
                   35
% identity
                  (Z98547) predicted using hexExon; MAL3P3.21 (PFC0360w),
NCBI Description
                   Hypothetical protein, len: 114 aa [Plasmodium falciparum]
                   204767
Seq. No.
                   LIB3083-066-Q1-L1-G7
Seq. ID
                   BLASTX
Method
                   g4455194
NCBI GI
                   307
BLAST score
                   4.0e-28
E value
                   70
Match length
                   80
% identity
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   204768
Seq. No.
                   LIB3083-066-Q1-L1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3763925
                   404
BLAST score
                   1.0e-39
E value
Match length
                   82
% identity
                   89
                   (AC004450) putative Af10-protein [Arabidopsis thaliana]
NCBI Description
                   204769
Seq. No.
                   LIB3083-066-Q1-L1-H10
Seq. ID
                   BLASTX
Method
                   q3747050
NCBI GI
BLAST score
                   503
E value
                   3.0e-51
                   113
Match length
% identity
                   (AF093540) ribosomal protein L26 [Zea mays]
NCBI Description
                   204770
Seq. No.
                   LIB3083-066-Q1-L1-H12
Seq. ID
```

```
BLAST score
                  612
                  6.0e-64
E value
                  120
Match length
                  92
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                  204771
Seq. No.
                  LIB3083-066-Q1-L1-H2
Seq. ID
                  BLASTX
Method
                  q4455208
NCBI GI
BLAST score
                  601
                  2.0e-62
E value
Match length
                  141
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   204772
Seq. No.
                  LIB3083-066-Q1-L1-H6
Seq. ID
Method
                   BLASTX
                   g3415117
NCBI GI
                   394
BLAST score
                   2.0e-38
E value
                   105
Match length
                   70
% identity
                  (AF081203) villin 3 [Arabidopsis thaliana]
NCBI Description
                   204773
Seq. No.
                   LIB3083-066-Q1-L1-H8
Seq. ID
                   BLASTX
Method
                   g3080390
NCBI GI
                   499
BLAST score
                   1.0e-50
E value
                   123
Match length
                   76
% identity
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                   204774
Seq. No.
                   LIB3083-067-Q1-L1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q135406
                   488
BLAST score
                   2.0e-49
E value
                   110
Match length
                   85
% identity
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir_ A32712 tubulin
NCBI Description
                   alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
                   204775
 Seq. No.
```

LIB3083-067-Q1-L1-B12 Seq. ID

Method BLASTX g1928981 NCBI GI 461 BLAST score E value 3.0e-46104 Match length 89 % identity

```
192651) tonoplast intrinsic protein bobTI
```

```
(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                    oleracea var. botrytis]
                    204776
Seq. No.
                    LIB3083-067-Q1-L1-C12
Seq. ID
Method
                    BLASTN
NCBI GI
                    g871769
                    33
BLAST score
                    4.0e-09
E value
                    258
Match length
% identity
NCBI Description V.unguiculata mRNA for glycin-rich protein
                    204777
Seq. No.
                    LIB3083-067-Q1-L1-D10
Seq. ID
                    BLASTX
Method
                    q464849
NCBI GI
BLAST score
                    518
                    5.0e-53
E value
                    107
Match length
                    97
% identity
                    TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha
NCBI Description
                    chain - almond >gi 20\overline{4}\overline{13} emb \overline{CAA4763}5 (X67162)
                    alpha-tubulin [Prunus dulcis]
                    204778
Seq. No.
                    LIB3083-067-Q1-L1-G9
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2149640
                    393
BLAST score
E value
                    3.0e-38
                    115
Match length
                    63
% identity
                    (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                    204779
Seq. No.
                    LIB3083-067-Q1-L1-H10
Seq. ID
                    BLASTX
Method
                    q4467147
NCBI GI
BLAST score
                    306
E value
                    4.0e-28
Match length
                    108
                    57
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                    204780
Seq. No.
                    LIB3083-067-Q1-L1-H9
Seq. ID
                    BLASTX
Method
NCBI GI
                    g119150
BLAST score
                    631
E value
                    4.0e-66
Match length
                    128
 % identity
                    93
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 NCBI Description
                    >gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
```

27983

1-alpha (AA 1-448) [Lycopersicon esculentum]





```
>gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                  [Lycopersicon esculentum]
                  204781
Seq. No.
                  LIB3083-068-Q1-L1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g729508
                  290
BLAST score
                  4.0e-26
E value
                  90
Match length
                  66
% identity
                  NARINGENIN, 2-OXOGLUTARATE 3-DIOXYGENASE
NCBI Description
                   (FLAVONONE-3-HYDROXYLASE) (FHT) >gi_499020_emb CAA53579_
                   (X75965) flavanone 3-hydroxylase [Vitis vinifera]
                   204782
Seq. No.
                  LIB3083-068-Q1-L1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706958
                   496
BLAST score
                   2.0e-50
E value
                   100
Match length
                   94
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204783
Seq. No.
                   LIB3083-068-Q1-L1-B11
Seq. ID
                   BLASTX
Method
                   q1666106
NCBI GI
BLAST score
                   216
                   1.0e-17
E value
                   96
Match length
                   48
% identity
                   (Z82098) hypothetical protein Rv3553 [Mycobacterium
NCBI Description
                   tuberculosis]
                   204784
Seq. No.
                   LIB3083-068-Q1-L1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2462929
                   185
BLAST score
E value
                   8.0e-14
                   48
Match length
                   67
% identity
                  (Y12295) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                   204785
Seq. No.
                   LIB3083-068-Q1-L1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q135434
BLAST score
                   144
                   4.0e-12
E value
```

Match length 93
% identity 48
NCBI Description TUBULIN ALPHA-1B CHAIN (TUBULIN ALPHA-N CHAIN)

Sq. 84170 pir S02130 tubulin alpha chain - slim

>gi\_84170\_pir\_\_S02130 tubulin alpha chain - slime mold
(Physarum polycephalum) >gi\_1213632\_emb\_CAA28712\_ (X05039)



## alpha-tubulin [Physarum polycephalum]

```
204786
Seq. No.
                  LIB3083-068-Q1-L1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3122673
                   350
BLAST score
                   2.0e-33
E value
                   95
Match length
                  74
% identity
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   204787
Seq. No.
Seq. ID
                   LIB3083-068-Q1-L1-E11
Method
                   BLASTX
NCBI GI
                   g2576255
BLAST score
                   143
                   4.0e-09
E value
                   96
Match length
                   41
% identity
                   (AJ001729) TH65 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204788
                   LIB3083-068-Q1-L1-E9
Seq. ID
                   BLASTX
Method
                   q4090884
NCBI GI
                   242
BLAST score
                   2.0e-20
E value
                   72
Match length
                   68
% identity
                   (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                   synaptobrevin 7B [Arabidopsis thaliana]
Seq. No.
                   204789
                   LIB3083-068-Q1-L1-F11
Seq. ID
                   BLASTX
Method
                   q1483563
NCBI GI
                   463
BLAST score
                   2.0e-46
E value
                   99
Match length
                   85
% identity
                   (X99825) leucine aminopeptidase [Petroselinum crispum]
NCBI Description
                   204790
Seq. No.
                   LIB3083-068-Q1-L1-H12
Seq. ID
                   BLASTX
Method
                   q1706956
NCBI GI
                   145
BLAST score
                   1.0e-09
E value
                   52
Match length
                   54
 % identity
                   (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204791
 Seq. No.
 Seq. ID
                   LIB3083-070-Q1-L1-A10
                   BLASTN
Method
```

```
g1143223
NCBI GI
                  190
BLAST score
                  1.0e-102
E value
                  331
Match length
% identity
                  56
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                  204792
Seq. No.
                  LIB3083-070-Q1-L1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1616613
BLAST score
                   40
                   3.0e-13
E value
                   83
Match length
% identity
                  N.plumbaginifolia mRNA for small GTP-binding protein, clone
NCBI Description
                  Np43GTP
                   204793
Seq. No.
                   LIB3083-070-Q1-L1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3860258
BLAST score
                   459
E value
                   6.0e-46
                   131
Match length
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                   204794
Seq. No.
                   LIB3083-070-Q1-L1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   564
                   5.0e-59
E value
Match length
                   122
% identity
                   10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   204795
Seq. No.
                   LIB3083-070-Q1-L1-C12
Seq. ID
```

Method BLASTX
NCBI GI g3738185
BLAST score 228
E value 2.0e-19
Match length 60
% identity 17

NCBI Description (AL031854) ubi4 - ubiquitin family protein

[Schizosaccharomyces pombe]

Seq. No. 204796

Seq. ID LIB3083-070-Q1-L1-C9

Method BLASTX
NCBI GI g267069
BLAST score 191
E value 8.0e-31
Match length 75
% identity 91



```
TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  204797
Seq. No.
                  LIB3083-070-Q1-L1-D9
Seq. ID
Method ·· *
                  BLASTX
                  q1174592
NCBI GI
BLAST score
                  547
                  3.0e-57
E value
Match length
                  115
% identity
                  96
                  TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                  - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                  sativum]
                  204798
Seq. No.
                  LIB3083-070-Q1-L1-E10
Seq. ID
                  BLASTX
Method
                  g485512
NCBI GI
                  398
BLAST score
E value
                   9.0e-39
Match length
                  103
                  71
% identity
                  salt-associated protein csaA - sweet orange
NCBI Description
                   204799
Seq. No.
                   LIB3083-070-Q1-L1-E11
Seq. ID
Method
                  BLASTX
                   g4206112
NCBI GI
                   303
BLAST score
E value
                   1.0e-27
Match length
                   58
% identity
                   100
                  (AF097662) alpha tubulin [Mesembryanthemum crystallinum]
NCBI Description
                   204800
Seq. No.
                   LIB3083-070-Q1-L1-E12
Seq. ID
                   BLASTN
Method
                   g3046853
NCBI GI
                   67
BLAST score
                   3.0e-29
E value
                   227
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRA19, complete sequence [Arabidopsis thaliana]
                   204801
Seq. No.
                   LIB3083-070-Q1-L1-E9
Seq. ID
                   BLASTX
Method
                   g1709761
NCBI GI
BLAST score
                   598
                   3.0e-62
E value
                   122
Match length
```

27987

NCBI Description PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

96

% identity



COMPLEX 27 KD SUBUNIT) >gi\_1262146\_emb\_CAA65660\_ (X96974) proteasome subunit [Spinacia oleracea]

Seq. No. 204802

Seq. ID LIB3083-070-Q1-L1-F10

Method BLASTX
NCBI GI g1848212
BLAST score 512
E value 4.0e-52
Match length 99

% identity 46 NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana

tabacum]

Seq. No. 204803

Seg. ID LIB3083-070-Q1-L1-F9

Method BLASTX
NCBI GI g4455208
BLAST score 285
E value 1.0e-25
Match length 96
% identity 65

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 204804

Seq. ID LIB3083-070-Q1-L1-G10

Method BLASTX
NCBI GI g125887
BLAST score 169
E value 6.0e-12
Match length 89
% identity 45

NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

>gi\_82092\_pir\_\_S04765 LAT52 protein precursor - tomato
>gi\_295812\_emb\_CAA33854\_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 204805

Seq. ID LIB3083-070-Q1-L1-G9

Method BLASTX
NCBI GI g1362005
BLAST score 230
E value 4.0e-19
Match length 110
% identity 50

NCBI Description secY protein homolog precursor - Arabidopsis thaliana

Seq. No. 204806

Seq. ID LIB3083-070-Q1-L1-H11

Method BLASTX
NCBI GI g1174592
BLAST score 657
E value 4.0e-69
Match length 135
% identity 96

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum



## sativum]

```
204807
Seq. No.
                  LIB3083-070-Q1-L1-H9
Seq. ID
                  BLASTX
Method
                  g731407
NCBI GI
                  241
BLAST score
                  2.0e-20
E value
                  114
Match length
% identity
NCBI Description HYPOTHETICAL 61.3 KD PROTEIN IN URA3-MMS21 INTERGENIC
                  REGION >gi_1077600_pir__S50439 hypothetical protein YEL020c
                  - yeast (Saccharomyces cerevisiae) >gi_602387 (U18530)
                  Yel020cp [Saccharomyces cerevisiae]
                  204808
Seq. No.
                  LIB3083-071-Q1-L1-A10
Seq. ID
                  BLASTX
Method
                  g4098244
NCBI GI
                  498
BLAST score
                  1.0e-50
E value
                  117
Match length
                  82
% identity
NCBI Description (U76409) homeobox 1 protein [Lycopersicon esculentum]
                  204809
Seq. No.
                  LIB3083-071-Q1-L1-A11
Seq. ID
                  BLASTX
Method
                  g421941
NCBI GI
                  413
BLAST score
                  1.0e-40
E value
Match length
                  90
                  88
% identity
                  GTP-binding protein, ras-related - common tobacco
NCBI Description
                  >qi 296878 emb CAA50609 (X71609) ras-related GTP-binding
                  protein [Nicotiana tabacum]
                   204810
Seq. No.
                  LIB3083-071-Q1-L1-A12
Seq. ID
                   BLASTX
Method
                   g1084335
NCBI GI
BLAST score
                   414
                   9.0e-41
E value
                   89
Match length
                   83
% identity
                  calcium-dependent protein kinase (EC 2.7.1.-) 2 -
NCBI Description
                   Arabidopsis thaliana >gi 604881_dbj_BAA04830_ (D21806)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
                   204811
Seq. No.
Seq. ID
                   LIB3083-071-Q1-L1-A4
                   BLASTX
Method
                   q1171978
NCBI GI
                   405
BLAST score
```

27989

9.0e-40

108

E value Match length

% identity



POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) NCBI Description (PABP 2) >gi\_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi\_2911051\_emb\_CAA17561\_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana] Seq. No. 204812

LIB3083-071-Q1-L1-A5 Seq. ID BLASTX Method NCBI GI q267082 595 BLAST score 6.0e-62 E value 112 Match length 97

% identity TUBULIN BETA-8 CHAIN >gi\_320189\_pir\_\_JQ1592 tubulin beta-8 NCBI Description chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

204813 Seq. No.

Seq. ID LIB3083-071-Q1-L1-B2

Method BLASTX g2160191 NCBI GI 584 BLAST score 1.0e-60 E value 111 Match length % identity

(AC000132) Identical to A. thaliana AtK-1 (gb X79279). NCBI Description

[Arabidopsis thaliana]

204814 Seq. No.

Seq. ID LIB3083-071-Q1-L1-B3

Method BLASTX q2828147 NCBI GI 181 BLAST score 2.0e-13 E value 56 Match length 62 % identity

(AF042384) BC-2 protein [Homo sapiens] NCBI Description

204815 Seq. No.

LIB3083-071-Q1-L1-B5 Seq. ID

Method BLASTX q4512699 NCBI GI BLAST score 453 2.0e-45 E value Match length 111 70 % identity

(AC006569) putative NADH-ubiquinone oxireductase NCBI Description

[Arabidopsis thaliana]

204816 Seq. No.

LIB3083-071-Q1-L1-B8 Seq. ID

Method BLASTX NCBI GI q3063653 BLAST score 140 1.0e-08 E value Match length 111 % identity 32



```
(AF057356) calcyclin binding protein [Homo sapiens]
NCBI Description
                  >gi 4200224 emb CAA22910 (AL035305) hypothetical protein
                   [Homo sapiens]
                   204817
Seq. No.
                  LIB3083-071-Q1-L1-B9
Seq. ID
                  BLASTX
Method
                   g1717952
NCBI GI
                   143
BLAST score
                   5.0e-09
E value
                   30
Match length
                   87
% identity
                   UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 4
NCBI Description
                   PRECURSOR (RIESKE IRON-SULFUR PROTEIN 4) (RISP4) >gi_530054
                   (L16812) Rieske iron-sulfur protein [Nicotiana tabacum]
                   204818
Seq. No.
                   LIB3083-071-Q1-L1-C1
Seq. ID
                   BLASTX
Method
                   g3080435
NCBI GI
BLAST score
                   524
                   1.0e-53
E value
                   119
Match length
                   84
% identity
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   204819
Seq. No.
                   LIB3083-071-Q1-L1-C10
Seq. ID
                   BLASTX
Method
                   g1524370
NCBI GI
BLAST score
                   342
E value
                   3.0e - 32
                   84
Match length
                   76
 % identity
                   (X92491) TOM20 [Solanum tuberosum]
NCBI Description
                   204820
 Seq. No.
 Seq. ID
                   LIB3083-071-Q1-L1-C11
                   BLASTX
Method
                   q2696804
NCBI GI
 BLAST score
                   164
                   1.0e-11
 E value
                   38
 Match length
                   68
 % identity
                   (AB009665) water channel protein [Oryza sativa]
 NCBI Description
                   204821
 Seq. No.
 Seq. ID
                   LIB3083-071-Q1-L1-C12
                   BLASTX
 Method
                   g1912453
 NCBI GI
                   144
 BLAST score
                   4.0e-09
 E value
                   95
 Match length
                   41
 % identity
                   (U49841) v-SNARE [Cricetulus griseus]
 NCBI Description
```

27991

204822

Seq. No.

BLAST score

E value

529 3.0e-54



```
LIB3083-071-Q1-L1-C2
Seq. ID
                  BLASTX
Method
                  g3868758
NCBI GI
                  476
BLAST score
                  5.0e-48
E value
                  91
Match length
                  93
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                  204823
Seq. No.
                  LIB3083-071-Q1-L1-C3
Seq. ID
Method
                  BLASTX
                  q3925703
NCBI GI
                   509
BLAST score
                   6.0e-52
E value
                   113
Match length
                   88
% identity
                   (X95905) 14-3-3 protein [Lycopersicon esculentum]
NCBI Description
                   204824
Seq. No.
                   LIB3083-071-Q1-L1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4234941
                   507
BLAST score
                   1.0e-51
E value
                   117
Match length
                   87
% identity
                   (AF097938) cytosolic phosphoglucomutase [Populus tremula x
NCBI Description
                   Populus tremuloides]
                   204825
Seq. No.
                   LIB3083-071-Q1-L1-D12
Seq. ID
                   BLASTX
Method
                   g3928089
NCBI GI
                   255
BLAST score
                   4.0e-22
E value
                   112
Match length
                   55
% identity
                   (AC005770) putative osr40 [Arabidopsis thaliana]
NCBI Description
                   204826
Seq. No.
                   LIB3083-071-Q1-L1-D2
Seq. ID
                   BLASTN
Method
NCBI GI
                   q525331
                   39
BLAST score
                   1.0e-12
E value
                   47
Match length
                   96
% identity
                   Pisum sativum Alaska alpha-tubulin (TubA1) gene, complete
NCBI Description
                   204827
Seq. No.
Seq. ID
                   LIB3083-071-Q1-L1-D4
                   BLASTX
Method
NCBI GI
                   q3790100
```



```
Match length
                   117
                   85
% identity
                   (AF095520) pyrophosphate-dependent phosphofructokinase beta
NCBI Description
                   subunit [Citrus X paradisi]
                   204828
Seq. No.
Seq. ID
                   LIB3083-071-Q1-L1-E10
                   BLASTX
Method
NCBI GI
                   q3928089
                   274
BLAST score
                   2.0e-24
E value
                   114
Match length
% identity
                  (AC005770) putative osr40 [Arabidopsis thaliana]
NCBI Description
                   204829
Seq. No.
Seq. ID
                   LIB3083-071-Q1-L1-E11
Method
                   BLASTX
                   q2501850
NCBI GI
BLAST score
                   569
                   6.0e-59
E value
                   116
Match length
% identity
                   (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
NCBI Description
                   204830
Seq. No.
Seq. ID
                   LIB3083-071-Q1-L1-E2
                   BLASTX
Method
                   g4427003
NCBI GI
BLAST score
                   259
E value
                   1.0e-22
                   111
Match length
% identity
                   (AF127664) NBD-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   204831
                   LIB3083-071-Q1-L1-E3
Seq. ID
                   BLASTX
Method
                   q3360291
NCBI GI
                   274
BLAST score
E value
                   2.0e-24
                   117
Match length
 % identity
                   55
                   (AF023165) leucine-rich repeat transmembrane protein kinase
NCBI Description
                   2 [Zea mays]
```

Seq. ID LIB3083-071-Q1-L1-E4

BLASTX Method g3928089 NCBI GI BLAST score 274 E value 2.0e-24 Match length 114 58 % identity

(AC005770) putative osr40 [Arabidopsis thaliana] NCBI Description

Seq. No. 204833



LIB3083-071-Q1-L1-F2 Seq. ID BLASTX Method g2653446 NCBI GI 568 BLAST score 8.0e-59 E value 121 Match length 89 % identity (AB009077) proton pyrophosphatase [Vigna radiata] NCBI Description 204834 Seq. No. LIB3083-071-Q1-L1-F3 Seq. ID BLASTX Method q1335862 NCBI GI 539 BLAST score 2.0e-55 E value 118 Match length % identity 88 NCBI Description (U42608) clathrin heavy chain [Glycine max] 204835 Seq. No. LIB3083-071-Q1-L1-F8 Seq. ID Method BLASTX g2529703 NCBI GI 327 BLAST score 1.0e-30 E value 101 Match length 68 % identity (AF000142) class II knotted-like homeodomain protein NCBI Description [Lycopersicon esculentum] 204836 Seq. No. Seq. ID LIB3083-071-Q1-L1-F9 Method BLASTX q2529680 NCBI GI 468 BLAST score 4.0e-47 E value 120 Match length 53 % identity (AC002535) putative protein disulfide-isomerase precursor NCBI Description [Arabidopsis thaliana] Seq. No. 204837 Seq. ID LIB3083-071-Q1-L1-G11 BLASTN Method g2267582 NCBI GI 69 BLAST score 5.0e-31 E value Match length 109 91 % identity Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA, NCBI Description complete cds 204838 Seq. No. LIB3083-071-Q1-L1-G2

Seq. ID

BLASTX Method NCBI GI q4415996 526 BLAST score

```
7.0e-54
E value
                   99
Match length
                   95
% identity
                  (AF059290) beta-tubulin 4 [Eleusine indica]
NCBI Description
                  204839
Seq. No.
Seq. ID
                  LIB3083-071-Q1-L1-G3
                  BLASTX
Method
NCBI GI
                  g2961377
BLAST score
                  148
                  2.0e-09
E value
                   62
Match length
                  16
% identity
                   (AL022141) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                   204840
Seq. No.
                  LIB3083-071-Q1-L1-G6
Seq. ID
                  BLASTX
Method
                   g3334405
NCBI GI
BLAST score
                   469
                   3.0e-47
E value
                  95
Match length
                   99
% identity
NCBI Description
```

VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >qi 2267583 (AF009338) vacuolar H+-ATPase subunit E

[Gossypium hirsutum]

204841 Seq. No.

Seq. ID LIB3083-071-Q1-L1-H1

BLASTX Method NCBI GI g3327868 BLAST score 188 3.0e-14 E value 66 Match length 59 % identity

(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis NCBI Description

thaliana]

204842 Seq. No.

Seq. ID LIB3083-071-Q1-L1-H5

Method BLASTX NCBI GI q1946300 313 BLAST score 6.0e-29 E value 89 Match length % identity

(Y12529) hypothetical protein [Silene latifolia] NCBI Description

204843 Seq. No.

LIB3083-071-Q1-L1-H6 Seq. ID

Method BLASTX NCBI GI q3204134 BLAST score 512 E value 3.0e-52Match length 114 % identity 80

Seq. ID



```
NCBI Description
                  (AJ006771) beta-galactosidase [Cicer arietinum]
Seq. No.
                  204844
Seq. ID
                  LIB3083-071-Q1-L1-H7
Method
                  BLASTX
NCBI GI
                  q4558591
BLAST score
                   471
                   2.0e-47
E value
Match length
                  118
                   71
% identity
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   204845
Seq. ID
                  LIB3083-071-Q1-L1-H9
Method
                  BLASTN
NCBI GI
                  g2695738
BLAST score
                   47
E value
                   2.0e-17
Match length
                  122
% identity
                   90
NCBI Description
                  Pisum sativum mitochondrial tRNA-Gly gene and flanking
                  sequences
                  204846
Seq. No.
Seq. ID
                  LIB3083-072-Q1-L1-A1
Method
                  BLASTX
NCBI GI
                  g2760830
BLAST score
                  187
E value
                   3.0e-14
Match length
                   59
% identity
                   56
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   204847
Seq. ID
                  LIB3083-072-Q1-L1-A10
Method
                  BLASTX
NCBI GI
                  g4415996
BLAST score
                  262
E value
                   2.0e-23
Match length
                  52
% identity
NCBI Description
                  (AF059290) beta-tubulin 4 [Eleusine indica]
Seq. No.
                  204848
Seq. ID
                  LIB3083-072-Q1-L1-A2
Method
                  BLASTX
NCBI GI
                  g4235430
BLAST score
                  399
E value
                  3.0e-39
Match length
                  94
% identity
                  81
NCBI Description
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.
                  204849
```

27996

LIB3083-072-Q1-L1-B12

```
Method
                  BLASTX
NCBI GI
                  q606942
BLAST score
                   390
                   2.0e-46
E value
Match length
                  104
% identity
                   96
NCBI Description
                  (U13760) unknown [Gossypium hirsutum]
Seq. No.
                  204850
                  LIB3083-072-Q1-L1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1854386
BLAST score
                  350
E value
                  3.0e-33
Match length
                  106
% identity
                  63
NCBI Description
                   (AB001375) similar to soluble NSF attachment protein [Vitis
                  vinifera]
Seq. No.
                  204851
Seq. ID
                  LIB3083-072-Q1-L1-B5
Method
                  BLASTX
NCBI GI
                  g2244806
BLAST score
                  290
E value
                  3.0e-26
Match length
                  66
% identity
                  73
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  204852
Seq. ID
                  LIB3083-072-Q1-L1-B7
Method
                  BLASTX
NCBI GI
                  q586076
BLAST score
                  537
E value
                  3.0e-55
Match length
                  107
                  93
% identity
NCBI Description
                  TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
                  chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                  tubulin 1 [Lupinus albus]
Seq. No.
                  204853
Seq. ID
                  LIB3083-072-Q1-L1-B8
Method
                  BLASTX
NCBI GI
                  q3819697
BLAST score
                  141
                  6.0e-09
E value
Match length
                  91
% identity
                  38
                  (AJ009608) BnMAP4K alpha1 [Brassica napus]
NCBI Description
Seq. No.
                  204854
Seq. ID
                  LIB3083-072-Q1-L1-C12
```

Method BLASTN NCBI GI q999314 BLAST score 93 E value 4.0e-45

```
Match length
                   145
% identity
                   95
NCBI Description
                   LTP=lipid transfer protein {clone GH3} [Gossypium
                   hirsutum=cotton, fiber, mRNA, 609 nt]
Seq. No.
                   204855
Seq. ID
                   LIB3083-072-Q1-L1-C2
Method
                   BLASTX
NCBI GI
                   g2731637
BLAST score
                   224
E value
                   2.0e-18
Match length
                   103
% identity
                   43
                  (U70667) Fas-ligand associated factor 1 [Homo sapiens]
NCBI Description
Seq. No.
                   204856
Seq. ID
                   LIB3083-072-Q1-L1-C3
Method
                   BLASTX
NCBI GI
                   ¢2435522
BLAST score
                   167
E value
                   3.0e-12
Match length
                   43
% identity
                   79
NCBI Description
                   (AF024504) contains similarity to other AMP-binding enzymes
                   [Arabidopsis thaliana]
Seq. No.
                   204857
Seq. ID
                  LIB3083-072-Q1-L1-C5
Method
                   BLASTX
NCBI GI
                  g1172977
BLAST score
                   336
E value
                  7.0e-32
Match length
                  74
% identity
                  86
NCBI Description
                  60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  204858
Seq. ID
                  LIB3083-072-Q1-L1-C6
Method
                  BLASTX
NCBI GI
                  g4337175
BLAST score
                  194
E value
                  6.0e-15
Match length
                  81
% identity
                  53
NCBI Description
                  (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
                  gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
```

Seq. ID LIB3083-072-Q1-L1-D10

Method BLASTX
NCBI GI g4567262
BLAST score 597
E value 6.0e-62
Match length 126

```
% identity
                  (AC006841) putative ubiquitin [Arabidopsis thaliana]
NCBI Description
                  204860
Seq. No.
                  LIB3083-072-Q1-L1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629806
```

6.0e-60 E value Match length 120 % identity

tubulin beta chain - rice >gi 493725 emb CAA55912 (X79367) NCBI Description

beta tubulin [Oryza sativa]

204861 Seq. No. Seq. ID LIB3083-072-Q1-L1-E4

578

BLASTX Method NCBI GI g2702273 BLAST score 291 E value 9.0e-30 Match length 117 62 % identity

BLAST score

(AC003033) carrot B2 protein-like [Arabidopsis thaliana] NCBI Description

204862 Seq. No.

Seq. ID LIB3083-072-Q1-L1-E7

BLASTX Method g1223579 NCBI GI BLAST score 179 2.0e-13 E value Match length 87 % identity 42

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 204863

Seq. ID LIB3083-072-Q1-L1-F4

Method BLASTX NCBI GI g3421090 BLAST score 202 E value 5.0e-16 Match length 45 % identity 91

NCBI Description (AF043525) 20S proteasome subunit PAE2 [Arabidopsis

thaliana]

Seq. No. 204864

Seq. ID LIB3083-072-Q1-L1-G1

BLASTX Method NCBI GI g2281115 BLAST score 324 2.0e-30 E value Match length 73 % identity

NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis

thaliana]

Seq. No. 204865

204870



```
LIB3083-072-Q1-L1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2414570
BLAST score
                  431
                  1.0e-42
E value
                  117
Match length
                  67
% identity
NCBI Description (Z99173) cysteine proteinase precursor [Nicotiana tabacum]
                  204866
Seq. No.
                  LIB3083-072-Q1-L1-G5
Seq. ID
                  BLASTX
Method
                  g81816
NCBI GI
                  258
BLAST score
                  6.0e-23
E value
                  58
Match length
                  81
% identity
NCBI Description tubulin beta-1 chain - soybean
                  204867
Seq. No.
Seq. ID
                  LIB3083-072-Q1-L1-G8
Method
                  BLASTX
                  g1709358
NCBI GI
                  350
BLAST score
                  3.0e-33
E value
                  122
Match length
                  55
% identity
                  NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
NCBI Description
                  PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir S48859
                  nucleoside triphosphatase - garden pea
                  >gi_2129890_pir__S65147 nucleoside triphosphatase
                  precursor, chromatin-associated - garden pea
                  >gi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase
                   [Pisum sativum] >gi 4519173 dbj BAA75506.1 (AB022319)
                  nucleoside triphosphatase (NTPase) [Pisum sativum]
Seq. No.
                   204868
Seq. ID
                  LIB3083-072-Q1-L1-H11
                  BLASTN
Method
                   g1143223
NCBI GI
BLAST score
                   110
                   5.0e-55
E value
                   200
Match length
                   90
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   204869
Seq. No.
Seq. ID
                   LIB3083-072-Q1-L1-H7
                   BLASTN
Method
                   g1143223
NCBI GI
                   72
BLAST score
E value
                   1.0e-32
                   197
Match length
                   25
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
```

```
LIB3083-073-Q1-L1-A11
Seq. ID
                  BLASTX
Method
                  g1706958
NCBI GI
                  353
BLAST score
                  7.0e-34
E value
                  85
Match length
                  81
% identity
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
                  204871
Seq. No.
                  LIB3083-073-Q1-L1-A2
Seq. ID
                  BLASTX
Method
                  g1706956
NCBI GI
                  450
BLAST score
                  3.0e-45
E value
                  85
Match length
% identity
                  98
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
                  204872
Seq. No.
Seq. ID
                  LIB3083-073-Q1-L1-A3
Method
                  BLASTX
                  q1129145
NCBI GI
                  238
BLAST score
                  2.0e-20
E value
                  81
Match length
% identity
                  62
NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
                  204873
Seq. No.
Seq. ID
                  LIB3083-073-Q1-L1-A4
                  BLASTX
Method
                  g322598
NCBI GI
BLAST score
                  248
                  1.0e-21
E value
                  76
Match length
                   66
% identity
NCBI Description St12p protein - Arabidopsis thaliana
                  204874
Seq. No.
Seq. ID
                  LIB3083-073-Q1-L1-B12
Method
                  BLASTX
NCBI GI
                  g3859116
                   246
BLAST score
                   3.0e-21
E value
                   77
Match length
                   60
% identity
NCBI Description (AF031609) unknown [Oryza sativa]
                   204875
```

LIB3083-073-Q1-L1-B3 Seq. ID

Method BLASTX NCBI GI g3983665 BLAST score 318 9.0e-30 E value Match length 85 % identity 72



258

63 68

1.0e-22

thaliana]

BLAST score

% identity

NCBI Description

E value Match length



```
(AB011271) importin-beta2 [Oryza sativa]
NCBI Description
                  204876
Seq. No.
                  LIB3083-073-Q1-L1-B6
Seq. ID
                  BLASTX
Method
                  g464849
NCBI GI
                   453
BLAST score
                  1.0e-45
E value
                  85
Match length
                   98
% identity
                  TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                  chain - almond >gi 2041\overline{3} emb_CAA47635_ (X67162)
                   alpha-tubulin [Prunus dulcis]
                   204877
Seq. No.
                  LIB3083-073-Q1-L1-B9
Seq. ID
Method
                  BLASTX
                   g2392771
NCBI GI
                   339
BLAST score
                   3.0e-32
E value
Match length
                   85
% identity
                   76
                   (AC002534) putative kinesin-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   204878
Seq. No.
                   LIB3083-073-Q1-L1-C10
Seq. ID
Method
                   BLASTX
                   g3421090
NCBI GI
                   318
BLAST score
                   9.0e-30
E value
                   68
Match length
% identity
                   91
                   (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
NCBI Description
                   thaliana]
                   204879
Seq. No.
                   LIB3083-073-Q1-L1-C3
Seq. ID
                   BLASTX
Method
                   g1335862
NCBI GI
                   404
BLAST score
                   7.0e-40
E value
                   85
Match length
                   95
% identity
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                   204880
Seq. No.
                   LIB3083-073-Q1-L1-C5
Seq. ID
                   BLASTX
Method
                   g3355471
NCBI GI
```

28002

(AC004218) putative lysophospholipase [Arabidopsis

W.

```
204881
Seq. No.
                  LIB3083-073-Q1-L1-C6
Seq. ID
                  BLASTX
Method
                  g1076685
NCBI GI
                  217
BLAST score
                  6.0e-18
E value
                  72
Match length
                  32
% identity
                  SPF1 protein - sweet potato >gi_484261 dbj BAA06278
NCBI Description
                   (D30038) SPF1 protein [Ipomoea batatas]
                  204882
Seq. No.
                  LIB3083-073-Q1-L1-C7
Seq. ID
                  BLASTX
Method
                  g3395425
NCBI GI
                   184
BLAST score
                   4.0e-14
E value
                   61
Match length
% identity
                   (AC004683) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   204883
Seq. No.
                   LIB3083-073-Q1-L1-D11
Seq. ID
                   BLASTX
Method
                   q267069
NCBI GI
                   385
BLAST score
                   1.0e-37
E value
                   70
Match length
                   100
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   204884
 Seq. No.
                   LIB3083-073-Q1-L1-D12
 Seq. ID
                   BLASTX
 Method
                   g2342719
 NCBI GI
                   258
 BLAST score
                   9.0e-23
 E value
                   68
 Match length
 % identity
                  (AC002341) SF16 protein isolog [Arabidopsis thaliana]
 NCBI Description
                   204885
 Seq. No.
                   LIB3083-073-Q1-L1-D2
 Seq. ID
                   BLASTX
 Method
                   q3097321
 NCBI GI
                   166
 BLAST score
                    6.0e-12
 E value
                    85
 Match length
```

% identity NCBI Description (AB013289) Bd 30K [Glycine max]

204886 Seq. No.

LIB3083-073-Q1-L1-D6 Seq. ID

42



```
Method
                   g3202040
NCBI GI
                   274
BLAST score
                   1.0e-24
E value
                   85
Match length
                   59
% identity
                   (AF069323) permease 1 [Mesembryanthemum crystallinum]
NCBI Description
                   204887
Seq. No.
                   LIB3083-073-Q1-L1-D7
Seq. ID
                   BLASTX
Method
                   g4467111
NCBI GI
                   322
BLAST score
                   3.0e-30
E value
                   84
Match length
                   70
% identity
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   204888
Seq. No.
                   LIB3083-073-Q1-L1-E1
Seq. ID
                   BLASTX
Method
                   g730512
NCBI GI
                   419
BLAST score
                   1.0e-41
E value
                   85
Match length
                   96
% identity
                   RAS-RELATED PROTEIN RIC2 >gi 481506 pir S38741 GTP-binding
NCBI Description
                   protein ric2 - rice >gi_2182\overline{2}8 dbj_\overline{B}AA0\overline{29}04_ (D13758)
                   ras-related GTP binding protein [Oryza sativa]
                   204889
Seq. No.
                   LIB3083-073-Q1-L1-E10
Seq. ID
                   BLASTX
Method
                    g1619602
NCBI GI
                    256
BLAST score
                    2.0e-22
E value
Match length
                    73
                    70
 % identity
                   (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                    204890
 Seq. No.
                    LIB3083-073-Q1-L1-E2
 Seq. ID
                    BLASTX
Method
                    g3789799
NCBI GI
                    149
 BLAST score
                    5.0e-10
 E value
                    75
 Match length
                    10
 % identity
                   (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens]
 NCBI Description
                    >gi_4557445_ref_NP_001259.1_pCHC1L_ RCC1-like G exchanging
                    factor RLG
```

Seq. ID LIB3083-073-Q1-L1-E3

BLASTX Method NCBI GI g417154 314 BLAST score



E value 3.0e-29
Match length 63
% identity 98
NCBI Description HEAT SH

HEAT SHOCK PROTEIN 82 >gi\_100685\_pir\_\_S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi\_20256\_emb\_CAA77978\_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 204892

Seq. ID LIB3083-073-Q1-L1-F1

Method BLASTX
NCBI GI g2827143
BLAST score 192
E value 5.0e-15
Match length 44
% identity 80

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 204893

Seq. ID LIB3083-073-Q1-L1-F10

Method BLASTX
NCBI GI g3850816
BLAST score 392
E value 2.0e-38
Match length 78
% identity 87

NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza

sativa]

Seq. No. 204894

Seq. ID LIB3083-073-Q1-L1-F11

Method BLASTX
NCBI GI g2347207
BLAST score 255
E value 2.0e-22
Match length 84
% identity 60

NCBI Description (AC002338) APG protein isolog [Arabidopsis thaliana]

>gi\_3150400 (AC004165) putative APG-like protein

[Arabidopsis thaliana]

Seq. No. 204895

Seq. ID LIB3083-073-Q1-L1-F12

Method BLASTX
NCBI GI g3650032
BLAST score 248
E value 1.0e-21
Match length 57
% identity 65

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No. 204896

Seq. ID LIB3083-073-Q1-L1-F2.

Method BLASTX NCBI GI g3334405



BLAST score 3.0e-35 E value 76 Match length 99 % identity

VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) NCBI Description >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E

[Gossypium hirsutum]

204897 Seq. No.

LIB3083-073-Q1-L1-F3 Seq. ID

BLASTX Method g549010 NCBI GI 383 BLAST score 2.0e-37 E value 84 Match length 87 % identity

EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) NCBI Description

(OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi\_322554\_pir\_\_S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi\_16514\_emb\_CAA49172\_ (X69375) similar to yeast

omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi 1402882\_emb CAA66813\_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis

thaliana] >gi\_1495249\_emb\_CAA66118\_ (X97486) eRF1-3

[Arabidopsis thaliana]

204898 Seq. No.

LIB3083-073-Q1-L1-F4 Seq. ID

BLASTX Method g4210504 NCBI GI BLAST score 240 1.0e-20 E value 72 Match length 68 % identity

(AC002392) putative cadmium-transporting ATPase NCBI Description

[Arabidopsis thaliana]

204899 Seq. No.

LIB3083-073-Q1-L1-F5 Seq. ID

BLASTX Method NCBI GI q464849 BLAST score 416 3.0e-41 E value Match length 85 99 % identity

TUBULIN ALPHA CHAIN >gi\_486847 pir S36232 tubulin alpha NCBI Description

chain - almond  $>gi_2041\overline{3}$  emb  $\overline{CAA47635}$  (X67162)

alpha-tubulin [Prunus dulcis]

204900 Seq. No.

Seq. ID LIB3083-073-Q1-L1-F7

BLASTX Method q267069 NCBI GI BLAST score 301 9.0e-28 E value 54 Match length



Seq. No. 204901

Seq. ID LIB3083-073-Q1-L1-F9

Method BLASTX
NCBI GI g2109293
BLAST score 278
E value 4.0e-25
Match length 59
% identity 86

NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 204902

Seq. ID LIB3083-073-Q1-L1-G10

Method BLASTX
NCBI GI g4210948
BLAST score 235
E value 5.0e-20
Match length 84
% identity 63

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 204903

Seq. ID LIB3083-073-Q1-L1-G4

Method BLASTX
NCBI GI g3893822
BLAST score 420
E value 1.0e-41
Match length 85
% identity 99

NCBI Description (U96498) ATPase beta subunit [Nicotiana sylvestris]

Seq. No. 204904

Seq. ID LIB3083-073-Q1-L1-G6

Method BLASTX
NCBI GI g3413706
BLAST score 341
E value 2.0e-32
Match length 85
% identity 65

NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No. 204905

Seq. ID LIB3083-073-Q1-L1-G8

Method BLASTX
NCBI GI g2827699
BLAST score 282
E value 1.0e-25
Match length 83
% identity 64

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]



Seq. ID LIB3083-073-Q1-L1-H1

Method BLASTN
NCBI GI g58066
BLAST score 37
E value 2.0e-11
Match length 200
% identity 84

NCBI Description pBluescript SK(-) vector DNA, phagemid excised from lambda

ZAP

Seq. No. 204907

Seq. ID LIB3083-073-Q1-L1-H12

Method BLASTX
NCBI GI g1729980
BLAST score 219
E value 4.0e-18
Match length 49
% identity 76

NCBI Description THAUMATIN-LIKE PROTEIN PRECURSOR >gi\_2129751\_pir\_\_S71175

thaumatin-like protein - Arabidopsis thaliana >gi 536825 (L34693) thaumatin-like protein [Arabidopsis thaliana]

>gi 1094863 prf 2106421A thaumatin-like protein

[Arabidopsis thaliana]

Seq. No. 204908

Seq. ID LIB3083-073-Q1-L1-H3

Method BLASTX
NCBI GI g1732511
BLAST score 280
E value 3.0e-25
Match length 59
% identity 90

NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis

thaliana]

Seq. No. 204909

Seq. ID LIB3083-073-Q1-L1-H7

Method BLASTX
NCBI GI g3513727
BLAST score 332
E value 2.0e-31
Match length 82
% identity 55

NCBI Description (AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi\_4539358\_emb\_CAB40052.1\_ (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 204910

Seq. ID LIB3083-073-Q1-L1-H8

Method BLASTX
NCBI GI g2865523
BLAST score 165
E value 8.0e-12
Match length 52



```
% identity
NCBI Description (AF044584) cold regulated LTCOR18 [Lavatera thuringiaca]
                  204911
Seq. No.
                  LIB3083-073-Q1-L1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3694872
BLAST score
                  296
                  3.0e-27
E value
Match length
                  62
% identity
                  85
NCBI Description (AF092547) profilin [Ricinus communis]
                  204912
Seq. No.
                  LIB3083-074-Q1-L1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2289012
BLAST score
                  155
E value
                  2.0e-10
Match length
                  55
% identity
                  51
NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]
                  204913
Seq. No.
Seq. ID
                  LIB3083-074-Q1-L1-A3
                  BLASTX
Method
NCBI GI
                  q4210948
                  552
BLAST score
                  7.0e-57
E value
                  131
Match length
                  85
% identity
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
                  204914
Seq. No.
Seq. ID
                  LIB3083-074-Q1-L1-A4
Method
                  BLASTX
NCBI GI
                  g2244772
BLAST score
                  520
                  4.0e-53
E value
Match length
                  130
% identity
                  75
NCBI Description (Z97335) transport protein [Arabidopsis thaliana]
                  204915
Seq. No.
                  LIB3083-074-Q1-L1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100439
BLAST score
                  300
E value
                  2.0e-27
Match length
                  69
```

87 % identity

NCBI Description heat shock protein 70 (clone DK) - potato (fragment)

>gi\_21481\_emb\_CAA78034\_ (Z11982) 70-kD heat shock protein

[Solanum tuberosum]

Seq. No. 204916

Seq. ID LIB3083-074-Q1-L1-A8

```
Method
NCBI GI
                  q4206765
BLAST score
                  232
                  2.0e-19
E value
                  90
Match length
                  54
% identity
NCBI Description
                  (AF104329) putative type 1 membrane protein [Arabidopsis
Seq. No.
                  204917
                  LIB3083-074-Q1-L1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351206
                  556
BLAST score
                  2.0e-57
E value
                  128
Match length
% identity
                  81
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                  4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >qi 629663 pir S44169 trans-cinnamate 4-monooxygenase (EC
                  1.14.13.11) cytochrome P450 73 - Madagascar periwinkle
                  >gi 2129922 pir S68204 trans-cinnamate 4-monooxygenase (EC
                  1.14.13.11) - Madagascar periwinkle
                  >gi 473229 emb CAA83552 (Z32563) cinnamate 4-hydroxylase
                  (CYP73) [Catharanthus roseus]
                  204918
Seq. No.
Seq. ID
                  LIB3083-074-Q1-L1-B4
Method
                  BLASTX
NCBI GI
                  q3702331
BLAST score
                  386
                  2.0e-37
E value
Match length
                  121
% identity
                  70
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
                  204919
Seq. No.
                  LIB3083-074-Q1-L1-B5
Seq. ID
Method
                  BLASTX
                  g3482967
NCBI GI
                  290
BLAST score
                  3.0e-26
E value
                  59
Match length
% identity
                  92
                 (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                  204920
                  LIB3083-074-Q1-L1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417154
                  513
BLAST score
                  2.0e-52
E value
                  98
Match length
                  98
% identity
```

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir\_\_S25541 heat shock



```
protein 82 - rice (strain Taichung Native One)
>gi 20256 emb CAA77978 (Z11920) heat shock protein 82
(HSP82) [Oryza sativa]
```

 Seq. ID
 LIB3083-074-Q1-L1-C3

 Method
 BLASTX

 NCBI GI
 g629791

 BLAST score
 575

 E value
 1.0e-59

 Match length
 114

 % identity
 96

NCBI Description tubulin beta chain - rice >gi\_460991\_emb\_CAA55022\_ (X78143)

beta tubulin [Oryza sativa]

Seq. No. 204922

Seq. No.

Seq. ID LIB3083-074-Q1-L1-C6

Method BLASTX
NCBI GI 94262241
BLAST score 332
E value 4.0e-31
Match length 121
% identity 61

NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 204923

Seq. ID LIB3083-074-Q1-L1-D1

Method BLASTX
NCBI GI g3252868
BLAST score 265
E value 3.0e-23
Match length 128
% identity 45

NCBI Description (AF033536) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 204924

Seq. ID LIB3083-074-Q1-L1-D3

Method BLASTX
NCBI GI g3608133
BLAST score 148
E value 2.0e-09
Match length 102
% identity 37

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 204925

Seq. ID LIB3083-074-Q1-L1-D4

Method BLASTX
NCBI GI g4454464
BLAST score 382
E value 6.0e-37
Match length 110
% identity 60

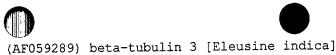
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 204926

Seq. ID LIB3083-074-Q1-L1-D5

```
Method
                  q3269288
NCBI GI
                   480
BLAST score
                   2.0e-48
E value
                  116
Match length
                   81
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   204927
Seq. No.
                   LIB3083-074-Q1-L1-D7
Seq. ID
                   BLASTX
Method
                   g1743277
NCBI GI
                   587
BLAST score
                   5.0e-61
E value
                   124
Match length
                   90
% identity
                  (Y09741) beta-tubulin 1 [Hordeum vulgare]
NCBI Description
                   204928
Seq. No.
                   LIB3083-074-Q1-L1-D8
Seq. ID
                   BLASTX
Method
                   g4204300
NCBI GI
                   191
BLAST score
                   1.0e-14
E value
                   77
Match length
                   57
% identity
                   (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   204929
Seq. No.
                   LIB3083-074-Q1-L1-E1
Seq. ID
                   BLASTN
Method
                   g606941
NCBI GI
                   291
BLAST score
                   1.0e-163
E value
                   303
Match length
                   99
 % identity
                   Gossypium hirsutum C312 clone Fb-B6 unidentified fiber
NCBI Description
                   mRNA, complete cds
                   204930
 Seq. No.
 Seq. ID
                   LIB3083-074-Q1-L1-E5
                   BLASTX
 Method
 NCBI GI
                   g3192881
                    569
 BLAST score
                    7.0e-59
 E value
                   124
 Match length
 % identity
                   (AF068834) starch synthase [Ipomoea batatas]
 NCBI Description
                    204931
 Seq. No.
 Seq. ID
                    LIB3083-074-Q1-L1-E6
                    BLASTX
 Method
                    q4415994
 NCBI GI
                    370
 BLAST score
                    1.0e-35
 E value
 Match length
                    74
```

% identity



204937

78

Match length

NCBI Description

% identity

Seq. No.

NCBI Description



```
204932
Seq. No.
Seq. ID
                  LIB3083-074-Q1-L1-E8
                  BLASTX
Method
                  g3367568
NCBI GI
                   382
BLAST score
                   6.0e-37
E value
                  86
Match length
                   85
% identity
                  (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   204933
Seq. No.
                   LIB3083-074-Q1-L1-F1
Seq. ID
                   BLASTX
Method
                   g1769528
NCBI GI
                   238
BLAST score
                   3.0e-20
E value
                   46
Match length
                   98
% identity
                  (U75868) beta-tubulin [Heliothis virescens]
NCBI Description
                   204934
Seq. No.
                   LIB3083-074-Q1-L1-F10
Seq. ID
                   BLASTX
Method
                   g232031
NCBI GI
                   266
BLAST score
                   3.0e-23
E value
                   85
Match length
% identity
                   ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224
NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                   204935
Seq. No.
                   LIB3083-074-Q1-L1-F2
Seq. ID
                   BLASTX
Method
                   q4098129
NCBI GI
BLAST score
                   241
                   1.0e-20
E value
                   83
Match length
                   59
% identity
                   (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   204936
Seq. No.
                   LIB3083-074-Q1-L1-F3
Seq. ID
                   BLASTX
Method
                   g2827082
NCBI GI
BLAST score
                   440
E value
                   7.0e-44
```

28013

(AF020272) malate dehydrogenase [Medicago sativa]



LIB3083-074-Q1-L1-F5 Seq. ID BLASTX Method g4417283 NCBI GI BLAST score 187 4.0e-14 E value 83 Match length % identity (AC007019) putative cytochrome p450 [Arabidopsis thaliana] NCBI Description 204938 Seq. No. LIB3083-074-Q1-L1-F6 Seq. ID BLASTX Method q1729980 NCBI GI 364 BLAST score 7.0e-35 E value 87 Match length 70 % identity THAUMATIN-LIKE PROTEIN PRECURSOR >gi\_2129751\_pir\_\_S71175 NCBI Description thaumatin-like protein - Arabidopsis thaliana >gi\_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >qi 1094863 prf 2106421A thaumatin-like protein [Arabidopsis thaliana] 204939 Seq. No. LIB3083-074-Q1-L1-F8 Seq. ID BLASTX Method g4512659 NCBI GI 267 BLAST score 2.0e-23 E value 120 Match length 49 % identity (AC006931) putative protein kinase [Arabidopsis thaliana] NCBI Description >gi\_4544465\_gb\_AAD22372.1\_AC006580\_4 (AC006580) putative protein kinase [Arabidopsis thaliana] 204940 Seq. No. LIB3083-074-Q1-L1-G1 Seq. ID BLASTX Method g2498490 NCBI GI 222 BLAST score 1.0e-18 E value 80 Match length % identity VIRAL INTEGRATION SITE PROTEIN INT-6 >gi\_1854579 (L35556) NCBI Description Int-6 [Mus musculus] >gi\_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi\_2351382 (U54562) eIF3-p48 [Homo sapiens]  $>gi_2688818$  (U8 $\overline{5}947$ ) Int-6 [Homo sapiens] >gi 2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi\_4503521\_ref\_NP\_001559.1\_pEIF3S6\_ murine mammary tumor integration site 6 (oncogene homolog) Seq. No. 204941

LIB3083-074-Q1-L1-G10 Seq. ID

BLASTX Method NCBI GI g3287696 BLAST score 174 1.0e-12 E value



Match length % identity

NCBI Description

(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

204942 Seq. No.

Seq. ID LIB3083-074-Q1-L1-G4

Method BLASTX g2244810 NCBI GI 287 BLAST score 2.0e-26 E value 65 Match length

88 % identity

(Z97336) CCAAT-binding transcription factor subunit NCBI Description

A(CBF-A) [Arabidopsis thaliana]

204943 Seq. No.

LIB3083-074-Q1-L1-G7 Seq. ID

Method BLASTX g4512667 NCBI GI 349 BLAST score 2.0e-33 E value 85 Match length 73 % identity

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

204944 Seq. No.

Seq. ID LIB3083-074-Q1-L1-H2

Method BLASTX NCBI GI g120668 332 BLAST score 4.0e-31 E value 67 Match length 93 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi 82399 pir A24159 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)

>qi 167044 (M36650) glyceraldehyde-3-phosphate

dehydrogenase [Hordeum vulgare] >gi\_225347\_prf\_\_1301218A dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.

distichum]

204945 Seq. No.

LIB3083-074-Q1-L1-H6 Seq. ID

Method BLASTX NCBI GI g3334113 BLAST score 341 3.0e-32 E value Match length 89 75 % identity

ACYL-COA-BINDING PROTEIN (ACBP) >gi\_1006831 (U35015) NCBI Description

acyl-CoA-binding protein [Gossypium hirsutum]

204946 Seq. No.

LIB3083-076-Q1-L1-A11 Seq. ID



```
BLASTX
Method
                  q2245087
NCBI GI
BLAST score
                  226
                   6.0e-19
E value
                  84
Match length
                   54
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  204947
Seq. No.
Seq. ID
                  LIB3083-076-Q1-L1-A2
                  BLASTX
Method
                   g1362117
NCBI GI
BLAST score
                   139
                   8.0e-09
E value
                   29
Match length
                   100
% identity
NCBI Description ribosomal protein S5 homolog - common tobacco (fragment)
                   204948
Seq. No.
Seq. ID
                   LIB3083-076-Q1-L1-A3
                   BLASTX
Method
                   g4101564
NCBI GI
                   189
BLAST score
                   1.0e-14
E value
                   88
Match length
                   47
% identity
NCBI Description (AF004556) IFA-binding protein [Arabidopsis thaliana]
                   204949
Seq. No.
                   LIB3083-076-Q1-L1-B1
Seq. ID
Method
                   BLASTX
                   q135452
NCBI GI
                   376
BLAST score
                   1.0e-36
E value
                   79
Match length
                   89
% identity
                   TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin
NCBI Description
                   [Glycine max]
                   204950
Seq. No.
Seq. ID
                   LIB3083-076-Q1-L1-B11
                   BLASTX
Method
NCBI GI
                   q3290020
BLAST score
                   305
                   3.0e-28
E value
                   67
Match length
% identity
                   90
                   (AF044172) cysteine synthase; CS-A; O-acetylserine (thiol)
NCBI Description
                   lyase; cytosolic isoform [Solanum tuberosum]
Seq. No.
                   204951
                   LIB3083-076-Q1-L1-B2
Seq. ID
```

Method BLASTX g1703375 NCBI GI BLAST score 221 2.0e-18 E value Match length 46

% identity NCBI Description

ADP-RIBOSYLATION FACTOR 1 >gi 965483\_dbj BAA08259\_ (D45420)

DcARF1 [Daucus carota]

204952 Seq. No.

Seq. ID LIB3083-076-Q1-L1-B4

BLASTX Method q2130073 NCBI GI BLAST score 291 1.0e-26 E value 63 Match length 90 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, NCBI Description

cytosolic - rice >gi\_786178\_dbj\_BAA08845\_ (D50307) aldolase

C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)

aldolase C-1 [Oryza sativa]

204953 Seq. No.

LIB3083-076-Q1-L1-B6 Seq. ID

Method BLASTX NCBI GI g461735 BLAST score 348 E value 2.0e-33 77 Match length

86 % identity

MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR NCBI Description

>gi 478785 pir \$29315 chaperonin 60 - cucurbit

>gi\_12544\_emb\_CAA50217\_ (X70867) chaperonin 60 [Cucurbita

sp.]

Seq. No. 204954

LIB3083-076-Q1-L1-B8 Seq. ID

BLASTX Method q1839188 NCBI GI BLAST score 232 E value 1.0e-19 83 Match length

55 % identity

(U86081) root hair defective 3 [Arabidopsis thaliana] NCBI Description

Seq. No. 204955

Seq. ID LIB3083-076-Q1-L1-B9

Method BLASTX NCBI GI q398849 BLAST score 268 E value 5.0e-24 Match length 52 90 % identity

NCBI Description (X74656) beta-5 tubulin [Zea mays]

Seq. No. 204956

LIB3083-076-Q1-L1-C1 Seq. ID

Method BLASTX g2119045 NCBI GI BLAST score 344 9.0e-33 E value Match length 85



```
% identity
                  small nuclear ribonucleoprotein U1A - potato
NCBI Description
                  >gi 1050840 emb CAA90282_ (Z49990) U1snRNP-specific
                  protein, UIA [Solanum tuberosum]
                  204957
Seq. No.
Seq. ID
                  LIB3083-076-Q1-L1-C4
Method
                  BLASTX
                  g3928099
NCBI GI
                  210
BLAST score
```

90 Match length 31 % identity NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

5.0e-17

204958 Seq. No. LIB3083-076-Q1-L1-C7 Seq. ID BLASTX Method g3820648 NCBI GI 145 BLAST score

E value 3.0e-09 Match length 76 % identity 46

E value

(Y12636) allene oxide synthase [Arabidopsis thaliana] NCBI Description

204959 Seq. No.

LIB3083-076-Q1-L1-D1 Seq. ID

Method BLASTX g3820648 NCBI GI 300 BLAST score 1.0e-27 E value Match length 86 % identity 67

NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana]

204960 Seq. No.

LIB3083-076-Q1-L1-D10 Seq. ID

BLASTX Method g4325369 NCBI GI BLAST score 467 4.0e-47 E value Match length 90 90 % identity

NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]

204961 Seq. No.

LIB3083-076-Q1-L1-D12 Seq. ID

BLASTX Method g2618688 NCBI GI 384 BLAST score 2.0e-37 E value Match length 91 % identity

(AC002510) putative esterase D [Arabidopsis thaliana] NCBI Description

Seq. No. 204962

LIB3083-076-Q1-L1-D2 Seq. ID



```
Method
                  q3860247
NCBI GI
BLAST score
                  185
                  3.0e-17
E value
                  51
Match length
                  78
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  204963
Seq. No.
                  LIB3083-076-Q1-L1-D3
Seq. ID
                  BLASTX
Method
                  g1352347
NCBI GI
                  161
BLAST score
                  2.0e-11
E value
                  62
Match length
                   53
% identity
                  ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
NCBI Description
                  >gi_480620_pir__S37103 translation elongation factor eEF-1
                  beta-A1 chain - Arabidopsis thaliana (cv. Colombia)
                   >gi 398608_emb_CAA52751_ (X74733) elongation factor-1 beta
                  Al [Arabidopsis thaliana]
                   204964
Seq. No.
                  LIB3083-076-Q1-L1-D4
Seq. ID
                  BLASTX
Method
                   g2980767
NCBI GI
                   150
BLAST score
                   5.0e-10
E value
                   77
Match length
                   48
% identity
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   204965
Seq. No.
Seq. ID
                   LIB3083-076-Q1-L1-D5
                   BLASTX
Method
NCBI GI
                   g3355468
                   291
BLAST score
                   1.0e-26
E value
                   80
Match length
                   79
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   204966
Seq. No.
                   LIB3083-076-Q1-L1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1703386
BLAST score
                   188
                   2.0e-14
E value
Match length
                   86
                   47
% identity
                   ACETYLORNITHINE DEACETYLASE (ACETYLORNITHINASE) (AO)
NCBI Description
                   (N-ACETYLORNITHINASE) (NAO) >gi 763048 (U23957)
```

204967 Seq. No.

LIB3083-076-Q1-L1-E1 Seq. ID

N-acetylornithine deacetylase  $[\overline{\mathtt{D}} \mathtt{ictyostelium} \ \mathtt{discoideum}]$ 

```
Method
                  g3695059
NCBI GI
                  323
BLAST score
                  3.0e-30
E value
                  86
Match length
                  78
% identity
                   (AF064787) rac GTPase activating protein 1 [Lotus
NCBI Description
                  japonicus]
                   204968
Seq. No.
                  LIB3083-076-Q1-L1-E10
Seq. ID
Method
                  BLASTX
                   q4490705
NCBI GI
                   398
BLAST score
                   4.0e-39
E value
                   91
Match length
                   88
% identity
                   (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   204969
Seq. No.
                   LIB3083-076-Q1-L1-E2
Seq. ID
Method
                   BLASTX
                   q1223922
NCBI GI
                   324
BLAST score
                   2.0e-30
E value
                   74
Match length
                   82
% identity
                   (U49445) Vigna radiata vicilin peptidohydrolase [Vigna
NCBI Description
                   radiata]
                   204970
Seq. No.
                   LIB3083-076-Q1-L1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q729505
BLAST score
                   265
                   9.0e-24
E value
                   72
Match length
                   71
% identity
                   NARINGENIN, 2-OXOGLUTARATE 3-DIOXYGENASE
NCBI Description
                   (FLAVONONE-3-HYDROXYLASE) (FHT) >gi_322680_pir__S31458
                   naringenin 3-dioxygenase (EC 1.14.11.9) - apple tree
                   >gi_19603_emb_CAA49353_ (X69664) naringenin, 2-oxoglutarate
                   3-dioxygenase [Malus sp.]
                   204971
 Seq. No.
                   LIB3083-076-Q1-L1-E8
 Seq. ID
Method
                   BLASTX
                   q464775
NCBI GI
                   344
 BLAST score
```

SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi\_542013\_pir\_\_S39492

superoxide dismutase (manganese) [Hevea brasiliensis]

superoxide dismutase - Para rubber tree >gi\_348137 (L11707)

8.0e-33

73

89

E value

Match length

NCBI Description

% identity



```
204972
Seq. No.
                  LIB3083-076-Q1-L1-E9
Seq. ID
Method
                  BLASTX
                  g2492953
NCBI GI
BLAST score
                  215
E value
                  1.0e-17
Match length
                  76
                  58
% identity
                  CHORISMATE SYNTHASE 2 PRECURSOR
NCBI Description
                  (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 2)
                  >gi 542027_pir__S40409 chorismate synthase (EC 4.6.1.4) 2
                  precursor - tomato >gi_410484_emb_CAA79854_ (Z21791)
                  chorismate synthase 2 [Lycopersicon esculentum]
                  204973
Seq. No.
                  LIB3083-076-Q1-L1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1729980
BLAST score
                  150
                  6.0e-10
E value
                  37
Match length
% identity
                  THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175
NCBI Description
                  thaumatin-like protein - Arabidopsis thaliana >gi_536825
                   (L34693) thaumatin-like protein [Arabidopsis thaliana]
                  >qi 1094863 prf 2106421A thaumatin-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   204974
                  LIB3083-076-Q1-L1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3176098
BLAST score
                   292
                   1.0e-26
E value
Match length
                   85
% identity
                   65
                  (Y15036) annexin [Medicago truncatula]
NCBI Description
Seq. No.
                   204975
                   LIB3083-076-Q1-L1-F6
Seq. ID
Method
                   BLASTX
                   g4218011
NCBI GI
                   407
BLAST score
                   4.0e-40
E value
                   88
Match length
                   88
% identity
                   (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_4309721 gb_AAD15491 (AC006439) putative
                   serine/threonine protein kinase [Arabidopsis thaliana]
```

204976 Seq. No.

Seq. ID LIB3083-076-Q1-L1-F8

BLASTX Method g1408471 NCBI GI BLAST score 390 4.0e-38 E value 89 Match length



% identity 79

NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi 3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No. 204977

Seq. ID LIB3083-076-Q1-L1-F9

Method BLASTX
NCBI GI g3377843
BLAST score 241
E value 4.0e-22

Match length 83 % identity 71

NCBI Description (AF076274) contains similarity to rat p47 protein

(GB:AB002086) [Arabidopsis thaliana]

Seq. No. 204978

Seq. ID LIB3083-076-Q1-L1-G1

Method BLASTX
NCBI GI g3738334
BLAST score 147
E value 6.0e-10
Match length 67
% identity 46

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 204979

Seq. ID LIB3083-076-Q1-L1-G10

Method BLASTX
NCBI GI g2832649
BLAST score 367
E value 2.0e-35
Match length 87
% identity 78

NCBI Description (AL021710) adenylosuccinate lyase - like protein

[Arabidopsis thaliana]

Seq. No. 204980

Seq. ID LIB3083-076-Q1-L1-G12

Method BLASTX
NCBI GI g136636
BLAST score 202
E value 4.0e-16
Match length 38
% identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 204981

Seq. ID LIB3083-076-Q1-L1-G2

Method

NCBI GI BLAST score

```
Method
                  g3915031
NCBI GI
                  489
BLAST score
                  9.0e-50
E value
                  89
Match length
                  100
% identity
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                  (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
                  204982
Seq. No.
                  LIB3083-076-Q1-L1-G5
Seq. ID
Method
                  BLASTX
                  g4539383
NCBI GI
                  282
BLAST score
                  1.0e-25
E value
                  79
Match length
% identity
                  63
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  204983
                  LIB3083-076-Q1-L1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3204134
BLAST score
                  348
E value
                  3.0e-33
                  86
Match length
                  72
% identity
                  (AJ006771) beta-galactosidase [Cicer arietinum]
NCBI Description
                  204984
Seq. No.
                  LIB3083-076-Q1-L1-H10
Seq. ID
                  BLASTX
Method
                  g485742
NCBI GI
                   409
BLAST score
                  2.0e-40
E value
                  82
Match length
                  98
% identity
NCBI Description (L32791) pyrophosphatase [Beta vulgaris]
                   204985
Seq. No.
Seq. ID
                  LIB3083-076-Q1-L1-H11
                  BLASTN
Method
                   g1143223
NCBI GI
BLAST score
                   265
                   1.0e-147
E value
                   277
Match length
                   34
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   204986
Seq. No.
Seq. ID
                   LIB3083-076-Q1-L1-H12
                   BLASTX
```

28023

g1345933



```
E value
                  79
Match length
                   94
% identity
                  CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)
NCBI Description
                   >gi_1084323_pir__S53007 citrate synthase - cucurbit
                   >gi_975633_dbj_BAA07328_ (D38132) glyoxysomal citrate
                   synthase [Cucurbita sp.]
                   204987
Seq. No.
                   LIB3083-076-Q1-L1-H2
Seq. ID
                   BLASTN
Method
                   g525331
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
                   57
Match length
                   91
% identity
                   Pisum sativum Alaska alpha-tubulin (TubA1) gene, complete
NCBI Description
                   204988
Seq. No.
                   LIB3083-076-Q1-L1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1706958
BLAST score
                   370
                   6.0e-36
E value
                   71
Match length
% identity
                   (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   204989
Seq. No.
                   LIB3083-076-Q1-L1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4159706
                   38
BLAST score
                   4.0e-12
E value
                   74
Match length
% identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGL6, complete sequence [Arabidopsis thaliana]
                   204990
Seq. No.
                   LIB3083-077-Q1-L1-A10
Seq. ID
                   {\tt BLASTX}
Method
                   g3281853
NCBI GI
                    437
BLAST score
                   1.0e-43
E value
                    88
Match length
                    98
 % identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                    204991
 Seq. No.
                    LIB3083-077-Q1-L1-A12
 Seq. ID
                    BLASTX
Method
                    g4539545
 NCBI GI
```

425

85

3.0e-42

BLAST score

Match length

E value

% identity



```
% identity
                   (Y16644) PRCI [Nicotiana tabacum]
NCBI Description
                    204992
Seq. No.
                    LIB3083-077-Q1-L1-A2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g730165
                    208
BLAST score
                    2.0e-16
E value
Match length
                    80
% identity
                    54
                   EARLY NODULIN 93 (N-93) >gi_486679_pir__S34801 nodulin (clone GmN93) - soybean >gi_218262_dbj_BAA02724_ (D13506) early nodulin [Glycine max] >gi_3763851_dbj_BAA33816_
NCBI Description
                    (AB018378) early nodulin [Glycine max]
                    >gi 447138_prf_ 1913422D nodulin [Glycine max]
Seq. No.
                    204993
Seq. ID
                    LIB3083-077-Q1-L1-A5
Method
                    BLASTX
NCBI GI
                    g3335359
BLAST score
                    557
E value
                    2.0e-57
Match length
                    127
% identity
                    80
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
                    204994
Seq. No.
                    LIB3083-077-Q1-L1-A7
Seq. ID
                    BLASTX
Method
NCBI GI
                    g1752734
                    329
BLAST score
                    1.0e-30
E value
                    88
Match length
% identity
NCBI Description (D78510) beta-qlucan-elicitor receptor [Glycine max]
Seq. No.
                    204995
Seq. ID
                    LIB3083-077-Q1-L1-B2
Method
                    BLASTX
NCBI GI
                    q4490300
BLAST score
                    479
                    3.0e-48
E value
                    130
Match length
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                    204996
Seq. No.
Seq. ID
                    LIB3083-077-Q1-L1-B4
Method
                    BLASTX
NCBI GI
                    g4490300
BLAST score
                    251
E value
                    1.0e-21
Match length
                    116
```

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]



```
204997
Seq. No.
                  LIB3083-077-Q1-L1-B8
Seq. ID
                  BLASTX
Method
                  g3834321
NCBI GI
                  520
BLAST score
                   4.0e-53
E value
Match length
                  111
                   91
% identity
                   (AC005679) Strong similarity to F13P17.9 gi_3337356
NCBI Description
                   transport protein SEC61 alpha subunit homolog from
                  Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis
                   thaliana]
                   204998
Seq. No.
                   LIB3083-077-Q1-L1-C2
Seq. ID
                   BLASTX
Method
                   g3641837
NCBI GI
BLAST score
                   498
                   2.0e-50
E value
                   128
Match length
                   77
% identity
                   (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   204999
Seq. No.
                   LIB3083-077-Q1-L1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2497743
BLAST score
                   177
                   6.0e-13
E value
Match length
                   57
                   61
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
NCBI Description
                   >gi 999315_bbs_166991 (S78173) LTP=lipid transfer protein
                   [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                   [Gossypium hirsutum]
                   205000
Seq. No.
                   LIB3083-077-Q1-L1-C5
Seq. ID
                   BLASTX
Method
                   g606942
NCBI GI
                   367
BLAST score
                   3.0e-35
E value
                   102
Match length
                   77
 % identity
                   (U13760) unknown [Gossypium hirsutum]
NCBI Description
                   205001
 Seq. No.
                   LIB3083-077-Q1-L1-C7
 Seq. ID
                   BLASTX
Method
                   g2558654
NCBI GI
                   142
 BLAST score
```

(AC002354) No definition line found [Arabidopsis thaliana]

8.0e-09

84

43

E value

Match length

NCBI Description

% identity

NCBI Description



```
Seq. No.
Seq. ID
                  LIB3083-077-Q1-L1-D10
                  BLASTX
Method
NCBI GI
                  g2244904
                  217
BLAST score
                  7.0e-18
E value
                  60
Match length
                  72
% identity
                  (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
NCBI Description
                  [Arabidopsis thaliana]
                  205003
Seq. No.
                  LIB3083-077-Q1-L1-D12
Seq. ID
                  BLASTX
Method
                  g170352
NCBI GI
                  111
BLAST score
                  1.0e-11
E value
                  40
Match length
                  17
% identity
                   (M74101) hexameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                  >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana]
                  >gi 4115333 (L81139) ubiquitin [Pisum sativum] >gi 4115335
                   (L81140) ubiquitin [Pisum sativum]
                  205004
Seq. No.
                  LIB3083-077-Q1-L1-D3
Seq. ID
                  BLASTX
Method
                   g4432837
NCBI GI
                   144
BLAST score
                   5.0e-09
E value
Match length
                   95
% identity
                   38
                   (AC006283) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205005
Seq. No.
Seq. ID
                   LIB3083-077-Q1-L1-D4
                   BLASTX
Method
                   q132944
NCBI GI
                   182
BLAST score
                   5.0e-14
E value
Match length
                   42
                   81
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                   protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   205006
Seq. ID
                   LIB3083-077-Q1-L1-D6
                   BLASTX
Method
NCBI GI
                   g4210334
BLAST score
                   277
                   1.0e-24
E value
Match length
                   55
                   95
% identity
```

[Arabidopsis thaliana]

(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit

```
205007
Seq. No.
                  LIB3083-077-Q1-L1-D9
Seq. ID
                  BLASTX
Method
                  g135449
NCBI GI
BLAST score
                  367
                  2.0e-35
E value
                  88
Match length
                  78
% identity
                  TUBULIN BETA-1 CHAIN >gi 100932 pir S14701 tubulin beta-1
NCBI Description
                  chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1
                  tubulin [Zea mays]
                  205008
Seq. No.
Seq. ID
                  LIB3083-077-Q1-L1-E1
                  BLASTX
Method
                  g2494034
NCBI GI
                  441
BLAST score
                  7.0e-44
E value
                  117
Match length
                  68
% identity
                  DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                  KINASE 1) >gi 2129573 pir S71467 diacylglycerol kinase -
                  Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)
                  diacylglycerol kinase [Arabidopsis thaliana]
                  205009
Seq. No.
                  LIB3083-077-Q1-L1-E2
Seq. ID
                  BLASTX
Method
                  g2500354
NCBI GI
                  280
BLAST score
                  3.0e-25
E value
Match length
                  77
                  77
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >qi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                  205010
Seq. ID
                  LIB3083-077-Q1-L1-E4
                  BLASTX
Method
                  g1709761
NCBI GI
BLAST score
                  609
E value
                  1.0e-63
                  126
Match length
% identity
                  94
                  PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX 27 KD SUBUNIT) >qi 1262146 emb CAA65660 (X96974)
                  proteasome subunit [Spinacia oleracea]
```

Seq. No. 205011

Seq. ID LIB3083-077-Q1-L1-E5

Method BLASTX
NCBI GI g1890311
BLAST score 248
E value 3.0e-21
Match length 63
% identity 71

NCBI Description (Y11789) peroxidase ATP23b [Arabidopsis thaliana]

BLAST score

E value Match length 281 4.0e-34

126



```
205012
Seq. No.
Seq. ID
                  LIB3083-077-Q1-L1-E6
Method
                  BLASTX
                  g3062806
NCBI GI
                  434
BLAST score
                  5.0e-43
E value
                  126
Match length
                  68
% identity
                  (D86198) dolichol-phosphate-mannose synthase [Homo sapiens]
NCBI Description
                  >gi_4503363_ref_NP_003850.1_pDPM1_ UNKNOWN
                  205013
Seq. No.
                  LIB3083-077-Q1-L1-E8
Seq. ID
                  BLASTX
Method
                  g136636
NCBI GI
                  406
BLAST score
                  9.0e-40
E value
                  91
Match length
                  72
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                  >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                  Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin
                   Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                  >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
                   205014
Seq. No.
Seq. ID
                   LIB3083-077-Q1-L1-F10
                   BLASTX
Method
                   g4415992
NCBI GI
                   268
BLAST score
                   8.0e-36
E value
Match length
                   86
                   91
% identity
                  (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
                   205015
Seq. No.
Seq. ID
                   LIB3083-077-Q1-L1-F11
                   BLASTX
Method
                   q4415992
NCBI GI
                   291
BLAST score
                   1.0e-26
E value
Match length
                   80
                   71
% identity
                  (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
                   205016
Seq. No.
                   LIB3083-077-Q1-L1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4193388
```



% identity

NCBI Description

```
% identity
                  (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
                  205017
Seq. No.
                  LIB3083-077-Q1-L1-F3
Seq. ID
                  BLASTX
Method
                  g1514639
NCBI GI
                  588
BLAST score
                  4.0e-61
E value
                  128
Match length
% identity
                  88
                  (X85181) alpha-glucan phosphorylase [Spinacia oleracea]
NCBI Description
                  205018
Seq. No.
                  LIB3083-077-Q1-L1-F4
Seq. ID
Method
                  BLASTX
                   g4056425
NCBI GI
                   250
BLAST score
                   2.0e-21
E value
                   59
Match length
                   80
% identity
                   (AC005322) ESTs gb H36249, gb_AA59732 and gb_AA651219 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
                   205019
Seq. No.
                   LIB3083-077-Q1-L1-F7
Seq. ID
                   BLASTX
Method
                   g3023841
NCBI GI
                   270
BLAST score
                   5.0e-24
E value
                   72
Match length
                   74
% identity
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
NCBI Description
                   >gi 1695179 emb CAA70704 (Y09513) G protein beta subunit
                   [Nicotiana plumbaginifolia]
                   205020
Seq. No.
                   LIB3083-077-Q1-L1-F9
Seq. ID
                   BLASTX
Method
                   g4098321
NCBI GI
                   486
BLAST score
                   2.0e-49
E value
                   90
Match length
                   99
 % identity
                   (U76745) beta-tubulin 2 [Triticum aestivum]
 NCBI Description
                   205021
 Seq. No.
                   LIB3083-077-Q1-L1-G1
 Seq. ID
                   BLASTX
 Method
                   g3023841
 NCBI GI
 BLAST score
                   354
                   1.0e-33
 E value
                   89
 Match length
```

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT

>gi 1695179\_emb\_CAA70704\_ (Y09513) G protein beta subunit



## [Nicotiana plumbaginifolia]

```
205022
Seq. No.
                  LIB3083-077-Q1-L1-G2
Seq. ID
                  BLASTX
Method
                  g3334261
NCBI GI
BLAST score
                  141
                  1.0e-08
E value
                  48
Match length
                  56
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1655851 (U61973)
NCBI Description
                  metallothionein-like protein [Malus domestica]
                  205023
Seq. No.
Seq. ID
                  LIB3083-077-Q1-L1-G3
                  BLASTX
Method
                  g3327868
NCBI GI
                  145
BLAST score
                  4.0e-09
E value
                  102
Match length
                  40
% identity
                   (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
NCBI Description
                  thaliana]
                  205024
Seq. No.
Seq. ID
                  LIB3083-077-Q1-L1-G6
                  BLASTN
Method
                  g2829205
NCBI GI
                  363
BLAST score
                  0.0e+00
E value
                   387
Match length
% identity
                  18
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                   205025
Seq. No.
Seq. ID
                  LIB3083-077-Q1-L1-G7
                  BLASTX
Method
NCBI GI
                   q464849
BLAST score
                   497
                   2.0e-50
E value
Match length
                   125
                   76
% identity
                  TUBULIN ALPHA CHAIN >qi 486847 pir S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 20413 emb CAA47635 (X67162)
                   alpha-tubulin [Prunus dulcis]
                   205026
Seq. No.
                   LIB3083-077-Q1-L1-H1
Seq. ID
                   BLASTX
Method
                   g1174592
NCBI GI
BLAST score
                   609
                   5.0e-64
E value
Match length
                   127
% identity
                   95
                   TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
```

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

E value

Match length

% identity

2.0e-54

113

90



## sativum]

```
205027
Seq. No.
                  LIB3083-077-Q1-L1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g421941
BLAST score
                  222
E value
                  2.0e-18
                  49
Match length
% identity
                  90
                  GTP-binding protein, ras-related - common tobacco
NCBI Description
                  >gi_296878_emb_CAA50609_ (X71609) ras-related GTP-binding
                  protein [Nicotiana tabacum]
                  205028
Seq. No.
Seq. ID
                  LIB3083-077-Q1-L1-H2
                  BLASTX
Method
                   g2529668
NCBI GI
BLAST score
                   355
                   9.0e-34
E value
Match length
                   121
                   55
% identity
                   (AC002535) putative photolyase/blue-light receptor
NCBI Description
                   [Arabidopsis thaliana] >gi_3319288 (AF053366)
                   photolyase/blue light photoreceptor PHR2 [Arabidopsis
                   thaliana]
                   205029
Seq. No.
Seq. ID
                   LIB3083-077-Q1-L1-H3
                   BLASTX
Method
NCBI GI
                   g2129473
BLAST score
                   295
                   1.0e-26
E value
                   105
Match length
                   56
% identity
                   arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                   205030
Seq. No.
                   LIB3083-077-Q1-L1-H5
Seq. ID
Method
                   BLASTX
                   q4580460
NCBI GI
BLAST score
                   436
                   3.0e-43
E value
                   109
Match length
                   82
% identity
                   (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                   thaliana]
                   205031
Seq. No.
                   LIB3083-077-Q1-L1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q804817
BLAST score
                   532
```



NCBI Description



```
205032
Seq. No.
                  LIB3083-078-Q1-L1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3924823
                  205
BLAST score
                  3.0e-16
E value
                  71
Match length
% identity
                  52
                  (Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST
NCBI Description
                  yk491a11.3 comes from this gene [Caenorhabditis elegans]
                  205033
Seq. No.
                  LIB3083-078-Q1-L1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3868758
BLAST score
                   386
                   2.0e-37
E value
Match length
                   111
                   62
% identity
                   (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
Seq. No.
                   205034
                   LIB3083-078-Q1-L1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3927831
BLAST score
                   567
                   1.0e-58
E value
Match length
                   128
% identity
                   81
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   205035
Seq. No.
                   LIB3083-078-Q1-L1-A6
Seq. ID
                   BLASTX
Method
                   g3641252
NCBI GI
BLAST score
                   411
                   2.0e-40
E value
                   122
Match length
                   5
% identity
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                   domestica]
                   205036
Seq. No.
                   LIB3083-078-Q1-L1-A9
Seq. ID
                   BLASTX
Method
                   g267073
NCBI GI
BLAST score
                   431
                   1.0e-42
E value
                   85
Match length
% identity
                   96
                   TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
NCBI Description
                   beta chain - Arabidopsis thaliana >gi_166898 (M84700)
```

(L36647) malic enzyme [Lycopersicon esculentum]

28033

beta-3 tubulin [Arabidopsis thaliana]

beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)



```
205037
Seq. No.
                   LIB3083-078-Q1-L1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3063469
BLAST score
                   381
E value
                   8.0e-37
Match length
                   114
                   73
% identity
NCBI Description (AC003981) F22013.31 [Arabidopsis thaliana]
Seq. No.
                   205038
                   LIB3083-078-Q1-L1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q123656
BLAST score
                   520
E value
                    4.0e-53
Match length
                    127
% identity
                    81
                   CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED
NCBI Description
                   PROTEIN >gi_285407_pir__A42582 heat shock protein SCE70 - spinach >gi_21338_emb_CAA43711_ (X61491) 70 kDa heat shock
                   protein [Spinacia oleracea]
Seq. No.
                    205039
                   LIB3083-078-Q1-L1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                    q1350720
BLAST score
                    430
E value
                    1.0e-42
Match length
                    90
% identity
                    88
NCBI Description
                   60S RIBOSOMAL PROTEIN L32
                    205040
Seq. No.
                    LIB3083-078-Q1-L1-B12
Seq. ID
Method
                    BLASTX
                    q3204134
NCBI GI
BLAST score
                    145
                    4.0e-09
E value
                    34
Match length
                    79
% identity
NCBI Description (AJ006771) beta-galactosidase [Cicer arietinum]
                    205041
Seq. No.
                    LIB3083-078-Q1-L1-B3
Seq. ID
                    BLASTX
Method
                    g267082
NCBI GI
                    581
BLAST score
                    3.0e-60
E value
                    106
Match length
                    99
% identity
                   TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
NCBI Description
                    chain - Arabidopsis thalīana >gī 166908 (M84705) beta-8
```

Seq. No. 205042

28034

tubulin [Arabidopsis thaliana]



```
LIB3083-078-Q1-L1-B4
Seq. ID
                   BLASTX
Method
                    q2194118
NCBI GI
                    204
BLAST score
                    4.0e-16
E value
                    71
Match length
% identity
                    (AC002062) F20P5.4 gene product [Arabidopsis thaliana]
NCBI Description
                    205043
Seq. No.
                    LIB3083-078-Q1-L1-B6
Seq. ID
                    BLASTX
Method
                    g2129575
NCBI GI
                    335
BLAST score
                    2.0e-31
E value
                    74
Match length
                    86
% identity
NCBI Description DNA repair protein homolog XPBara - Arabidopsis thaliana
                    205044
Seq. No.
                    LIB3083-078-Q1-L1-B7
Seq. ID
                    BLASTX
Method
                    g4531440
NCBI GI
                    142
BLAST score
                    8.0e-09
E value
                    100
Match length
                    40
% identity
                    (AC006224) unknown protein [Arabidopsis thaliana]
NCBI Description
                    205045
Seq. No.
                    LIB3083-078-Q1-L1-C1
Seq. ID
                    BLASTX
Method
                     g1076708
NCBI GI
                     591
BLAST score
                     2.0e-61
E value
                     119
Match length
                     27
 % identity
                     seed tetraubiquitin - common sunflower
 NCBI Description
                    >gi 303901 dbj BAA03764 (D16248) ubiquitin [Glycine max] >gi 456714 dbj BAA05670 (D28123) Ubiquitin [Glycine max] >gi 556688 emb CAA84440 (Z34988) seed tetraubiquitin
                     [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
                     Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                     putative polyubiquitin [Arabidopsis thaliana]
                     >gi 1096513 prf 2111434A tetraubiquitin [Helianthus
                     annuus]
                     205046
 Seq. No.
                     LIB3083-078-Q1-L1-C11
 Seq. ID
                     BLASTX
 Method
 NCBI GI
                     q3608485
                     638
 BLAST score
                     6.0e-67
 E value
                     127
 Match length
                     95
 % identity
 NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]
```



```
205047
Seq. No.
                  LIB3083-078-Q1-L1-C12
Seq. ID
                  BLASTX
Method
                  g120673
NCBI GI
                  524
BLAST score
                  1.0e-53
E value
Match length
                  128
                  81
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >qi 66013 pir DEPJG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - garden petunia
                  >gi 20551_emb CAA42904_ (X60346) glyceraldehyde
                  3-phosphate dehydrogenase [Petunia x hybrida]
                  205048
Seq. No.
                  LIB3083-078-Q1-L1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2098709
                   431
BLAST score
                  1.0e-42
E value
                  123
Match length
                   72
% identity
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
                   205049
Seq. No.
                   LIB3083-078-Q1-L1-C7
Seq. ID
                   BLASTN
Method
                   q1143223
NCBI GI
BLAST score
                   133
                   1.0e-68
E value
                   375
Match length
                   55
% identity
                  Gossypium barbadense FbLate-2 gene, complete cds
NCBI Description
                   205050
Seq. No.
                   LIB3083-078-Q1-L1-C9
Seq. ID
                   BLASTX
Method
                   q2129495
NCBI GI
BLAST score
                   571
                   4.0e-59
E value
                   119
Match length
                   90
% identity
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                   (U30508) E6 [Gossypium barbadense]
                   205051
 Seq. No.
                   LIB3083-078-Q1-L1-D1
 Seq. ID
                   BLASTX
 Method
                   g3033400
 NCBI GI
```

NCBI GI g3033400
BLAST score 603
E value 7.0e-63
Match length 126
% identity 94

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]



67

Match length

NCBI Description

% identity

```
205052
Seq. No.
                  LIB3083-078-Q1-L1-D11
Seq. ID
                  BLASTX
Method
                  g1729980
NCBI GI
                  392
BLAST score
                  3.0e-38
E value
                  85
Match length
                  76
% identity
                  THAUMATIN-LIKE PROTEIN PRECURSOR >gi 2129751_pir__S71175
NCBI Description
                  thaumatin-like protein - Arabidopsis thaliana >gi_536825
                   (L34693) thaumatin-like protein [Arabidopsis thaliana]
                  >gi 1094863 prf__2106421A thaumatin-like protein
                   [Arabidopsis thaliana]
                  205053
Seq. No.
                  LIB3083-078-Q1-L1-D12
Seq. ID
Method
                  BLASTN
                   q1143223
NCBI GI
                  89
BLAST score
                   2.0e-42
E value
Match length
                   271
                   24
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   205054
Seq. No.
                   LIB3083-078-Q1-L1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4371292
BLAST score
                   491
                   1.0e-49
E value
Match length
                   120
                   72
% identity
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205055
Seq. No.
                   LIB3083-078-Q1-L1-D5
Seq. ID
                   {\tt BLASTX}
Method
                   g267069
NCBI GI
                   568
BLAST score
                   9.0e-59
E value
                   106
Match length
                   99
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   205056
Seq. No.
                   LIB3083-078-Q1-L1-D6
Seq. ID
                   BLASTX
Method
                   g2098709
NCBI GI
BLAST score
                   357
                   5.0e-34
E value
```

(U82975) pectinesterase [Citrus sinensis]



```
Seq. No.
                  LIB3083-078-Q1-L1-D8
Seq. ID
                  BLASTX
Method
                  g2673910
NCBI GI
BLAST score
                  190
                  2.0e-14
E value
                  94
Match length
                  48
% identity
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  205058
Seq. No.
                  LIB3083-078-Q1-L1-D9
Seq. ID
Method
                  BLASTX
                  q4510383
NCBI GI
                   476
BLAST score
                   6.0e-48
E value
Match length
                  128
                  76
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205059
Seq. No.
Seq. ID
                  LIB3083-078-Q1-L1-E1
Method
                  BLASTX
NCBI GI
                   g2708324
BLAST score
                   191
E value
                   1.0e-14
Match length
                   57
                   67
% identity
                   (AF037455) glutaredoxin type 1 [Fritillaria agrestis]
NCBI Description
                   >gi 2724048 (AF037984) glutaredoxin type II [Fritillaria
                   agrestis] >gi 2724050 (AF037985) glutaredoxin type I
                   [Fritillaria agrestis] >gi 2724052 (AF037986) glutaredoxin
                   type I [Fritillaria agrest\overline{i}s] >gi_2724054 (AF0\overline{3}7987)
                   glutaredoxin type I [Fritillaria agrestis] >gi_2724056
                   (AF037988) glutaredoxin type I [Fritillaria agrestis]
                   205060
Seq. No.
                   LIB3083-078-Q1-L1-E10
Seq. ID
                   BLASTN
Method
                   g2829205
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
Match length
                   366
                   26
% identity
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
                   205061
Seq. No.
Seq. ID
                   LIB3083-078-Q1-L1-E11
                   BLASTX
Method
                   g4098129
NCBI GI
BLAST score
                   660
```

(U73588) sucrose synthase [Gossypium hirsutum]

2.0e-69

128

98

E value

Match length

NCBI Description

% identity

```
205062
Seq. No.
                  LIB3083-078-Q1-L1-E2
Seq. ID
                  BLASTX
Method
                  g806310
NCBI GI
                  177
BLAST score
                  7.0e-13
E value
Match length
                  124
% identity
                  (J02746) proline-rich protein [Glycine max]
NCBI Description
Seq. No.
                   205063
                   LIB3083-078-Q1-L1-E3
Seq. ID
Method
                  BLASTX
                   g1706958
NCBI GI
                   697
BLAST score
                   7.0e-74
E value
Match length
                   127
                   100
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   205064
Seq. No.
                   LIB3083-078-Q1-L1-E4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1143223
                   236
BLAST score
                   1.0e-130
E value
                   363
Match length
                   28
% identity
                   Gossypium barbadense FbLate-2 gene, complete cds
NCBI Description
                   205065
Seq. No.
                   LIB3083-078-Q1-L1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1518540
                   211
BLAST score
E value
                   4.0e-20
Match length
                   112
                   53
% identity
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   205066
Seq. No.
                   LIB3083-078-Q1-L1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1518540
BLAST score
                   482
                   9.0e-49
E value
Match length
                   111
% identity
                   88
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
```

205067 Seq. No.

LIB3083-078-Q1-L1-F2 Seq. ID

BLASTX Method g4220521 NCBI GI 158 BLAST score 1.0e-10 E value 97 Match length

NCBI Description

```
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  205068
Seq. No.
                  LIB3083-078-Q1-L1-F4
Seq. ID
                  BLASTX
Method
                  g136739
NCBI GI
                  530
BLAST score
                  2.0e-54
E value
                  123
Match length
                  80
% identity
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                   205069
                  LIB3083-078-Q1-L1-F8
Seq. ID
                  BLASTX
Method
                   g1335862
NCBI GI
BLAST score
                   476
                   3.0e-48
E value
                   125
Match length
                   75
% identity
NCBI Description (U42608) clathrin heavy chain [Glycine max]
                   205070
Seq. No.
                   LIB3083-078-Q1-L1-F9
Seq. ID
                   BLASTX
Method
                   g2065531
NCBI GI
                   359
BLAST score
                   3.0e-34
E value
                   73
Match length
                   89
% identity
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
                   205071
Seq. No.
                   LIB3083-078-Q1-L1-G11
Seq. ID
                   BLASTX
Method
                   g606942
NCBI GI
                   607
BLAST score
                   2.0e-63
E value
                   121
Match length
                   98
% identity
                  (U13760) unknown [Gossypium hirsutum]
NCBI Description
                   205072
Seq. No.
                   LIB3083-078-Q1-L1-G12
Seq. ID
                   BLASTX
Method
                   g1418319
NCBI GI
BLAST score
                   195
                   4.0e-15
E value
                   101
Match length
                   43
 % identity
```

(X95965) CER1-like [Arabidopsis thaliana]

```
205073
Seq. No.
                  LIB3083-078-Q1-L1-G3
Seq. ID
                  BLASTX
Method
                   g3608154
NCBI GI
                   397
BLAST score
                   1.0e-38
E value
                   122
Match length
                   66
% identity
                   (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 205074 Seq. ID LIB3083-078-Q1-L1-G5

Method BLASTX
NCBI GI g2864609
BLAST score 158
E value 1.0e-11
Match length 71
% identity 55

NCBI Description (AL021811) putative protein [Arabidopsis thaliana] >gi 4049337 emb CAA22562\_ (AL034567) putative protein

[Arabidopsis thaliana]

 Seq. No.
 205075

 Seq. ID
 LIB3083-078-Q1-L1-G6

 Method
 BLASTX

NCBI GI g1771780
BLAST score 483
E value 8.0e-49
Match length 120
% identity 79

NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 205076

Seq. ID LIB3083-078-Q1-L1-G8

Method BLASTX
NCBI GI g1552169
BLAST score 210
E value 9.0e-17
Match length 114
% identity 43

NCBI Description (D42138) PIG-B [Homo sapiens]

Seq. No. 205077

Seq. ID LIB3083-078-Q1-L1-G9

Method BLASTX
NCBI GI g1814403
BLAST score 299
E value 2.0e-27
Match length 76
% identity 72

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 205078

Seq. ID LIB3083-078-Q1-L1-H1

Method BLASTN NCBI GI g2829205



```
BLAST score
                   0.0e + 00
E value
                   384
Match length
                   18
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
Seq. No.
                   205079
                  LIB3083-078-Q1-L1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4325369
                   147
BLAST score
                   1.0e-09
E value
                   98
Match length
                   38
% identity
                  (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
NCBI Description
                   205080
Seq. No.
                   LIB3083-078-Q1-L1-H11
Seq. ID
Method
                   BLASTX
                   g3511285
NCBI GI
BLAST score
                   460
E value
                   4.0e-46
```

122 Match length 71 % identity

(AF081534) cellulose synthase [Populus alba x Populus NCBI Description

tremula]

205081 Seq. No.

LIB3083-078-Q1-L1-H12 Seq. ID

BLASTN Method NCBI GI g3241920 BLAST score 36 7.0e-11 E value 88 Match length 85 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MAE1, complete sequence [Arabidopsis thaliana]

205082 Seq. No.

Seq. ID LIB3083-078-Q1-L1-H2

BLASTX Method NCBI GI g421929 BLAST score 239 3.0e-20 E value 89 Match length % identity

ubiquitin - tomato >qi 312160 emb CAA51679 (X73156) NCBI Description

ubiquitin [Lycopersicon esculentum]

205083 Seq. No.

Seq. ID LIB3083-078-Q1-L1-H3

Method BLASTX g4539335 NCBI GI BLAST score 186 E value 6.0e-14Match length 51



% identity 59
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No. 205084
Seq. ID LIB3083-078-Q1-L1-H5

Method BLASTX
NCBI GI g2780194
BLAST score 607
E value 2.0e-63
Match length 123

% identity 62

NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No. 205085

Seq. ID LIB3083-078-Q1-L1-H6

Method BLASTX
NCBI GI g4544432
BLAST score 487
E value 3.0e-49
Match length 120
% identity 78

NCBI Description (AC006955) putative mannose-1-phosphate guanyltransferase

[Arabidopsis thaliana]

Seq. No. 205086

Seq. ID LIB3083-078-Q1-L1-H8

Method BLASTN
NCBI GI g1143223
BLAST score 188
E value 1.0e-101
Match length 385
% identity 32

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205087

Seq. ID LIB3083-078-Q1-L1-H9

Method BLASTX
NCBI GI g2499710
BLAST score 482
E value 1.0e-48
Match length 112
% identity 85

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>qi 1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No. 205088

Seq. ID LIB3083-079-Q1-L1-A10

Method BLASTX
NCBI GI g4469023
BLAST score 550
E value 1.0e-56
Match length 123
% identity 83

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 205089

BLAST score

174

```
LIB
```

```
LIB3083-079-Q1-L1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1619602
                   368
BLAST score
                   3.0e-35
E value
                   100
Match length
                   72
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                   205090
Seq. No.
                  LIB3083-079-Q1-L1-A9
Seq. ID
                   BLASTX
Method
                   g481526
NCBI GI
                   309
BLAST score
                   2.0e-28
E value
                   122
Match length
                   57
% identity
NCBI Description probable ribosomal protein S1 - wheat mitochondrion
                   205091
Seq. No.
                   LIB3083-079-Q1-L1-B10
Seq. ID
Method
                   BLASTX
                   g123620
NCBI GI
                   407
BLAST score
                   7.0e-40
E value
                   110
Match length
                   75
% identity
                   HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950
NCBI Description
                   heat shock cognate protein 70 - tomato
                   >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
                   70 [Lycopersicon esculentum]
                   205092
Seq. No.
Seq. ID
                   LIB3083-079-Q1-L1-B11
                   BLASTX
Method
                   g1895084
NCBI GI
BLAST score
                   535
                   7.0e-55
E value
                   110
Match length
                   90
% identity
                  (U89897) golgi associated protein se-wap41 [Zea mays]
NCBI Description
                   205093
Seq. No.
                   LIB3083-079-Q1-L1-B9
Seq. ID
                   BLASTX
Method
                   q606942
NCBI GI
BLAST score
                   453
                   3.0e-45
E value
                   117
Match length
                   81
 % identity
                  (U13760) unknown [Gossypium hirsutum]
NCBI Description
                   205094
 Seq. No.
Seq. ID
                   LIB3083-079-Q1-L1-C10
Method
                   BLASTX
NCBI GI
                   q1171577
```



E value 1.0e-12 Match length 98 % identity 38

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.

205095

Seq. ID

LIB3083-079-Q1-L1-C12

Method NCBI GI BLAST score BLASTX g312179 223

8.0e-19

49

86

E value
Match length
% identity

NCBI Description

(X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi\_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi\_1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No.

205096

Seq. ID

LIB3083-079-Q1-L1-C9

Method BLASTX
NCBI GI g4126473
BLAST score 601
E value 1.0e-62
Match length 115
% identity 99

NCBI Description (AB014884) adenylyl cyclase associated protein [Gossypium

hirsutum]

Seq. No.

205097

Seq. ID

LIB3083-079-Q1-L1-D10

Method BLASTX
NCBI GI g4522004
BLAST score 164
E value 2.0e-11
Match length 118
% identity 36

NCBI Description (AC007069) putative histidine kinase, sensory transduction

[Arabidopsis thaliana]

Seq. No.

205098

Seq. ID

LIB3083-079-Q1-L1-D11

Method BLASTX
NCBI GI g3688178
BLAST score 186
E value 6.0e-14
Match length 100
% identity 41

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No.

205099

Seq. ID

LIB3083-079-Q1-L1-D12

Method BLASTN
NCBI GI g1143223
BLAST score 243
E value 1.0e-134



Match length 26 % identity

Gossypium barbadense FbLate-2 gene, complete cds NCBI Description

Seq. No.

205100

Seq. ID

LIB3083-079-Q1-L1-D9

Method NCBI GI BLAST score BLASTX q2275196 368

3.0e-35 E value 75 Match length 95 % identity

(AC002337) water stress-induced protein, WSI76 isolog NCBI Description

[Arabidopsis thaliana]

Seq. No.

205101

Seq. ID

LIB3083-079-Q1-L1-E11

BLASTX Method g2245378 NCBI GI BLAST score 160 6.0e-11 E value 36 Match length

75 % identity

(U83245) auxin response factor 1 [Arabidopsis thaliana] NCBI Description

Seq. No.

205102

Seq. ID

LIB3083-079-Q1-L1-E9

BLASTX Method q4580523 NCBI GI 425 BLAST score 5.0e-42 E value 122 Match length 70 % identity

(AF036305) scarecrow-like 8 [Arabidopsis thaliana] NCBI Description

Seq. No.

205103

Seq. ID

LIB3083-079-Q1-L1-F11

BLASTX Method q2738998 NCBI GI 570 BLAST score E value 5.0e-59 123 Match length % identity 85

(AF022458) CYP98A2p [Glycine max] NCBI Description

Seq. No.

205104

Seq. ID

LIB3083-079-Q1-L1-F12

BLASTX Method NCBI GI g1518540 BLAST score 172 1.0e-12 E value Match length 94 51 % identity

(U53418) UDP-glucose dehydrogenase [Glycine max] NCBI Description

Seq. No.

205105

Seq. ID

LIB3083-079-Q1-L1-F9



```
Method
                  g2245091
NCBI GI
                  162
BLAST score
                   4.0e-11
E value
                   46
Match length
                   74
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205106
Seq. No.
                  LIB3083-079-Q1-L1-G10
Seq. ID
                  BLASTX
Method
                   g2827699
NCBI GI
                   496
BLAST score
                   2.0e-50
E value
                   123
Match length
                   75
% identity
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   205107
Seq. No.
                   LIB3083-079-Q1-L1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3236252
BLAST score
                   410
                   3.0e-40
E value
Match length
                   126
                   60
% identity
                   (AC004684) CER1-like protein [Arabidopsis thaliana]
NCBI Description
                   205108
Seq. No.
                   LIB3083-079-Q1-L1-H10
Seq. ID
                   BLASTX
Method
                   g2739376
NCBI GI
BLAST score
                   409
                   4.0e-40
E value
                   126
Match length
                   64
% identity
                   (AC002505) putative permease [Arabidopsis thaliana]
NCBI Description
                   205109
Seq. No.
                   LIB3083-079-Q1-L1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4417283
                   232
BLAST score
                   2.0e-19
E value
                   121
Match length
                   40
% identity
```

(AC007019) putative cytochrome p450 [Arabidopsis thaliana] NCBI Description

205110 Seq. No.

Seq. ID LIB3083-080-Q1-L1-A1

BLASTX Method NCBI GI g1076387 280 BLAST score 2.0e-25 E value Match length 66 77 % identity

NCBI Description protein kinase homolog - Arabidopsis thaliana





>gi\_717180\_emb\_CAA55866\_ (X79279) protein kinase homologous
to shaggy and glycogen synthase kinase-3 [Arabidopsis
thaliana]

 Seq. No.
 205111

 Seq. ID
 LIB3083-080-Q1-L1-A3

 Method
 BLASTN

NCBI GI g4322254
BLAST score 53
E value 5.0e-21
Match length 144
% identity 91

NCBI Description Corythophora alta rp120-5'-rps12 intergenic region,

chloroplast sequence

Seq. No. 205112

Seq. ID LIB3083-080-Q1-L1-A6

Method BLASTX
NCBI GI g2653446
BLAST score 432
E value 6.0e-43
Match length 108
% identity 80

NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]

Seq. No. 205113

Seq. ID LIB3083-080-Q1-L1-A9

Method BLASTX
NCBI GI g2500345
BLAST score 259
E value 5.0e-23
Match length 60
% identity 85

NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)

>qi 2618578 dbj BAA23363 (D50420) OTK27 [Homo sapiens]

>gi\_3859990 (AF091076) OTK27 [Homo sapiens]

>gi\_1589072\_prf\_\_2210268A nuclear protein-NHP2-like protein

[Homo sapiens]

Seq. No. 205114

Seq. ID LIB3083-080-Q1-L1-B1

Method BLASTN
NCBI GI g1143223
BLAST score 189
E value 1.0e-102
Match length 205
% identity 38

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205115

Seq. ID LIB3083-080-Q1-L1-B10

Method BLASTX
NCBI GI g2306917
BLAST score 435
E value 3.0e-43
Match length 96



```
% identity
                   (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                   thaliana]
                   205116
Seq. No.
Seq. ID
                   LIB3083-080-Q1-L1-B11
Method
                   BLASTX
NCBI GI
                   g2499611
BLAST score
                   477
E value
                   4.0e-48
Match length
                   99
% identity
                   92
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
NCBI Description
                   (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                   >qi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis
                   thaliana]
                   205117
Seq. No.
                   LIB3083-080-Q1-L1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3415115
BLAST score
                   510
E value
                   6.0e-52
Match length
                   125
                   37
% identity
NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]
Seq. No.
                   205118
                   LIB3083-080-Q1-L1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1669573
BLAST score
                   336
                   5.0e-32
E value
Match length
                   73
% identity
                   89
NCBI Description (D88399) endosperm kinase [Oryza sativa]
Seq. No.
                   205119
                   LIB3083-080-Q1-L1-B3
Seq. ID
Method
                   BLASTX
                   g606942
NCBI GI
BLAST score
                   365
                   2.0e-35
E value
                   73
Match length
                   99
% identity
                   (U13760) unknown [Gossypium hirsutum]
NCBI Description
                   205120
Seq. No.
                   LIB3083-080-Q1-L1-B5
Seq. ID
                   BLASTX
Method
                   g4371290
NCBI GI
BLAST score
                   145
                   3.0e-09
E value
                   39
Match length
```

28049

NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

64

% identity

Seq. ID

Method



```
205121
Seq. No.
                  LIB3083-080-Q1-L1-B6
Seq. ID
                  BLASTX
Method
                  g1710780
NCBI GI
                  343
BLAST score
                  3.0e-32
E value
                  74
Match length
                  85
% identity
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917_emb CAA65433_
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
                  205122
Seq. No.
                  LIB3083-080-Q1-L1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204765
                  308
BLAST score
                  8.0e-29
E value
                  70
Match length
% identity
                  84
NCBI Description (U51194) peroxidase [Glycine max]
                  205123
Seq. No.
                  LIB3083-080-Q1-L1-B9
Seq. ID
                  BLASTX
Method
                   g4102839
NCBI GI
                   293
BLAST score
                   6.0e-27
E value
                   76
Match length
                   74
% identity
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
                   205124
Seq. No.
                   LIB3083-080-Q1-L1-C1
Seq. ID
                   BLASTX
Method
                   g1657948
NCBI GI
                   274
BLAST score
                   1.0e-24
E value
                   77
Match length
                   74
% identity
                  (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
                   205125
Seq. No.
                   LIB3083-080-Q1-L1-C11
Seq. ID
                   BLASTX
Method
                   g3342552
NCBI GI
BLAST score
                   220
                   6.0e-18
E value
                   94
Match length
                   48
% identity
                  (AF076979) putative strictosidine synthase [Arabidopsis
NCBI Description
                   thaliana]
                   205126
Seq. No.
```

28050

LIB3083-080-Q1-L1-C12

BLASTX



```
NCBI GI
BLAST score
                  659
E value
                  2.0e-69
                  126
Match length
% identity
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                   (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
Seq. No.
                   205127
                   LIB3083-080-Q1-L1-C2
Seq. ID
Method
                   BLASTX
                   g1657621
NCBI GI
                   219
BLAST score
                   4.0e-18
E value
                   53
Match length
                   75
% identity
                  (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
NCBI Description
                   putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                   205128
Seq. No.
                   LIB3083-080-Q1-L1-C3
Seq. ID
Method
                   BLASTX
                   g2995990
NCBI GI
BLAST score
                   344
                   1.0e-32
E value
                   105
Match length
                   64
% identity
                   (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2995992 (AF053747) dormancy-associated
                   protein [Arabidopsis thaliana]
                   205129
Seq. No.
                   LIB3083-080-Q1-L1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1708721
                   197
BLAST score
E value
                   2.0e-15
Match length
                   94
% identity
                   41
                   (U60075) 13.pep [Solanum tuberosum]
NCBI Description
                   205130
Seq. No.
                   LIB3083-080-Q1-L1-C5
 Seq. ID
                   BLASTX
Method
                   g2245394
 NCBI GI
 BLAST score
                   273
                   4.0e-24
 E value
 Match length
                   85
```

% identity 61

(U89771) ARF1-binding protein [Arabidopsis thaliana] NCBI Description

Seq. No.

205131

Seq. ID

LIB3083-080-Q1-L1-C6

Method NCBI GI BLASTX g2262173



BLAST score 8.0e-55 E value Match length 117 % identity (AC002329) NADPH thioredoxin reductase [Arabidopsis NCBI Description thaliana] 205132 Seq. No.

Seq. ID LIB3083-080-01-L1-C7

BLASTX Method g549000 NCBI GI 163 BLAST score 1.0e-11 E value 78 Match length 47 % identity

SUCROSE TRANSPORT PROTEIN (SUCROSE PERMEASE) NCBI Description

(SUCROSE-PROTON SYMPORTER) >gi 282839 pir\_\_S28052 sucrose

transport protein - spinach >gi\_21319\_emb\_CAA47604\_

(X67125) sucrose permease [Spinacia oleracea]

205133 Seq. No.

LIB3083-080-Q1-L1-D2 Seq. ID

BLASTN Method g2829205 NCBI GI 243 BLAST score 1.0e-134 E value 243 Match length 23 % identity

Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein NCBI Description

precursor (PRP) mRNA, complete cds

Seq. No. 205134

LIB3083-080-Q1-L1-D3 Seq. ID

BLASTX Method q559684 NCBI GI 433 BLAST score 4.0e-43 E value 94 Match length 88 % identity

(L36097) aquaporin [Mesembryanthemum crystallinum] NCBI Description

Seq. No. 205135

Seq. ID LIB3083-080-Q1-L1-D5

BLASTX Method NCBI GI q3983665 382 BLAST score 4.0e-37 E value 99 Match length 71 % identity

(AB011271) importin-beta2 [Oryza sativa] NCBI Description

Seq. No. 205136

LIB3083-080-Q1-L1-D6 Seq. ID

BLASTX Method NCBI GI q135452 BLAST score 553 4.0e-57 E value



Match length 89 % identity

TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin NCBI Description

[Glycine max]

205137 Seq. No.

LIB3083-080-Q1-L1-D8 Seq. ID

BLASTX Method NCBI GI g1082054 157 BLAST score 6.0e-11 E value 73 Match length

% identity (Z49859) copper transporter protein [Arabidopsis thaliana] NCBI Description

205138 Seq. No.

LIB3083-080-Q1-L1-D9 Seq. ID

45

BLASTX Method g3769472 NCBI GI 153 BLAST score 3.0e-10 E value Match length 44 % identity 57

(AF064732) putative phospholipase A2 [Dianthus NCBI Description

caryophyllus]

205139 Seq. No.

LIB3083-080-Q1-L1-E11 Seq. ID

Method BLASTX g4314378 NCBI GI 303 BLAST score 8.0e-28 E value Match length 107 51 % identity

(AC006232) putative lipase [Arabidopsis thaliana] NCBI Description

205140 Seq. No.

LIB3083-080-Q1-L1-E12 Seq. ID

BLASTX Method NCBI GI g1706958 BLAST score 451 4.0e-45 E value 121 Match length 66 % identity

(U58284) cellulose synthase [Gossypium hirsutum] NCBI Description

205141 Seq. No.

Seq. ID LIB3083-080-Q1-L1-E4

BLASTX Method NCBI GI q404688 159 BLAST score 6.0e-11 E value Match length 64 48 % identity

(L19074) cytochrome P450 [Catharanthus roseus] NCBI Description

Seq. No. 205142

```
LIB3083-080-Q1-L1-E5
Seq. ID
                  BLASTN
Method
                  g1143223
NCBI GI
                  199
BLAST score
                  1.0e-108
E value
                  331
Match length
                  28
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                  205143
Seq. No.
                  LIB3083-080-Q1-L1-E8
Seq. ID
Method
                  BLASTX
                  q3790102
NCBI GI
                  406
BLAST score
                  6.0e-40
E value
                  86
Match length
% identity
                  88
                   (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                  alpha subunit [Citrus X paradisi]
                  205144
Seq. No.
Seq. ID
                  LIB3083-080-Q1-L1-E9
Method
                  BLASTX
                  g547683
NCBI GI
BLAST score
                   412
                   1.0e-40
E value
                   78
Match length
                   97
% identity
                  HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat
NCBI Description
                   shock cognate protein 80 [Solanum lycopersicum]
                   >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
                   205145
Seq. No.
                   LIB3083-080-Q1-L1-F1
Seq. ID
                   BLASTX
Method
                   q1706958
NCBI GI
                   285
BLAST score
                   1.0e-25
E value
                   102
Match length
                   66
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   205146
Seq. No.
                   LIB3083-080-Q1-L1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3202040
                   332
BLAST score
                   4.0e-31
E value
                   92
Match length
% identity
```

NCBI Description (AF069323) permease 1 [Mesembryanthemum crystallinum]

Seq. No.

205147

Seq. ID

LIB3083-080-Q1-L1-F11

Method NCBI GI BLASTX q1737222

```
BLAST score
                  2.0e-63
E value
                  114
Match length
                  90
% identity
                  (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]
NCBI Description
                  205148
Seq. No.
                  LIB3083-080-Q1-L1-F3
Seq. ID
                  BLASTX
Method
                  g2529680
NCBI GI
                  307
BLAST score
                  2.0e-28
E value
                  88
Match length
                   40
% identity
                   (AC002535) putative protein disulfide-isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   205149
Seq. No.
                  LIB3083-080-Q1-L1-F5
Seq. ID
                  BLASTX
                   g2104949
                   539
                   2.0e-55
                   118
```

Method NCBI GI BLAST score E value Match length % identity 86 (U96716) MAP kinase-like protein [Selaginella lepidophylla] NCBI Description

205150 Seq. No. LIB3083-080-Q1-L1-F6 Seq. ID BLASTX Method

g2495365 NCBI GI BLAST score 557 2.0e-57 E value Match length 113 96 % identity

HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B NCBI Description heat shock protein HSP81-2 [Arabidopsis thaliana]

205151 Seq. No. LIB3083-080-Q1-L1-F9 Seq. ID

BLASTX Method NCBI GI q135452 BLAST score 391 2.0e-38 E value Match length 80 88 % identity

TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin NCBI Description [Glycine max]

Seq. No. 205152

Seq. ID LIB3083-080-Q1-L1-G10

BLASTX Method g3522956 NCBI GI 406 BLAST score E value 1.0e-39 132 Match length % identity 61

Method

BLASTX



```
(AC004411) putative pectinacetylesterase precursor
NCBI Description
                  [Arabidopsis thaliana]
                  205153
Seq. No.
                  LIB3083-080-Q1-L1-G12
Seq. ID
                  BLASTX
Method
                  g3482933
NCBI GI
                  353
BLAST score
                  2.0e-35
E value
                  97
Match length
                  66
% identity
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                  thaliana]
                  205154
Seq. No.
                  LIB3083-080-Q1-L1-G3
Seq. ID
                  BLASTX
Method
                   g2347199
NCBI GI
                   254
BLAST score
                   4.0e-22
E value
                   80
Match length
% identity
                   68
                   (AC002338) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
                   205155
Seq. No.
                   LIB3083-080-Q1-L1-G4
Seq. ID
                   BLASTX
Method
                   g4432855
NCBI GI
BLAST score
                   292
                   2.0e-26
E value
                   107
Match length
                   62
% identity
                  (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205156
Seq. No.
Seq. ID
                   LIB3083-080-Q1-L1-G6
                   BLASTX
Method
                   g2828296
NCBI GI
BLAST score
                   310
                   4.0e-51
E value
                   111
Match length
                   51
% identity
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
NCBI Description
                   205157
Seq. No.
Seq. ID
                   LIB3083-080-Q1-L1-G8
                   BLASTX
Method
                   q4098331
NCBI GI
BLAST score
                   537
                   3.0e-55
E value
                   101
Match length
% identity
                   97
                   (U76896) beta-tubulin 5 [Triticum aestivum]
NCBI Description
Seq. No.
                   205158
                   LIB3083-080-Q1-L1-G9
Seq. ID
```

```
g3360289
NCBI GI
                   343
BLAST score
                  1.0e-32
E value
                   92
Match length
                   72
% identity
                   (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                   1 [Zea mays]
                   205159
Seq. No.
                   LIB3083-080-Q1-L1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4415942
                   353
BLAST score
                   8.0e-34
E value
                   83
Match length
                   81
% identity
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205160
Seq. No.
                   LIB3083-080-Q1-L1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g629692
BLAST score
                   440
                   9.0e-44
E value
                   124
Match length
                   69
% identity
                   hypothetical protein - common tobacco
NCBI Description
                   >gi 506471 emb CAA56189 (X79794) unnamed protein product
                   [Nicotiana tabacum]
                   205161
Seq. No.
                   LIB3083-080-Q1-L1-H2
Seq. ID
Method
                   BLASTX
                   g1518540
NCBI GI
                   305
BLAST score
                   3.0e-28
E value
                   62
Match length
                   92
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   205162
Seq. No.
                   LIB3083-080-Q1-L1-H3
Seq. ID
                   BLASTX
Method
                   g2244736
NCBI GI
                   521
BLAST score
                   2.0e-53
E value
                   96
Match length
                   99
% identity
                  (D88415) expansin [Gossypium hirsutum]
NCBI Description
```

BLAST score 141

205163

BLASTX

q3868853

LIB3083-080-Q1-L1-H4

E value 1.0e-08 Match length 51

Seq. No. Seq. ID

Method

NCBI GI

```
% identity
                  (AB013853) GPI-anchored protein [Vigna radiata]
NCBI Description
Seq. No.
                  205164
                  LIB3083-080-Q1-L1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4098331
BLAST score
                  578
E value
                  6.0e-60
                  106
Match length
% identity
                  96
                  (U76896) beta-tubulin 5 [Triticum aestivum]
NCBI Description
Seq. No.
                  205165
                  LIB3083-080-Q1-L1-H8
Seq. ID
Method
                  BLASTX
                  g1903364
NCBI GI
BLAST score
                  373
                  5.0e-36
E value
Match length
                  103
% identity
                   71
                   (AC000104) EST gb_T45093 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                   205166
Seq. No.
Seq. ID
                  LIB3083-080-Q1-L1-H9
                  BLASTX
Method
NCBI GI
                   g1706958
BLAST score
                   441
                   5.0e-44
E value
Match length
                   98
                   86
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   205167
Seq. No.
                   LIB3083-081-Q1-L1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2829894
BLAST score
                   357
                   6.0e - 34
E value
Match length
                   122
                   57
% identity
                  (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205168
Seq. ID
                   LIB3083-081-Q1-L1-A11
Method
                   BLASTX
NCBI GI
                   g3355470
BLAST score
                   275
                   2.0e-24
E value
Match length
                   76
% identity
                   67
                  (AC004218) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana]
                   205169
Seq. No.
                   LIB3083-081-Q1-L1-A12
Seq. ID
```

28058

a)

```
BLASTX
Method
NCBI GI
                  g1706956
BLAST score
                   638
                   6.0e-67
E value
Match length
                   124
% identity
                   100
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   205170
                  LIB3083-081-Q1-L1-A2
Seq. ID
                   BLASTX
Method
                   q4097569
NCBI GI
BLAST score
                   148
                   2.0e-09
E value
                   36
Match length
                   78
% identity
                  (U64915) GMFP4 [Glycine max]
NCBI Description
                   205171
Seq. No.
Seq. ID
                   LIB3083-081-Q1-L1-A3
                   BLASTX
Method
                   q4454026
NCBI GI
                   350
BLAST score
                   3.0e-33
E value
Match length
                   115
% identity
                   64
NCBI Description
```

(AL035394) phosphatase like protein [Arabidopsis thaliana]

205172 Seq. No. Seq. ID LIB3083-081-Q1-L1-A4 Method BLASTX q1076274 NCBI GI BLAST score 269 1.0e-23 E value

Match length 114 % identity 48

cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment) NCBI Description

Seq. No. 205173

Seq. ID LIB3083-081-Q1-L1-A5

Method BLASTX NCBI GI q4510345 BLAST score 232 E value 2.0e-19 Match length 121 % identity 44

(AC006921) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 205174

LIB3083-081-Q1-L1-A6 Seq. ID

Method BLASTX g4309760 NCBI GI BLAST score 211 6.0e-17 E value Match length 88 55 % identity

NCBI Description (AC006217) unknown protein [Arabidopsis thaliana]

Seq. ID

```
205175
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-A7
                  BLASTX
Method
NCBI GI
                  g4262240
BLAST score
                  195
                  2.0e-15
E value
                  78
Match length
                  53
% identity
                  (AC006200) putative stress protein [Arabidopsis thaliana]
NCBI Description
                  205176
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-A8
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  305
                  1.0e-171
E value
                  321
Match length
                  20
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  205177
Seq. No.
                  LIB3083-081-Q1-L1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3128234
BLAST score
                   425
                   6.0e-42
E value
                   89
Match length
                   85
% identity
                  (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205178
Seq. No.
                  LIB3083-081-Q1-L1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076580
BLAST score
                   321
                   8.0e-30
E value
Match length
                   96
                   65
% identity
                   alcohol dehydrogenase homolog ADH3b - tomato
NCBI Description
                   >gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH
                   {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red
                   cherry, Peptide, 390 aa] [Lycopersicon esculentum]
Seq. No.
                   205179
                   LIB3083-081-Q1-L1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3402722
BLAST score
                   244
E value
                   8.0e-21
Match length
                   84
% identity
                   58
                   (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
                   205180
Seq. No.
```

28060

LIB3083-081-Q1-L1-B12

```
BLASTX
Method
                  g2459412
NCBI GI
                   431
BLAST score
                  1.0e-42
E value
                  105
Match length
                  70
% identity
                  (AC002332) putative G9a protein [Arabidopsis thaliana]
NCBI Description
                  205181
Seq. No.
                  LIB3083-081-Q1-L1-B2
Seq. ID
                  BLASTX
Method
                   q1143445
NCBI GI
                   478
BLAST score
                   3.0e-48
E value
                   108
Match length
% identity
                   81
                  (X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]
NCBI Description
                   205182
Seq. No.
                   LIB3083-081-Q1-L1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510345
BLAST score
                   167
                   1.0e-11
E value
Match length
                   80
                   46
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205183
Seq. No.
                   LIB3083-081-Q1-L1-B4
Seq. ID
                   BLASTX
Method
                   q4033838
NCBI GI
BLAST score
                   399
                   4.0e-39
E value
Match length
                   102
% identity
                   46
                  (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                   205184
Seq. No.
                   LIB3083-081-Q1-L1-B6
Seq. ID
                   BLASTX
Method
                   g3785995
NCBI GI
BLAST score
                   222
                   1.0e-18
E value
                   52
Match length
                   85
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
```

Seq. No. 205185

Seq. ID LIB3083-081-Q1-L1-B8

Method BLASTX
NCBI GI g3122703
BLAST score 468
E value 5.0e-47
Match length 111
% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi\_2641201 (AF031542) ribosomal



## protein L23a [Fritillaria agrestis]

```
205186
Seq. No.
                  LIB3083-081-Q1-L1-C1
Seq. ID
                  BLASTX
Method
                  g3608154
NCBI GI
BLAST score
                  440
                  1.0e-43
E value
                  133
Match length
                  67
% identity
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
                  205187
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-C11
                  BLASTX
Method
                  g3513727
NCBI GI
                   458
BLAST score
                   7.0e-46
E value
                  122
Match length
                   57
% identity
                   (AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                  TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                   kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                   thaliana] >gi 4539358 emb CAB40052.1_ (AL049525) putative
                  protein [Arabidopsis Thaliana]
                   205188
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-C12
                   BLASTX
Method
                   g2688822
NCBI GI
BLAST score
                   204
E value
                   5.0e-16
                   52
Match length
                   69
% identity
                   (U93272) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Prunus armeniaca]
                   205189
Seq. No.
Seq. ID
                   LIB3083-081-Q1-L1-C2
                   BLASTX
Method
NCBI GI
                   g1169384
                   432
BLAST score
                   8.0e-43
E value
Match length
                   111
                   75
% identity
                   DNAJ PROTEIN HOMOLOG ANJ1 >gi 543510 pir JQ2142 chaperone
NCBI Description
                   ANJ1 protein - Atriplex nummularia
                   205190
Seq. No.
                   LIB3083-081-Q1-L1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1665817
BLAST score
                   164
                   2.0e-11
E value
Match length
                   96
% identity
                   35
```

NCBI Description (D87466) Similar to S.cerevisiae hypothetical protein L3111



## (S59316) [Homo sapiens]

```
205191
  Seq. No.
                    LIB3083-081-Q1-L1-C6
  Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q4545262
                    165
 BLAST score
                    2.0e-11
 E value
                    44
 Match length
  % identity
                    66
                    (AF118230) metallothionein-like protein [Gossypium
. NCBI Description
                    hirsutum]
                    205192
  Seq. No.
                    LIB3083-081-Q1-L1-C7
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3107931
  BLAST score
                    587
                    6.0e-61
  E value
  Match length
                    130
  % identity
                    88
                    (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
  NCBI Description
                    205193
  Seq. No.
                    LIB3083-081-Q1-L1-C8
  Seq. ID
  Method
                    BLASTX
                    g3386619
  NCBI GI
  BLAST score
                    232
                     2.0e-19
  E value
                    102
  Match length
                     47
  % identity
                    (AC004665) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                    205194
  Seq. No.
                    LIB3083-081-Q1-L1-C9
  Seq. ID
                    BLASTX
  Method
                    g4490756
  NCBI GI
                     101
  BLAST score
                     1.0e-08
  E value
                     69
  Match length
                     51
  % identity
                    (AL035708) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     205195
  Seq. No.
  Seq. ID
                     LIB3083-081-Q1-L1-D1
  Method
                     BLASTX
                     g2102696
  NCBI GI
  BLAST score
                     301
                     2.0e-27
  E value
                     120
  Match length
                     51
  % identity
                     (U72761) karyopherin beta 3 [Homo sapiens]
  NCBI Description
                     >gi 4504909_ref_NP_002262.1_pKPNB3_ karyopherin (importin)
                     beta
                     205196
  Seq. No.
  Seq. ID
                     LIB3083-081-Q1-L1-D11
```



```
Method
NCBI GI
                  q1045052
BLAST score
                  174
                  2.0e-12
E value
Match length
                  33
                  97
% identity
                  (X88776) alpha tubulin [Eimeria acervulina]
NCBI Description
                  205197
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-D12
                  BLASTX
Method
                  g2462749
NCBI GI
                  298
BLAST score
                  4.0e-27
E value
Match length
                  109
                  58
% identity
                  (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  205198
                  LIB3083-081-Q1-L1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4234941
BLAST score
                  376
                  9.0e-38
E value
Match length
                  120
                  73
% identity
                  (AF097938) cytosolic phosphoglucomutase [Populus tremula x
NCBI Description
                  Populus tremuloides]
Seq. No.
                  205199
                  LIB3083-081-Q1-L1-D3
Seq. ID
                  BLASTX
Method
                  q3334113
NCBI GI
BLAST score
                  466
E value
                  9.0e-47
                  89
Match length
                  100
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
NCBI Description
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  205200
Seq. ID
                  LIB3083-081-Q1-L1-D4
Method
                  BLASTX
NCBI GI
                  g2129473
BLAST score
                  259
                  2.0e-22
E value
Match length
                  94
                  52
% identity
                  arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                  205201
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-D5
Method
                  BLASTX
```

28064

q2098709

318

NCBI GI BLAST score E value 105 Match length 56 % identity (U82975) pectinesterase [Citrus sinensis] NCBI Description 205202 Seq. No. Seq. ID LIB3083-081-Q1-L1-D6 BLASTX Method NCBI GI g4510363 189 BLAST score 2.0e-14 E value 39 Match length 87 % identity (AC007017) putative DNA-binding protein [Arabidopsis NCBI Description thaliana] 205203 Seq. No. LIB3083-081-Q1-L1-D7 Seq. ID BLASTX Method g1203832 NCBI GI BLAST score 560 8.0e-58 E value 131 Match length 77 % identity (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII NCBI Description [Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan exohydrolase [Hordeum vulgare] 205204 Seq. No. LIB3083-081-Q1-L1-D8 Seq. ID BLASTX Method NCBI GI g1351135 BLAST score 613

5.0e-64 E value 129 Match length 89 % identity

SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) NCBI Description

>qi 436792 emb CAA50317 (X70990) sucrose synthase

[Arabidopsis thaliana]

205205 Seq. No.

Seq. ID LIB3083-081-Q1-L1-D9

BLASTN Method g536660 NCBI GI 33 BLAST score 6.0e-09 E value 41 Match length 56 % identity

NCBI Description S.cerevisiae chromosome II reading frame ORF YBR247c

205206 Seq. No.

Seq. ID LIB3083-081-Q1-L1-E1

BLASTX Method NCBI GI q3983665 BLAST score 521 E value 3.0e-53 130 Match length



% identity (AB011271) importin-beta2 [Oryza sativa] NCBI Description

205207 Seq. No.

LIB3083-081-Q1-L1-E3 Seq. ID

BLASTN Method NCBI GI g166919

82 BLAST score

3.0e-38 E value Match length 94 97 % identity

Arabidopsis thaliana alpha-6 tubulin (TUA6) gene, complete NCBI Description

cds

205208 Seq. No.

LIB3083-081-Q1-L1-E4 Seq. ID

Method BLASTX NCBI GI g120673 BLAST score 450 5.0e-45 E value Match length 105 81 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi 66013 pir DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >qi 20551 emb CAA42904 (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

205209 Seq. No.

LIB3083-081-Q1-L1-E6 Seq. ID

BLASTX Method g398845 NCBI GI BLAST score 645 9.0e-68 E value 127 Match length 95

% identity

(X74654) beta3 tubulin [Zea mays] NCBI Description

205210 Seq. No.

Seq. ID LIB3083-081-Q1-L1-E7

BLASTX Method g1946355 NCBI GI BLAST score 222 3.0e-18 E value 127 Match length 39 % identity

(U93215) maize transposon MuDR mudrA protein isolog NCBI Description

[Arabidopsis thaliana] >gi 2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

205211 Seq. No.

LIB3083-081-Q1-L1-F1 Seq. ID

BLASTX Method NCBI GI g3927830 BLAST score 326 2.0e-30 E value Match length 121

% identity (AC005727) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 205212 Seq. ID LIB3083-081-Q1-L1-F10 BLASTX Method NCBI GI g3080420 BLAST score 378 1.0e-36 E value Match length 103 % identity 68 (AL022604) putative sugar transporter protein [Arabidopsis NCBI Description thaliana] 205213 Seq. No. Seq. ID LIB3083-081-Q1-L1-F12 BLASTX Method NCBI GI g3033397 353 7 BLAST score 1.0e-33 E value Match length 95 73 % identity (AC004238) unknown protein [Arabidopsis thaliana] NCBI Description 205214 Seq. No. Seq. ID LIB3083-081-Q1-L1-F3 Method BLASTX g4455206 NCBI GI BLAST score 473 1.0e-47 E value 111 Match length 77 % identity (AL035440) putative beta-1, 3-glucanase [Arabidopsis NCBI Description thaliana] 205215 Seq. No. Seq. ID LIB3083-081-Q1-L1-F4 BLASTX Method

Method BLASTX
NCBI GI g4454051
BLAST score 324
E value 4.0e-30
Match length 112
% identity 58

NCBI Description (AL035394) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 205216

Seq. ID LIB3083-081-Q1-L1-F5

Method BLASTX
NCBI GI g1362086
BLAST score 505
E value 2.0e-51
Match length 113
% identity 90

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_2129919\_pir\_\_\$65957



205217



5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase [Catharanthus roseus]

Seq. ID LIB3083-081-Q1-L1-F6
Method BLASTX
NCBI GI g2829204
BLAST score 513
E value 3.0e-52
Match length 120
% identity 87

NCBI Description (AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

Seq. No. 205218

Seq. No.

Seq. ID LIB3083-081-Q1-L1-F7

Method BLASTX
NCBI GI g1171577
BLAST score 219
E value 8.0e-18
Match length 123
% identity 33

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 205219

Seq. ID LIB3083-081-Q1-L1-F8

Method BLASTX
NCBI GI g4544403
BLAST score 318
E value 2.0e-29
Match length 89
% identity 63

NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase

precursor [Arabidopsis thaliana]

Seq. No. 205220

Seq. ID LIB3083-081-Q1-L1-G10

Method BLASTX
NCBI GI g1332579
BLAST score 491
E value 8.0e-50
Match length 100
% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 205221

Seq. ID LIB3083-081-Q1-L1-G11

Method BLASTX
NCBI GI g3236252
BLAST score 197
E value 1.0e-15
Match length 80
% identity 51

NCBI Description (AC004684) CER1-like protein [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-G12
Method
                  BLASTX
NCBI GI
                  q3548804
BLAST score
                  429
E value
                  2.0e-42
Match length
                  131
                  62
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                  205223
Seq. No.
Seq. ID
                  LIB3083-081-Q1-L1-G2
Method
                  BLASTX
NCBI GI
                  g2144270
BLAST score
                  226
                  4.0e-19
E value
Match length
                  48
% identity
                  88
NCBI Description
                  trans-cinnamate 4-monooxygenase (EC 1.14.13.11) B - Populus
                  kitakamiensis (fragment) >gi 1777371 dbj BAA11577 (D82813)
                  cinnamic acid 4-hydroxylase [Populus kitakamiensis]
Seq. No.
                  205224
                  LIB3083-081-Q1-L1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3834317
BLAST score
                  312
                  1.0e-28
E value
Match length
                  72
% identity
                  75
NCBI Description
                  (AC005679) Similar to CDC16 protein gb U18291 (CDC16Hs)
                  from Homo sapiens. [Arabidopsis thaliana]
Seq. No.
                  205225
Seq. ID
                  LIB3083-081-Q1-L1-G4
Method
                  BLASTX
NCBI GI
                  g2605932
BLAST score
                  331
E value
                  6.0e-31
Match length
                  85
% identity
                  78
NCBI Description
                 (AF029898) aspartate aminotransferase [Lotus corniculatus]
Seq. No.
                  205226
Seq. ID
                  LIB3083-081-Q1-L1-G5
Method
                  BLASTX
NCBI GI
                  g2950210
BLAST score
                  324
E value
                  4.0e-30
Match length
                  87
% identity
                  76
NCBI Description
                 (Y14615) Importin alpha-like protein [Arabidopsis thaliana]
```

Seq. No. 205227

 Seq. ID
 LIB3083-081-Q1-L1-G7

 Method
 BLASTX

 NCBI GI
 q1619602

28069

5 (1) 35 (1)



BLAST score 455 E value 2.0e-45 Match length 129 % identity 67

NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No.

205228

Seq. ID LIB3083-081-Q1-L1-G8

Method BLASTX
NCBI GI g2760832
BLAST score 162
E value 4.0e-11
Match length 80
% identity 46

NCBI Description (AC003105) similar to barley ids-4 gene product

[Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3083-081-Q1-L1-H10

205229

Method BLASTX
NCBI GI g3201615
BLAST score 324
E value 4.0e-30
Match length 121
% identity 56

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 205230

Seq. ID LIB3083-081-Q1-L1-H3

Method BLASTX
NCBI GI g1702983
BLAST score 356
E value 7.0e-34
Match length 111
% identity 59

NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850

hypothetical protein - garden strawberry

>gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria
x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 205231

Seq. ID LIB3083-081-Q1-L1-H5

Method BLASTX
NCBI GI g2213628
BLAST score 210
E value 9.0e-17
Match length 128
% identity 41

NCBI Description (AC000103) F21J9.20 [Arabidopsis thaliana]

Seq. No. 205232

Seq. ID LIB3083-081-Q1-L1-H7

Method BLASTN
NCBI GI g2828278
BLAST score 40
E value 4.0e-13



Match length 82 % identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 205233

Seq. ID LIB3083-081-Q1-L1-H8

Method BLASTX
NCBI GI g3650032
BLAST score 237
E value 6.0e-20
Match length 49
% identity 73

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No. 205234

Seq. ID LIB3083-081-Q1-L1-H9

Method BLASTX
NCBI GI g1076737
BLAST score 279
E value 7.0e-25
Match length 130
% identity 65

NCBI Description beta-tubulin R1623 - rice

Seq. No. 205235

Seq. ID LIB3083-082-Q1-L1-A10

Method BLASTX
NCBI GI g4432841
BLAST score 411
E value 3.0e-40
Match length 132
% identity 58

NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No. 205236

Seq. ID LIB3083-082-Q1-L1-A11

Method BLASTX
NCBI GI g2129955
BLAST score 229
E value 6.0e-19
Match length 84
% identity 58

NCBI Description photoassimilate-responsive protein PAR-1b precursor -

common tobacco >gi\_871487\_emb\_CAA58731\_ (X83851) mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Nicotiana tabacum]

Seq. No. 205237

Seq. ID LIB3083-082-Q1-L1-A12

Method BLASTX
NCBI GI g1706956
BLAST score 661
E value 1.0e-69
Match length 130
% identity 99





```
(U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
Seq. No.
                  205238
Seq. ID
                  LIB3083-082-Q1-L1-A2
Method
                  BLASTN
NCBI GI
                  q2829205
BLAST score
                  348
                  0.0e + 00
E value
Match length
                  384
                  17
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
Seq. No.
                  205239
                  LIB3083-082-Q1-L1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  551
E value
                  1.0e-56
Match length
                  102
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  205240
Seq. No.
                  LIB3083-082-Q1-L1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3176072
BLAST score
                  509
                  8.0e-52
E value
Match length
                  108
                  91
% identity
                  (AJ002485) protein phosphatase 1, catalytic beta subunit
NCBI Description
                   [Medicago sativa]
Seq. No.
                   205241
                  LIB3083-082-Q1-L1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g226261
BLAST score
                  377
                   2.0e-36
E value
Match length
                  78
                   92
% identity
                  alphal tubulin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205242
```

Seq. ID LIB3083-082-Q1-L1-B1

Method BLASTX NCBI GI g3320120 BLAST score 157 1.0e-10 E value 94 Match length 36 % identity

(U66669) 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo NCBI Description

sapiens]

Method

NCBI GI

BLASTX

q538502

```
205243
Seq. No.
Seq. ID
                  LIB3083-082-Q1-L1-B11
Method
                  BLASTX
NCBI GI
                  g1706956
                  673
BLAST score
                  5.0e-71
E value
                  127
Match length
                  100
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  205244
Seq. No.
                  LIB3083-082-Q1-L1-B12
Seq. ID
Method
                  BLASTX
                  g3511285
NCBI GI
BLAST score
                  356
                  6.0e-34
E value
                  118
Match length
                  62
% identity
                   (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
                  tremula]
                  205245
Seq. No.
                  LIB3083-082-Q1-L1-B3
Seq. ID
                  BLASTX
Method
                  q4490737
NCBI GI
                  282
BLAST score
                   4.0e-25
E value
                  120
Match length
                  51
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205246
Seq. ID
                  LIB3083-082-Q1-L1-B5
                  BLASTN
Method
NCBI GI
                  q166919
BLAST score
                   62
                   3.0e - 26
E value
                   81
Match length
                   94
% identity
                  Arabidopsis thaliana alpha-6 tubulin (TUA6) gene, complete
NCBI Description
                   205247
Seq. No.
Seq. ID
                  LIB3083-082-Q1-L1-B7
Method
                  BLASTX
NCBI GI
                  g3687223
                   460
BLAST score
                   4.0e-46
E value
                   126
Match length
% identity
NCBI Description
                  (AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   205248
Seq. ID
                  LIB3083-082-Q1-L1-B8
```

```
BLAST score
                   396
E value
                   1.0e-38
Match length
                   103
% identity
                   72
NCBI Description
                  (L36231) peroxidase [Stylosanthes humilis]
Seq. No.
                   205249
Seq. ID
                   LIB3083-082-Q1-L1-C1
Method
                   BLASTX
NCBI GI
                   q3935145
BLAST score
                   299
E value
                   3.0e-27
Match length
                   85
% identity
                   65
NCBI Description (AC005106) T25N20.9 [Arabidopsis thaliana]
Seq. No.
                   205250
Seq. ID
                   LIB3083-082-Q1-L1-C10
Method
                  BLASTX
NCBI GI
                   q3820614
BLAST score
                   160
E value
                   6.0e-11
Match length
                   120
% identity
                   36
NCBI Description (AF094516) E1-like protein [Homo sapiens]
Seq. No.
                  205251
Seq. ID
                  LIB3083-082-Q1-L1-C12
Method
                  BLASTX
NCBI GI
                  q3367571
BLAST score
                  182
E value
                  1.0e-13
Match length
                  71
% identity
                  55
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                  205252
Seq. ID
                  LIB3083-082-Q1-L1-C3
```

Method BLASTX NCBI GI g2467274 BLAST score 160 E value 6.0e-11 Match length 43 % identity 65

NCBI Description (Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 205253

Seq. ID LIB3083-082-Q1-L1-C7

Method BLASTX NCBI GI g755150 BLAST score 413 E value 1.0e-40 Match length 97 % identity 57

NCBI Description (U13670) vacuolar H+-ATPase proteolipid (16 kDa) subunit

[Gossypium hirsutum]



```
Seq. No.
                   205254
Seq. ID
                   LIB3083-082-Q1-L1-C9
Method
                   BLASTX
NCBI GI
                   g2511590
BLAST score
                   646
E value
                   8.0e-68
Match length
                   138
% identity
                   89
NCBI Description
                   (Y13692) multicatalytic endopeptidase complex, proteasome
                   component, beta subunit [Arabidopsis thaliana] >gi_3421111
                   (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis
                   thaliana]
Seq. No.
                   205255
Seq. ID
                   LIB3083-082-Q1-L1-D10
Method
                   BLASTN
NCBI GI
                   g212850
BLAST score
                   38
E value
                   3.0e-12
Match length
                   85
% identity
                   87
NCBI Description Chicken ubiquitin mRNA, from heat shocked embryo cells
Seq. No.
                   205256
Seq. ID
                   LIB3083-082-Q1-L1-D12
Method
                   BLASTX
NCBI GI
                   g2244816
BLAST score
                   456
E value
                   1.0e-45
Match length
                   125
% identity
                   30
NCBI Description
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  205257
Seq. ID
                  LIB3083-082-01-L1-D5
Method
                  BLASTX
NCBI GI
                  g3860255
BLAST score
                  164
E value
                  2.0e-11
Match length
                  60
% identity
                   62
NCBI Description
                  (AC005824) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  205258
Seq. ID
                  LIB3083-082-Q1-L1-D6
Method
                  BLASTX
NCBI GI
                  g120669
BLAST score
                  518
E value
                  7.0e-53
```

Match length 104 % identity 93

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]



```
Seq. No.
                   205259
Seq. ID
                   LIB3083-082-Q1-L1-D8
Method
                   BLASTX
NCBI GI
                   g4006914
BLAST score
                   407
                   6.0e-40
E value
Match length
                   117
% identity
                   64
NCBI Description
                  (Z99708) serine C-palmitoyltransferase like protein
                   [Arabidopsis thaliana]
Seq. No.
                   205260
Seq. ID
                  LIB3083-082-Q1-L1-E1
Method
                  BLASTX
NCBI GI
                  g3142290
BLAST score
                  495
E value
                   4.0e-50
Match length
                  130
% identity
                  78
NCBI Description
                  (AC002411) Contains similarity to gb Z69902 from C.
                  elegans. [Arabidopsis thaliana]
Seq. No.
                  205261
                  LIB3083-082-Q1-L1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4193382
BLAST score
                  384
                  4.0e-37
E value
Match length
                  86
% identity
                  83
NCBI Description
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
                  >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
Seq. No.
                  205262
Seq. ID
                  LIB3083-082-Q1-L1-E12
Method
                  BLASTX
NCBI GI
                  g3142290
BLAST score
                  496
E value
                  3.0e-50
Match length
                  131
% identity
                  78
                  (AC002411) Contains similarity to gb_Z69902 from C.
NCBI Description
                  elegans. [Arabidopsis thaliana]
Seq. No.
                  205263
Seq. ID
                  LIB3083-082-Q1-L1-E2
```

Method BLASTX NCBI GI g1706956 BLAST score 579 E value 5.0e-60 Match length 132 % identity 78

NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 205264

Seq. ID LIB3083-082-Q1-L1-E4

```
本
Method
                   BLASTX
NCBI GI
                  g2098709
BLAST score
                  477
                  4.0e-48
E value
Match length
                  132
% identity
                  67
NCBI Description
                  (U82975) pectinesterase [Citrus sinensis]
                  205265
Seq. No.
Seq. ID
                  LIB3083-082-Q1-L1-E5
Method
                  BLASTX
NCBI GI
                  q3935157
BLAST score
                  422
                  1.0e-41
E value
Match length
                  132
                  59
% identity
NCBI Description
                  (AC005106) T25N20.21 [Arabidopsis thaliana]
                  205266
Seq. No.
Seq. ID
                  LIB3083-082-Q1-L1-E7
Method
                  BLASTX
NCBI GI
                  g3212865
BLAST score
                  578
E value
                  6.0e-60
Match length
                  130
                  88
% identity
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  205267
Seq. ID
                  LIB3083-082-Q1-L1-E8
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  631
```

4.0e-66 E value Match length 132 % identity 51

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

thaliana]

205268 Seq. No.

Seq. ID LIB3083-082-Q1-L1-F1

Method BLASTX NCBI GI g1326163 BLAST score 210 9.0e-17 E value Match length 52 % identity 75

NCBI Description (U54704) stress related protein PvSRP [Phaseolus vulgaris]

Seq. No. 205269

Seq. ID LIB3083-082-Q1-L1-F10

Method BLASTX NCBI GI g2118017 BLAST score 561 E value 7.0e-58 Match length 124 % identity 74

NCBI Description

thaliana]





```
NCBI Description
                   non-S-RNase (EC 3.1.-.-) - Japanese pear
                   >gi_1526417_dbj BAA08475 (D49529) ribonuclease [Pyrus
                   pyrifolia]
Seq. No.
                   205270
Seq. ID
                   LIB3083-082-Q1-L1-F11
Method
                   BLASTN
NCBI GI
                   q1143223
BLAST score
                   269
E value
                   1.0e-150
Match length
                   381
% identity
                   30
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                   205271
Seq. ID
                   LIB3083-082-Q1-L1-F3
Method
                   BLASTX
NCBI GI
                   q2435518
BLAST score
                   459
E value
                   6.0e-46
Match length
                   119
% identity
                   82
NCBI Description
                  (AF024504) contains similarity to C3HC4-type zinc fingers
                   [Arabidopsis thaliana]
Seq. No.
                   205272
Seq. ID
                   LIB3083-082-Q1-L1-F5
Method
                   BLASTX
NCBI GI
                   g2160175
BLAST score
                   286
E value
                   1.0e-25
Match length
                   131
% identity
                   40
                   (AC000132) Strong similarity to Dianthus cysteine
NCBI Description
                  proteinase (gb_U17135). [Arabidopsis thaliana]
Seq. No.
                  205273
Seq. ID
                  LIB3083-082-Q1-L1-F6
Method
                  BLASTX
NCBI GI
                  g2292959
BLAST score
                  350
E value
                   4.0e-33
Match length
                  130
% identity
                  57
NCBI Description
                  (Z98209) hflX [Mycobacterium tuberculosis]
Seq. No.
                  205274
Seq. ID
                  LIB3083-082-Q1-L1-G12
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  276
E value
                  1.0e-24
Match length
                  104
% identity
                  70
```

28078

(U90439) Cys3His zinc finger protein isolog [Arabidopsis



```
Seq. No.
                   205275
Seq. ID
                   LIB3083-082-Q1-L1-G2
Method
                   BLASTX
NCBI GI
                   g2493906
BLAST score
                   201
E value
                   1.0e-15
Match length
                   129
% identity
                   33
NCBI Description
                   CULLIN HOMOLOG 1 (CUL-1) >gi 1381142 (U58087) Hs-CUL-1
                   [Homo sapiens] >gi_4503161_ref_NP_003583.1 pCUL1 cullin
Seq. No.
                   205276
Seq. ID
                   LIB3083-082-Q1-L1-G3
Method
                   BLASTN
NCBI GI
                   g3449327
BLAST score
                   58
E value
                   6.0e-24
Match length
                   146
% identity
                   85
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   205277
Seq. ID
                   LIB3083-082-Q1-L1-G5
Method
                   BLASTX
NCBI GI
                   q3805845
BLAST score
                   156
E value
                   2.0e-10
Match length
                   39
% identity
                   72
NCBI Description
                  (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.
                   205278
Seq. ID
                   LIB3083-082-Q1-L1-G7
Method
                   BLASTX
NCBI GI
                   g1655536
BLAST score
                   335
E value
                   2.0e-31
Match length
                   89
% identity
                   67
NCBI Description
                   (Y09095) chloride channel [Arabidopsis thaliana]
                   >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel
                  protein [Arabidopsis thaliana]
Seq. No.
                   205279
Seq. ID
                  LIB3083-082-Q1-L1-G8
Method
                  BLASTX
NCBI GI
```

g116923 BLAST score 180 E value 3.0e-13 Match length 131 % identity 35

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi\_111414 pir\_\_S13520 beta-COP protein - rat >gi\_55819\_emb\_CAA40505\_ (X57228) beta COP [Rattus

norvegicus]

```
Seq. No.
                   205280
Seq. ID
                   LIB3083-082-Q1-L1-H1
Method
                   BLASTX
NCBI GI
                   q2911148
BLAST score
                   520
E value
                   4.0e-53
Match length
                   127
% identity
                   81
NCBI Description
                  (AB005808) NADP-malic enzyme [Aloe arborescens]
Seq. No.
                   205281
Seq. ID
                   LIB3083-082-Q1-L1-H3
Method
                   BLASTN
NCBI GI
                   g1143223
BLAST score
                   121
E value
                   2.0e-61
Match length
                   287
% identity
                   88
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                   205282
Seq. ID
                   LIB3083-082-Q1-L1-H4
Method
                   BLASTX
NCBI GI
                   g2244899
BLAST score
                   295
E value
                   5.0e-27
Match length
                   85
% identity
                   69
NCBI Description
                  (Z97338) similar to UFD1 protein [Arabidopsis thaliana]
Seq. No.
                   205283
Seq. ID
                   LIB3083-082-Q1-L1-H5
Method
                   BLASTX
NCBI GI
                   g2829899
BLAST score
                   295
E value
                   1.0e-26
Match length
                   125
% identity
                   46
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   205284
Seq. ID
                  LIB3083-082-Q1-L1-H7
Method
                  BLASTX
NCBI GI
                  g1709251
BLAST score
                  144
E value
                  1.0e-09
Match length
                  64
% identity
                  44
```

NCBI Description SERINE/THREONINE-PROTEIN KINASE NEK1 (NIMA-RELATED PROTEIN KINASE 1) >gi 110860 pir S25284 protein kinase nek1 (EC

2.7.1.-) - mouse >gi 256855 bbs 114985 (S45828)

serine/threonine- and tyrosine-specific protein kinase,

Nek1=NIMA cell cycle regulator homolog [mice, erythroleukemia cells, Peptide, 774 aa] [Mus sp.]



Seq. No. 205285
Seq. ID LIB308

LIB3083-082-Q1-L1-H8

Method BLASTX
NCBI GI g81816
BLAST score 553
E value 6.0e-57
Match length 114
% identity 88

NCBI Description tubulin beta-1 chain - soybean

Seq. No. 205286

Seq. ID LIB3083-082-Q1-L1-H9

Method BLASTX
NCBI GI g3075394
BLAST score 487
E value 3.0e-49
Match length 134
% identity 73

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana] >gi\_3559809\_emb\_CAA09311\_ (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

Seq. No. 205287

Seq. ID LIB3083-083-Q1-L1-A1

Method BLASTX
NCBI GI g1171866
BLAST score 166
E value 1.0e-11
Match length 59
% identity 54

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR

(COMPLEX I-20KD) (CI-20KD) >gi\_629601\_pir\_\_S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi\_562282\_emb\_CAA57725\_ (X82274) PSST subunit of

NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 205288

Seq. ID LIB3083-083-Q1-L1-A10

Method BLASTX
NCBI GI g1171978
BLAST score 533
E value 1.0e-54
Match length 128
% identity 20

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi\_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi\_2911051\_emb\_CAA17561\_ (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 205289

Seq. ID LIB3083-083-Q1-L1-A11

Method BLASTX
NCBI GI g4204263
BLAST score 207
E value 2.0e-16
Match length 84
% identity 49

```
NCBI Description
                  (AC005223) 40409 [Arabidopsis thaliana]
Seq. No.
                  205290
Seq. ID
                  LIB3083-083-Q1-L1-A2
Method
                  BLASTX
NCBI GI
                  q3869088
BLAST score
                  535
E value
                  6.0e - 55
Match length
                  102
% identity
                  99
NCBI Description
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                  205291
Seq. No.
Seq. ID
                  LIB3083-083-Q1-L1-A3
Method
                  BLASTX
NCBI GI
                  g2150027
BLAST score
                  242
E value
                  1.0e-20
Match length
                  114
% identity
                  52
NCBI Description
                  (AF001269) NADP-malic enzyme [Lycopersicon esculentum]
Seq. No.
                  205292
Seq. ID
                  LIB3083-083-Q1-L1-A8
Method
                  BLASTX
NCBI GI
                  g464987
BLAST score
                  150
E value
                  8.0e-10
Match length
                  32
% identity
                  88
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
                  LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                  >gi_421858_pir__S32672 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC10 - Arabidopsis thaliana
                  >gi_297878_emb CAA78715 (Z14991) ubiquitin conjugating
                  enzyme [Arabidopsis thaliana] >gi 349213 (L00640) ubiquitin
                  conjugating enzyme [Arabidopsis thaliana]
```

Seq. No. 205293

Seq. ID LIB3083-083-Q1-L1-B1

Method BLASTX NCBI GI q960289 BLAST score 258 E value 2.0e-22 Match length 67 % identity 73

NCBI Description (L34343) anthranilate synthase alpha subunit [Ruta

graveolens]

Seq. No. 205294

Seq. ID LIB3083-083-Q1-L1-B10

Method BLASTX NCBI GI g125887 BLAST score 204 E value 5.0e-16 Match length 106 % identity 45



```
NCBI Description
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                  >gi 82092 pir S04765 LAT52 protein precursor - tomato
                  >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                  esculentum]
Seq. No.
                  205295
                  LIB3083-083-Q1-L1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406372
                  471
BLAST score
                  2.0e-47
E value
Match length
                  120
% identity
                  72
                  (AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                  glomerata]
                  205296
Seq. No.
Seq. ID
                  LIB3083-083-Q1-L1-B12
Method
                  BLASTX
NCBI GI
                  g1172874
BLAST score
                  170
E value
                  4.0e-12
                  35
Match length
                  77
% identity
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                  >gi 479589 pir S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                   [Arabidopsis thaliana] >gi 447134 prf 1913421A rd22 gene
                   [Arabidopsis thaliana]
Seq. No.
                  205297
                  LIB3083-083-Q1-L1-B3
Seq. ID
Method
                  BLASTN
                  q1000085
NCBI GI
BLAST score
                  80
E value
                  1.0e-37
Match length
                  84
                  99
% identity
NCBI Description Gossypium hirsutum clone CKE6-4A E6 gene, complete cds
Seq. No.
                  205298
                  LIB3083-083-Q1-L1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641837
BLAST score
                  374
                  5.0e-36
E value
Match length
                  130
```

% identity 61

(AL023094) Nonclathrin coat protein gamma - like protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 205299

Seq. ID LIB3083-083-Q1-L1-B7

Method BLASTX NCBI GI q4140622 BLAST score 190 E value 6.0e-15



Match length % identity 58

NCBI Description (AF090160) alcohol dehydrogenase A [Gossypium hirsutum]

>gi 4140624 (AF090161) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140626 (AF090162) alcohol dehydrogenase A

[Gossypium hirsutum]

Seq. No. 205300

Seq. ID LIB3083-083-Q1-L1-B9

Method BLASTX NCBI GI g125887 BLAST score 176 E value 5.0e-13 Match length 90 44 % identity

NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

>gi 82092 pir S04765 LAT52 protein precursor - tomato >gi\_295812\_emb\_CAA33854\_ (X15855) LAT52 [Lycopersicon

esculentum]

205301 Seq. No.

Seq. ID LIB3083-083-Q1-L1-C1

Method BLASTX NCBI GI q2388575 BLAST score 258 E value 2.0e-22 Match length 122 40 % identity

NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 205302

Seq. ID LIB3083-083-Q1-L1-C11

Method BLASTN NCBI GI q3046906 BLAST score 46 E value 9.0e-17 74 Match length

91 % identity

NCBI Description Onchocerca volvulus beta-tubulin (tub) gene, complete cds

Seq. No. 205303

Seq. ID LIB3083-083-Q1-L1-C12

Method BLASTX NCBI GI g3169287 BLAST score 603 E value 7.0e-63 Match length 124 97 % identity

NCBI Description (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium

hirsutum]

Seq. No. 205304

Seq. ID LIB3083-083-Q1-L1-C3

Method BLASTX NCBI GI q4098128 BLAST score 598 E value 3.0e-62



Match length % identity 88

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.

205305

46

Seq. ID

LIB3083-083-Q1-L1-C5

Method BLASTX NCBI GI g4006868 BLAST score 220 E value 6.0e-18 Match length 97

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No.

% identity

205306 Seq. ID LIB3083-083-Q1-L1-C6

Method BLASTX NCBI GI q3249064 BLAST score 529 E value 4.0e-54 Match length 129 75 % identity

NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate

synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana]

Seq. No. 205307

Seq. ID LIB3083-083-Q1-L1-C8

Method BLASTX NCBI GI q4098129 BLAST score 309 E value 2.0e-28 Match length 59 % identity 100

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 205308

LIB3083-083-Q1-L1-C9 Seq. ID

Method BLASTX NCBI GI g3114901 BLAST score 238 E value 5.0e-20 Match length 69 % identity 70

NCBI Description (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa]

>gi 3114905 emb CAA06709 (AJ005806) pceberh [Populus

balsamifera subsp. trichocarpa]

Seq. No. 205309

Seq. ID LIB3083-083-Q1-L1-D10

Method BLASTX NCBI GI g4544399 BLAST score 328 E value 6.0e-31 Match length 88 % identity 70

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

% identity

NCBI Description

47

thaliana]



## thaliana]

```
Seq. No.
                   205310
Seq. ID
                   LIB3083-083-Q1-L1-D11
Method
                   BLASTX
NCBI GI
                   g115492
BLAST score
                   657
                   3.0e-69
E value
Match length
                   128
% identity
                   58
NCBI Description
                  CALMODULIN-RELATED PROTEIN >qi 169205 (M80831)
                   calmodulin-related protein [Petunia hybrida]
Seq. No.
                   205311
Seq. ID
                   LIB3083-083-Q1-L1-D12
Method
                   BLASTX
NCBI GI
                   q3687389
BLAST score
                   617
E value
                   2.0e-64
                   126
Match length
% identity
                   97
NCBI Description
                  (Y16124) putative cullin protein [Lycopersicon esculentum]
Seq. No.
                   205312
Seq. ID
                   LIB3083-083-Q1-L1-D3
Method
                   BLASTX
NCBI GI
                   g1706956
BLAST score
                   694
E value
                   2.0e-73
Match length
                   127
% identity
                   98
NCBI Description
                  (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   205313
Seq. ID
                  LIB3083-083-Q1-L1-D4
Method
                  BLASTX
NCBI GI
                   g547683
BLAST score
                   673
E value
                   5.0e-71
Match length
                  133
% identity
                   95
NCBI Description
                  HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
                  205314
Seq. No.
Seq. ID
                  LIB3083-083-Q1-L1-D5
Method
                  BLASTX
NCBI GI
                  g3342552
BLAST score
                  222
E value
                  4.0e-18
Match length
                  93
```

28086

(AF076979) putative strictosidine synthase [Arabidopsis



```
Seq. No.
                   205315
Seq. ID
                   LIB3083-083-Q1-L1-D6
Method
                   BLASTX
NCBI GI
                   q3413167
BLAST score
                   214
E value
                   3.0e-17
Match length
                   42
% identity
                   100
                  (AJ010225) elongation factor 1-alpha [Cicer arietinum]
NCBI Description
Seq. No.
                   205316
Seq. ID
                   LIB3083-083-Q1-L1-D8
Method
                   BLASTX
NCBI GI
                   g3935145
BLAST score
                   299
E value
                   3.0e-27
Match length
                   85
% identity
                   65
NCBI Description
                  (AC005106) T25N20.9 [Arabidopsis thaliana]
Seq. No.
                   205317
Seq. ID
                   LIB3083-083-Q1-L1-E12
Method
                   BLASTX
NCBI GI
                   q1350977
BLAST score
                   148
E value
                   1.0e-09
Match length
                   33
% identity
                   85
NCBI Description
                  PROBABLE 40S RIBOSOMAL PROTEIN S30
Seq. No.
                   205318
Seq. ID
                   LIB3083-083-Q1-L1-E2
Method
                   BLASTX
NCBI GI
                   g1220453
BLAST score
                   355
E value
                   9.0e-34
Match length
                   122
% identity
                   51
NCBI Description
                   (M79328) alpha-amylase [Solanum tuberosum]
Seq. No.
                   205319
Seq. ID
                   LIB3083-083-Q1-L1-E4
Method
                   BLASTX
NCBI GI
                   g3892054
BLAST score
                   402
E value
                   3.0e-39
Match length
                   97
% identity
                   69
                   (AC002330) putative glycosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                  205320
Seq. No.
```

Seq. ID LIB3083-083-Q1-L1-E5

Method BLASTN NCBI GI g1143223 BLAST score 151 E value 2.0e-79



Match length 25 % identity

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No.

205321

Seq. ID

LIB3083-083-Q1-L1-E6

Method BLASTX NCBI GI q2497702 BLAST score 195 E value 5.0e-15 Match length 123 % identity 38

NCBI Description OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR

> >gi 2121019 pir I40710 outer membrane lipoprotein -Citrobacter freundii >gi 717136 (U21727) lipocalin

precursor [Citrobacter freundii]

Seq. No. 205322

Seq. ID LIB3083-083-Q1-L1-F10

Method BLASTX NCBI GI g3114901 BLAST score 274 3.0e-24E value Match length 68

% identity 78 (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] NCBI Description

>gi\_3114905\_emb\_CAA06709\_ (AJ005806) pceberh [Populus

balsamifera subsp. trichocarpa]

Seq. No. 205323

Seq. ID LIB3083-083-Q1-L1-F11

Method BLASTN NCBI GI g2244733 BLAST score 111 E value 1.0e-55 Match length 308 84 % identity

NCBI Description Cotton mRNA for actin, clone CF456, partial cds

Seq. No. 205324

Seq. ID LIB3083-083-Q1-L1-F3

Method BLASTX NCBI GI g2245135 BLAST score 488 E value 2.0e-49 Match length 120 % identity 72

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 205325

Seq. ID LIB3083-083-Q1-L1-F4

Method BLASTX NCBI GI g3183640 BLAST score 258 E value 2.0e-22 Match length 50 % identity 96

```
NCBI Description
                  (AJ005869) transmembrane channel protein [Cicer arietinum]
Seq. No.
                  205326
Seq. ID
                  LIB3083-083-Q1-L1-F6
Method
                  BLASTX
NCBI GI
                  q3668092
BLAST score
                  306
E value
                  2.0e-28
Match length
                  75
% identity
                  81
NCBI Description
                  (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  205327
Seq. ID
                  LIB3083-083-Q1-L1-F7
Method
                  BLASTX
NCBI GI
                  q2493852
BLAST score
                  291
E value
                  3.0e-26
Match length
                  63
% identity
                  84
NCBI Description
                  CYTOCHROME C OXIDASE POLYPEPTIDE VC
                  >gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc
                  subunit [Hordeum vulgare]
Seq. No.
                  205328
                  LIB3083-083-Q1-L1-F8
                  BLASTX
                  q1170373
BLAST score
                  611
```

Seq. ID Method NCBI GI

E value 9.0e-64 Match length 127 % identity 91

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi\_397482 emb CAA52684 (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

Seq. No. 205329

Seq. ID LIB3083-083-Q1-L1-F9

Method BLASTN NCBI GI g2271476 BLAST score 43 1.0e-15 E value 75 Match length 89 % identity

NCBI Description Arabidopsis thaliana AP47/50p mRNA, complete cds

Seq. No. 205330

Seq. ID LIB3083-083-Q1-L1-G10

Method BLASTX NCBI GI g4371295 BLAST score 442 E value 5.0e-44Match length 120 % identity 76

NCBI Description (AC006260) putative CCAAT-binding transcription factor

[Arabidopsis thaliana]

```
Seq. No.
                  205331
Seq. ID
                  LIB3083-083-Q1-L1-G3
Method
                  BLASTX
                  g3882081
NCBI GI
BLAST score
                  309
E value
                  2.0e-28
Match length
                  62
% identity
                  33
NCBI Description
                  (AJ012552) polyubiquitin [Vicia faba]
Seq. No.
                  205332
Seq. ID
                  LIB3083-083-Q1-L1-G6
Method
                  BLASTX
NCBI GI
                  g4218011
BLAST score
                  109
                  2.0e-09
E value
Match length
                  76
% identity
                  51
NCBI Description
                  (AC006135) putative protein kinase [Arabidopsis thaliana]
                  >gi_4309721 gb AAD15491 (AC006439) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                  205333
Seq. ID
                  LIB3083-083-Q1-L1-G8
Method
                  BLASTX
NCBI GI
                  g2154609
BLAST score
                  612
                  6.0e-64
E value
Match length
                  127
% identity
                  84
NCBI Description
                  (D63509) endoxyloglucan transferase related protein
                  [Arabidopsis thaliana] >gi_4522010 gb AAD21783.1
                   (AC007069) endoxyloglucan transferase [Arabidopsis
                  thaliana]
Seq. No.
                  205334
Seq. ID
                  LIB3083-083-Q1-L1-G9
Method
                  BLASTX
NCBI GI
                  g3236248
BLAST score
                  381
E value
                  7.0e-37
Match length
                  102
% identity
                  75
NCBI Description
                  (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                  205335
Seq. ID
                  LIB3083-083-Q1-L1-H10
Method
                  BLASTX
NCBI GI
                  g3786000
BLAST score
                  164
```

E value 2.0e-11 Match length 74 % identity 42

(AC005499) hypothetical protein [Arabidopsis thaliana] NCBI Description

205336 Seq. No.



```
Seq. ID
                  LIB3083-083-Q1-L1-H11
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                  260
E value
                  9.0e-23
Match length
                  108
% identity
                  47
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
                  205337
Seq. No.
                  LIB3083-083-Q1-L1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170409
BLAST score
                  375
E value
                  3.0e-36
Match length
                  104
                  71
% identity
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)
NCBI Description
                  >gi 549887 (U09336) homeobox protein [Arabidopsis thaliana]
                  >gi 549888 (U09337) homeobox protein [Arabidopsis thaliana]
                  >gi_4490724_emb_CAB38927.1 (AL035709) homeobox protein
                  HAT22 [Arabidopsis thaliana]
                  205338
Seq. No.
Seq. ID
                  LIB3083-083-Q1-L1-H4
Method
                  BLASTX
NCBI GI
                  g4105772
BLAST score
                  242
                  1.0e-20
E value
Match length
                  52
% identity
                  40
NCBI Description
                  (AF049917) PGP9B [Petunia x hybrida]
                  205339
Seq. No.
                  LIB3083-083-Q1-L1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539301
BLAST score
                  165
                  1.0e-11
E value
Match length
                  77
% identity
                  45
                  (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  205340
Seq. ID
                  LIB3083-083-Q1-L1-H7
Method
                  BLASTN
                  q1143223
                  224
                  1.0e-123
                  380
```

NCBI GI BLAST score E value Match length % identity 33

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205341

Seq. ID LIB3083-083-01-L1-H9

Method BLASTN

E value

Match length

% identity

6.0e-24

90

67



```
NCBI GI
                  g1143223
BLAST score
                  63
E value
                  2.0e-27
Match length
                  94
% identity
                  91
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                  205342
Seq. ID
                  LIB3083-086-Q1-L1-A12
                  BLASTX
Method
NCBI GI
                  g3928084
BLAST score
                  188
                  2.0e-14
E value
Match length
                  94
                  44
% identity
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  205343
Seq. ID
                  LIB3083-086-Q1-L1-C9
Method
                  BLASTX
NCBI GI
                  g2702272
BLAST score
                  157
E value
                  1.0e-10
Match length
                  59
                  49
% identity
NCBI Description (AC003033) hypothetical protein [Arabidopsis thaliana]
                  205344
Seq. No.
Seq. ID
                  LIB3083-086-Q1-L1-D10
Method
                  BLASTX
NCBI GI
                  g2851455
BLAST score
                  291
E value
                  1.0e-26
Match length
                  61
% identity
                  95
NCBI Description
                  DYNAMIN-LIKE PROTEIN >gi 2267213 (L36939) dynamin-like GTP
                  binding protein [Arabidopsis thaliana]
Seq. No.
                  205345
Seq. ID
                  LIB3083-086-Q1-L1-D9
                  BLASTN
Method
NCBI GI
                  q1143223
BLAST score
                  95
                  4.0e-46
E value
Match length
                  267
% identity
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                  205346
Seq. ID
                  LIB3083-086-Q1-L1-F12
Method
                  BLASTX
NCBI GI
                  q1168328
BLAST score
                  226
```

Match length

% identity

130

87



```
NCBI Description
                  ACTIN-LIKE PROTEIN 3 >gi 629878 pir S48844 actin-like
                  protein - slime mold (Dictyostelium discoideum)
                   >gi 2130164_pir S69002 actin-like protein - slime mold
                   (Dictyostelium discoideum) >gi_563346_emb_CAA86553
                   (Z46418) actin-like protein [Dictyostelium discoideum]
Seq. No.
                  205347
Seq. ID
                  LIB3083-087-Q1-L1-A11
Method
                  BLASTX
NCBI GI
                  g2129495
BLAST score
                  575
E value
                  1.0e-59
Match length
                  120
                  90
% identity
NCBI Description
                  fiber protein E6 (clone SIE6-2A) - sea-island cotton
                  >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                   (U30508) E6 [Gossypium barbadense]
Seq. No.
                  205348
Seq. ID
                  LIB3083-087-Q1-L1-A2
Method
                  BLASTX
NCBI GI
                  g2244799
BLAST score
                  358
E value
                  4.0e-34
Match length
                  107
% identity
                  61
NCBI Description
                  (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
Seq. No.
                  205349
Seq. ID
                  LIB3083-087-Q1-L1-A3
Method
                  BLASTX
NCBI GI
                  g2511533
BLAST score
                  201
E value
                  1.0e-15
                  39
Match length
% identity
                  97
NCBI Description
                  (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.
                  205350
Seq. ID
                  LIB3083-087-Q1-L1-A4
Method
                  BLASTX
NCBI GI
                  g1850546
BLAST score
                  227
E value
                  4.0e-19
Match length
                  77
                  68
% identity
NCBI Description
                  (U88045) syntaxin related protein AtVam3p [Arabidopsis
                  thaliana]
Seq. No.
                  205351
Seq. ID
                  LIB3083-087-Q1-L1-A6
Method
                  BLASTX
NCBI GI
                  q2388689
BLAST score
                  598
E value
                  3.0e-62
```

28093

æ.



```
NCBI Description
                   (AF016633) GH1 protein [Glycine max]
                   205352
Seq. No.
Seq. ID
                   LIB3083-087-Q1-L1-A9
                   BLASTX
Method
NCBI GI
                   g2129495
BLAST score
                   152
E value
                   5.0e-10
Match length
                   99
% identity
                   43
NCBI Description
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
                   >gi 1000088 (U30507) E6 [Gossypium barbadense] >qi 1000090
                   (U30508) E6 [Gossypium barbadense]
Seq. No.
                   205353
Seq. ID
                   LIB3083-087-Q1-L1-B10
Method
                   BLASTX
NCBI GI
                   g2065531
BLAST score
                   506
E value
                   2.0e-51
Match length
                   127
                   71
% identity
NCBI Description
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
Seq. No.
                   205354
Seq. ID
                   LIB3083-087-Q1-L1-B11
Method
                   BLASTX
NCBI GI
                   g2829893
BLAST score
                   231
E value
                   2.0e-19
Match length
                   112
% identity
                   46
                   (AC002311) phosphoglucomutase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205355
Seq. ID
                  LIB3083-087-Q1-L1-B4
Method
                  BLASTX
NCBI GI
                   g2129473
BLAST score
                   295
E value
                   1.0e-26
Match length
                   105
% identity
                   56
                  arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                  205356
Seq. ID
                  LIB3083-087-Q1-L1-B5
Method
                  BLASTX
NCBI GI
                  g2323344
BLAST score
                  552
E value
                  7.0e-57
Match length
                  126
% identity
                  79
```

Seq. No. 205357

NCBI Description

Seq. ID LIB3083-087-Q1-L1-B8

(AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]

% identity

91



```
Method
                   BLASTX
NCBI GI
                   g3641868
BLAST score
                   412
E value
                   2.0e-40
Match length
                   110
% identity
                   71
NCBI Description
                   (AJ011012) hypothetical protein [Cicer arietinum]
Seq. No.
                   205358
Seq. ID
                   LIB3083-087-Q1-L1-C2
Method
                   BLASTX
NCBI GI
                   q4098129
BLAST score
                   694
E value
                   2.0e-73
Match length
                   130
% identity
                   98
NCBI Description
                   (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                   205359
Seq. ID
                   LIB3083-087-Q1-L1-C3
Method
                   BLASTX
NCBI GI
                   q4235430
BLAST score
                   481
E value
                   2.0e-48
Match length
                   113
                   81
% identity
NCBI Description
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.
                   205360
Seq. ID
                   LIB3083-087-Q1-L1-C4
Method
                   BLASTX
NCBI GI
                   q4235430
BLAST score
                   146
E value
                   9.0e-14
Match length
                   91
% identity
                   52
NCBI Description
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.
                   205361
Seq. ID
                  LIB3083-087-Q1-L1-C7
Method
                  BLASTX
NCBI GI
                   g1174171
BLAST score
                   190
                   2.0e-14
E value
Match length
                  70
% identity
                   54
NCBI Description
                  (U44947) NTH1 [Pisum sativum]
Seq. No.
                  205362
Seq. ID
                  LIB3083-087-Q1-L1-C9
Method
                  BLASTX
NCBI GI
                  g2500354
BLAST score
                  605
E value
                  4.0e-63
Match length
                  124
```

28095

NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi\_1902894\_dbj\_BAA19462\_

Seq. ID





## (AB001891) QM family protein [Solanum melongena]

```
Seq. No.
                  205363
Seq. ID
                  LIB3083-087-Q1-L1-D1
Method
                  BLASTX
NCBI GI
                  g2829899
BLAST score
                  291
                   3.0e-26
E value
Match length
                  125
% identity
                   46
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp AJ001449 2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
                  205364
Seq. No.
                  LIB3083-087-Q1-L1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1143223
BLAST score
                  131
E value
                  2.0e-67
Match length
                   376
% identity
                   50
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                  205365
                  LIB3083-087-Q1-L1-E1
Seq. ID
Method
                  BLASTX
                  g3927825
NCBI GI
BLAST score
                   467
E value
                   5.0e-47
Match length
                   103
                   85
% identity
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   205366
Seq. ID
                  LIB3083-087-Q1-L1-E10
Method
                  BLASTX
NCBI GI
                   g3063447
BLAST score
                   153
E value
                   4.0e-10
Match length
                   129
% identity
NCBI Description
                   (AC003981) F22013.9 [Arabidopsis thaliana]
Seq. No.
                   205367
                  LIB3083-087-Q1-L1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1143223
BLAST score
                   144
E value
                   3.0e-75
Match length
                   378
% identity
                   50
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                  205368
```

28096

LIB3083-087-Q1-L1-E3

```
BLASTX
Method
NCBI GI
                   g170354
BLAST score
                   207
E value
                   1.0e-16
Match length
                   52
% identity
                   16
NCBI Description
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                  205369
Seq. ID
                  LIB3083-087-Q1-L1-E4
Method
                  BLASTN
NCBI GI
                   g3108237
BLAST score
                   64
E value
                   2.0e-27
Match length
                  195
                   45
% identity
NCBI Description
                  Gossypium barbadense clone pXP004 repetitive DNA sequence
                  205370
Seq. No.
Seq. ID
                  LIB3083-087-Q1-L1-E9
Method
                  BLASTX
NCBI GI
                  g2501490
BLAST score
                  154
E value
                   3.0e-10
Match length
                  80
                   47
% identity
NCBI Description
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID
                   3-O-GLUCOSYLTRANSFERASE) >gi 1620013 dbj BAA12737 (D85186)
                  UDP-glucose:flavonoid-3-glucosyltransferase [Gentiana
                   triflora]
Seq. No.
                  205371
                  LIB3083-087-Q1-L1-F4
Seq. ID
Method
                  BLASTX
                  g3367523
                   405
                  1.0e-39
                  117
                   64
NCBI Description
                   (AC004392) ESTs gb AA728658 and gb N95943 come from this
```

NCBI GI BLAST score E value Match length % identity

gene. [Arabidopsis thaliana]

Seq. No. 205372

LIB3083-087-Q1-L1-F6 Seq. ID

Method BLASTN g4151090 NCBI GI BLAST score 33 E value 5.0e-09 53 Match length 91 % identity

NCBI Description Stylosanthes guianensis microsatellite SSR1-24

Seq. No. 205373

LIB3083-087-Q1-L1-F7 Seq. ID

Method BLASTX NCBI GI g4325367 BLAST score 173



E value 1.0e-12 Match length 42 % identity 74

NCBI Description (AF128396) contains similarity to Nicotiana tabacum B-type

cyclin (GB:D50737) [Arabidopsis thaliana]

Seq. No. 205374

Seq. ID LIB3083-087-Q1-L1-F9

Method BLASTX
NCBI GI g2160156
BLAST score 463
E value 2.0e-46
Match length 127
% identity 66

NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA

synthetase (gb\_Z73100). [Arabidopsis thaliana]

Seq. No. 205375

Seq. ID LIB3083-087-Q1-L1-G11

Method BLASTX
NCBI GI g2935416
BLAST score 157
E value 4.0e-11
Match length 53
% identity 66

NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No. 205376

Seq. ID LIB3083-087-Q1-L1-G2

Method BLASTX
NCBI GI g4218011
BLAST score 272
E value 5.0e-24
Match length 125
% identity 51

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi 4309721 gb AAD15491 (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 205377

Seq. ID LIB3083-087-Q1-L1-G6

Method BLASTN
NCBI GI g1143223
BLAST score 139
E value 3.0e-72
Match length 372
% identity 50

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205378

Seq. ID LIB3083-087-Q1-L1-H1

Method BLASTN
NCBI GI g1143223
BLAST score 252
E value 1.0e-139
Match length 380
% identity 52





## NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205379

Seq. ID LIB3083-087-Q1-L1-H2

Method BLASTX
NCBI GI g267069
BLAST score 613
E value 4.0e-64
Match length 116
% identity 97

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >qi 320183 pir JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 205380

Seq. ID LIB3083-087-Q1-L1-H3

Method BLASTX
NCBI GI g2129495
BLAST score 229
E value 4.0e-31
Match length 115
% identity 64

NCBI Description fiber protein E6 (clone SIE6-2A) - sea-island cotton

>gi\_1000088 (U30507) E6 [Gossypium barbadense] >gi\_1000090

(U30508) E6 [Gossypium barbadense]

Seq. No. 205381

Seq. ID LIB3083-087-Q1-L1-H4

Method BLASTX
NCBI GI g3511285
BLAST score 382
E value 6.0e-37
Match length 90
% identity 79

NCBI Description (AF081534) cellulose synthase [Populus alba x Populus

tremula]

Seq. No. 205382

Seq. ID LIB3083-087-Q1-L1-H5

Method BLASTX
NCBI GI g466160
BLAST score 373
E value 7.0e-36
Match length 84
% identity 85

NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III

>gi\_630771\_pir\_\_S44903 ZK652.3 protein - Caenorhabditis
elegans >gi 289769 (L14429) putative [Caenorhabditis

elegans]

Seq. No. 205383

Seq. ID LIB3083-087-Q1-L1-H6

Method BLASTX
NCBI GI g136636
BLAST score 406
E value 9.0e-40



Match length 80 % identity 93

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi\_442594 pdb\_1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894 pdb\_2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 205384

Seq. ID LIB3083-087-Q1-L1-H7

Method BLASTX
NCBI GI g2129473
BLAST score 198
E value 2.0e-15
Match length 77
% identity 49

NCBI Description arabinogalactan-like protein - loblolly pine >gi 607774

(U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 205385

Seq. ID LIB3083-087-Q1-L1-H8

Method BLASTN
NCBI GI g1143223
BLAST score 119
E value 2.0e-60
Match length 336
% identity 91

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205386

Seq. ID LIB3083-088-Q1-L1-A11

Method BLASTX
NCBI GI g1666234
BLAST score 509
E value 5.0e-52
Match length 95
% identity 98

NCBI Description (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin

[Pisum sativum]

Seq. No. 205387

Seq. ID LIB3083-088-Q1-L1-A2

Method BLASTX
NCBI GI g100203
BLAST score 210
E value 5.0e-17
Match length 80
% identity 61

NCBI Description cysteine proteinase (EC 3.4.22.-) precursor - tomato

>gi\_19195\_emb\_CAA78403\_ (Z14028) pre-pro-cysteine

proteinase [Lycopersicon esculentum]

Seq. No. 205388



```
LIB3083-088-Q1-L1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760330
BLAST score
                   259
E value
                  7.0e-23
Match length
                   58
                  79
% identity
NCBI Description
                  (AC002130) F1N21.15 [Arabidopsis thaliana]
                  205389
Seq. No.
Seq. ID
                  LIB3083-088-Q1-L1-B2
Method
                  BLASTN
NCBI GI
                   g451543
BLAST score
                   234
                   1.0e-129
E value
                   329
Match length
                   93
% identity
                  Gossypium barbadense Sea Island proline-rich cell wall
NCBI Description
                  protein gene complete cds. >gi 1598725 gb I18370 I18370
                  Sequence 25 from patent US
                   205390
Seq. No.
                  LIB3083-088-Q1-L1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3290020
                   334
BLAST score
E value
                   2.0e-33
Match length
                   103
% identity
                   78
NCBI Description
                   (AF044172) cysteine synthase; CS-A; O-acetylserine (thiol)
                  lyase; cytosolic isoform [Solanum tuberosum]
                   205391
Seq. No.
Seq. ID
                   LIB3083-088-Q1-L1-B9
                   BLASTX
Method
NCBI GI
                   g3172538
BLAST score
                   377
                   2.0e-36
E value
Match length
                   116
                   69
% identity
                  (AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205392
                   LIB3083-088-Q1-L1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2065531
BLAST score
                   457
E value
                   9.0e-46
Match length
                   112
% identity
                   73
NCBI Description
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
```

205393 Seq. No.

Seq. ID LIB3083-088-Q1-L1-C12

Method BLASTX NCBI GI g4512712 BLAST score 380



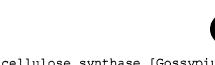
```
0e-37
E value
Match length
                  88
% identity
                  73
                   (AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205394
Seq. ID
                  LIB3083-088-Q1-L1-C4
Method
                  BLASTX
NCBI GI
                  q4415992
BLAST score
                   634
                   2.0e-66
E value
                   121
Match length
% identity
                   99
                   (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
                   205395
Seq. No.
                  LIB3083-088-Q1-L1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1314712
BLAST score
                   589
E value
                   3.0e-61
Match length
                   132
% identity
                   83
                   (U54615) calcium-dependent protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   205396
Seq. No.
                   LIB3083-088-Q1-L1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q435039
BLAST score
                   163
                   3.0e-11
E value
                   31
Match length
                   100
% identity
                   (L17308) proline-rich cell wall protein [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   205397
Seq. ID
                   LIB3083-088-Q1-L1-D10
Method
                   BLASTX
NCBI GI
                   q1256830
BLAST score
                   322
                   2.0e-30
E value
Match length
                   75
                   76
% identity
NCBI Description
                   (U52970) cysteine endopeptidase 1 [Phaseolus vulgaris]
                   >gi 2959418 emb CAA12118 (AJ224766) cysteine protease
                   [Phaseolus vulgaris]
                   205398
Seq. No.
```

Seq. ID LIB3083-088-Q1-L1-D11

Method BLASTX
NCBI GI g1706956
BLAST score 566
E value 1.0e-61
Match length 122
% identity 99

Seq. ID





```
NCBI Description
                   (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   205399
Seq. ID
                   LIB3083-088-Q1-L1-D12
Method
                   BLASTX
NCBI GI
                   g2244732
BLAST score
                   318
E value
                   2.0e-29
Match length
                   62
% identity
                   92
                   (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
NCBI Description
                   205400
Seq. No.
Seq. ID
                   LIB3083-088-Q1-L1-D4
                   BLASTX
Method
NCBI GI
                   q1706956
BLAST score
                   534
E value
                   6.0e-55
                   105
Match length
% identity
                   96
                   (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   205401
Seq. No.
Seq. ID
                   LIB3083-088-Q1-L1-D6
Method
                   BLASTX
NCBI GI
                   g2252840
BLAST score
                   164
                   2.0e-11
E value
Match length
                   61
% identity
                   56
NCBI Description
                   (AF013293) contains regions of similarity to Haemophilus
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                   205402
Seq. ID
                   LIB3083-088-Q1-L1-D9
Method
                   BLASTX
NCBI GI
                   g1854386
BLAST score
                   440
                   8.0e-44
E value
Match length
                   117
% identity
                   72
NCBI Description
                   (AB001375) similar to soluble NSF attachment protein [Vitis
                   vinifera]
                   205403
Seq. No.
Seq. ID
                   LIB3083-088-Q1-L1-E2
Method
                   BLASTX
NCBI GI
                   g4263695
BLAST score
                   193
                   6.0e-15
E value
Match length
                   105
                   20
% identity
                   (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   205404
```

28103

LIB3083-088-Q1-L1-E4



```
Method
                  g3080420
NCBI GI
BLAST score
                  381
E value
                  8.0e-37
                  132
Match length
                  56
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  205405
Seq. ID
                  LIB3083-088-Q1-L1-E6
                  BLASTX
Method
                  g4263695
NCBI GI
                  180
BLAST score
E value
                  2.0e-13
                  108
Match length
                  12
% identity
                   (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  205406
                  LIB3083-088-Q1-L1-E8
Seq. ID
                  BLASTX
Method
                  g4150963
NCBI GI
                  191
BLAST score
E value
                  1.0e-14
Match length
                  76
                  50
% identity
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]
                   205407
Seq. No.
                  LIB3083-088-Q1-L1-E9
Seq. ID
                  BLASTX
Method
                   g1351856
NCBI GI
BLAST score
                   600
                   2.0e-62
E value
Match length
                   121
                   95
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                   [Cucurbita sp.]
Seq. No.
                   205408
                   LIB3083-088-Q1-L1-F11
Seq. ID
Method
                   BLASTX
                   q2500521
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
                   48
Match length
                   81
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15)
NCBI Description
                   >gi_485945_emb_CAA55739_ (X79138) NeIF-4A15 [Nicotiana
                   tabacum]
```

205409 Seq. No.

LIB3083-088-Q1-L1-F12 Seq. ID

Method BLASTX

```
NCBI GI
                  g1703375
                  496
BLAST score
                  2.0e-50
E value
                  96
Match length
                  100
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi 965483_dbj_BAA08259_ (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
                  205410
Seq. No.
Seq. ID
                  LIB3083-088-Q1-L1-F4
                  BLASTX
Method
NCBI GI
                  g1703380
BLAST score
                  358
                  3.0e-34
E value
                  71
Match length
                  100
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
                  205411
Seq. No.
                  LIB3083-088-Q1-L1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4008072
                  320
BLAST score
                  1.0e-29
E value
                  119
Match length
                  49
% identity
NCBI Description (AF105425) chitinase [Cynodon dactylon]
                  205412
Seq. No.
Seq. ID
                  LIB3083-088-Q1-L1-G4
                  BLASTX
Method
NCBI GI
                  g1173209
                  336
BLAST score
                  2.0e-31
E value
                   68
Match length
                   99
% identity
                  40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
NCBI Description
                  protein S16 protein - upland cotton
                  >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
                   205413
Seq. No.
                  LIB3083-088-Q1-L1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1279588
BLAST score
                   406
                  1.0e-39
E value
Match length
                  117
% identity
                   66
                  (Z71749) glutathione S-transferase [Nicotiana
NCBI Description
                  plumbaginifolia]
```

Seq. No. 205414

Seq. ID LIB3083-088-Q1-L1-G7

Method BLASTX NCBI GI g134101



BLAST score 587 E value 6.0e-61 Match length 133 % identity 90

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD

CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi\_72958\_pir\_\_HHCSBA ribulose-bisphosphate carboxylase

subunit-binding protein alpha chain - castor bean

(fragment)

Seq. No. 205415

Seq. ID LIB3083-088-Q1-L1-H10

Method BLASTX
NCBI GI g4512658
BLAST score 146
E value 1.0e-09
Match length 79
% identity 35

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No. 205416

Seq. ID LIB3083-088-Q1-L1-H11

Method BLASTX
NCBI GI g1256830
BLAST score 517
E value 8.0e-53
Match length 119
% identity 80

NCBI Description (U52970) cysteine endopeptidase 1 [Phaseolus vulgaris]

>gi\_2959418\_emb\_CAA12118\_ (AJ224766) cysteine protease

[Phaseolus vulgaris]

Seq. No. 205417

Seq. ID LIB3083-088-Q1-L1-H12

Method BLASTX
NCBI GI g547684
BLAST score 408
E value 3.0e-40
Match length 92
% identity 89

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100336 pir S18865 heat shock

protein 82 - common tobacco (fragment)

>gi\_19880\_emb\_CAA44877\_ (X63195) heat shock protein 82

[Nicotiana tabacum]

Seq. No. 205418

Seq. ID LIB3083-088-Q1-L1-H2

Method BLASTX
NCBI GI g4115933
BLAST score 407
E value 8.0e-40
Match length 116
% identity 76

NCBI Description (AF118223) contains similarity to human RNA polymerase II

complex component SRB7 (GB:U52960) [Arabidopsis thaliana]

Seq. No. 205419

```
LIB3083-088-Q1-L1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129473
BLAST score
                  196
                  4.0e-15
E value
                  114
Match length
                  43
% identity
                  arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                  (U09556) arabinogalactan-like protein [Pinus taeda]
                  205420
Seq. No.
Seq. ID
                  LIB3083-088-Q1-L1-H5
                  BLASTX
Method
                  g3327868
                  168
                  6.0e-12
```

NCBI GI BLAST score E value Match length 112

38 % identity

(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis NCBI Description

thaliana]

Seq. No. 205421

LIB3083-088-Q1-L1-H6 Seq. ID

Method BLASTN g2829205 NCBI GI 394 BLAST score 0.0e+00E value 402 Match length 19 % identity

Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein NCBI Description

precursor (PRP) mRNA, complete cds

205422 Seq. No.

Seq. ID LIB3083-088-Q1-L1-H7

BLASTX Method NCBI GI q3342552 BLAST score 254 6.0e-22 E value Match length 101 48 % identity

NCBI Description (AF076979) putative strictosidine synthase [Arabidopsis

thaliana]

205423 Seq. No.

LIB3083-088-Q1-L1-H9 Seq. ID

BLASTX Method NCBI GI q728938 BLAST score 422 8.0e-42 E value Match length 102 75 % identity

PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP NCBI Description

(PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)

(H+-PPASE) >gi\_322841\_pir\_\_JC1466 inorganic pyrophosphatase

(EC 3.6.1.1) - barley >gi 285638 dbj BAA02717 (D13472)

inorganic pyrophosphatse ase' [Hordeum vulgare]

Method

NCBI GI

BLAST score

BLASTX

295

q3115374



```
Seq. No.
                  LIB3083-089-Q1-L1-A11
Seq. ID
                  BLASTX
Method
                  g1350956
NCBI GI
BLAST score
                  483
                  8.0e-49
E value
                  100
Match length
                  94
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
                  205425
Seq. No.
                  LIB3083-089-Q1-L1-B10
Seq. ID
                  BLASTX
Method
                  q3184054
NCBI GI
                  561
BLAST score
                  5.0e-58
E value
                  130
Match length
                  85
% identity
                  (AJ223318) MADS-box transcription factor [Pisum sativum]
NCBI Description
                   205426
Seq. No.
                  LIB3083-089-Q1-L1-B11
Seq. ID
Method
                  BLASTX
                   q4091008
NCBI GI
                   302
BLAST score
                   2.0e-27
E value
                   108
Match length
% identity
                   56
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
                   205427
Seq. No.
Seq. ID
                   LIB3083-089-Q1-L1-C10
Method
                   BLASTX
                   g2129932
NCBI GI
                   660
BLAST score
                   1.0e-69
E value
                   120
Match length
                   96
% identity
                  myb-related transcription factor TMH1 - tomato
NCBI Description
                   >gi 1167486 emb CAA64615 (X95297) transcription factor
                   [Lycopersicon esculentum]
    ١.
                   205428
Seq. No.
                   LIB3083-089-Q1-L1-C11
Seq. ID
Method
                   BLASTX
                   q3668086
NCBI GI
BLAST score
                   306
                   9.0e-32
E value
                   131
Match length
% identity
                   58
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205429
Seq. No.
                   LIB3083-089-Q1-L1-C2
Seq. ID
```

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score



```
E value
                  104
Match length
% identity
                  (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]
NCBI Description
                  205430
Seq. No.
Seq. ID
                  LIB3083-089-Q1-L1-C6
Method
                  BLASTX
NCBI GI
                  q2618699
                  233
BLAST score
                  2.0e-19
E value
                  116
Match length
                  41
% identity
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                  205431
Seq. No.
                  LIB3083-089-Q1-L1-C8
Seq. ID
Method
                  BLASTX
                  g4539324
NCBI GI
                  364
BLAST score
E value
                  8.0e-35
                  121
Match length
% identity
                  64
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
                  205432
Seq. No.
                  LIB3083-089-Q1-L1-C9
Seq. ID
                  BLASTX
Method
                  g3582436
NCBI GI
                  507
BLAST score
E value
                  1.0e-51
Match length
                  121
                  81
% identity
                  (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
NCBI Description
Seq. No.
                   205433
                  LIB3083-089-Q1-L1-D10
Seq. ID
Method
                  BLASTX
                   g1362086
NCBI GI
BLAST score
                   666
E value
                   3.0e-70
                   129
Match length
% identity
                   97
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >qi 2129919 pir S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 886471 emb CAA58474 (X83499) methionine synthase
                   [Catharanthus roseus]
                   205434
```

28109

LIB3083-089-Q1-L1-D11

BLASTX

370 2.0e-35

g1171866



205435

Match length % identity 63

NCBI Description (COMPLEX I-20KD) (CI-20KD) >gi\_629601\_pir\_\_S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi\_562282\_emb\_CAA57725\_ (X82274) PSST subunit of NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. ID LIB3083-089-Q1-L1-D12
Method BLASTX
NCBI GI g1703375
BLAST score 441
E value 8.0e-44
Match length 85
% identity 100

Seq. No.

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi\_965483\_dbj\_BAA08259\_ (D45420)

DcARF1 [Daucus carota]

 Seq. No.
 205436

 Seq. ID
 LIB3083-089-Q1-L1-D6

 Method
 BLASTX

 NCBI GI
 g1706958

BLAST score 465 E value 1.0e-46 Match length 137 % identity 63

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 205437

Seq. ID LIB3083-089-Q1-L1-D9

Method BLASTX
NCBI GI g4104242
BLAST score 318
E value 2.0e-29
Match length 62

% identity 100

NCBI Description (AF034266) palmitoyl-acyl carrier protein thioesterase

[Gossypium hirsutum]

Seq. No. 205438

Seq. ID LIB3083-089-Q1-L1-E10

Method BLASTX
NCBI GI g2864609
BLAST score 183
E value 1.0e-13
Match length 68
% identity 54

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

>gi 4049337 emb\_CAA22562\_ (AL034567) putative protein

[Arabidopsis thaliana]

Seq. No. 205439

Seq. ID LIB3083-089-Q1-L1-E2

Method BLASTX NCBI GI g1706956 BLAST score 507



```
1.0e-51
E value
                   98
Match length
                   100
% identity
                   (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   205440
                   LIB3083-089-Q1-L1-E4
Seq. ID
                   BLASTX
Method
                   q398847
NCBI GI
BLAST score
                   219
                   1.0e-37
E value
Match length
                   111
% identity
                  (X74655) beta-4 tubulin [Zea mays]
NCBI Description
                   205441
Seq. No.
                   LIB3083-089-Q1-L1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172557
BLAST score
                   183
                   1.0e-13
E value
Match length
                   55
% identity
                   OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
NCBI Description
                   ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   >gi_422030_pir__S34146 porin por1 - maize
>gi_626044_pir__A55017 porin, plastid - maize
                   >gi 313136_emb_CAA51828_ (X73429) porin [Zea mays]
                   205442
Seq. No.
                   LIB3083-089-Q1-L1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3142289
                   149
BLAST score
                   1.0e-09
E value
                   50
Match length
                   62
% identity
                   (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                   gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
                   205443
Seq. No.
Seq. ID
                   LIB3083-089-Q1-L1-F4
                   BLASTX
Method
                   g3142300
NCBI GI
BLAST score
                   503
                   4.0e-51
E value
                   126
Match length
                   73
% identity
                   (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                   protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
                   and gb T88158, gb N38703 and gb AA651043 come from this
                   gene. [Arabidopsis thaliana]
```

205444 Seq. No.

Seq. ID LIB3083-089-Q1-L1-F6

BLASTX Method q3549666 NCBI GI



```
BLAST score
                   5.0e-34
E value
Match length
                   87
                   78
% identity
                   (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205445
                   LIB3083-089-Q1-L1-F8
Seq. ID
                   BLASTX
Method
                   g82426
NCBI GI
                   604
BLAST score
                   6.0e-63
E value
                   126
Match length
```

45 % identity ubiquitin precursor - barley (fragment) NCBI Description

>gi 755763\_emb CAA27751\_ (X04133) ubiquitin polyprecursor

(171 aa) [Hordeum vulgare]

205446 Seq. No. Seq. ID LIB3083-089-Q1-L1-F9 Method BLASTX NCBI GI g267069 BLAST score 592 E value 1.0e-61

109 Match length 99 % identity

TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183\_pir\_\_JQ1594 NCBI Description

tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 205447

LIB3083-089-Q1-L1-G10 Seq. ID

BLASTX Method q1174592 NCBI GI BLAST score 573 5.0e-67 E value 132 Match length % identity

TUBULIN ALPHA-1 CHAIN >gi 2119270\_pir\_\_S60233 alpha-tubulin NCBI Description

- garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 205448

LIB3083-089-Q1-L1-G12 Seq. ID

Method BLASTX NCBI GI g2501490 BLAST score 280 6.0e-25 E value Match length 125 43 % identity

FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID NCBI Description

3-O-GLUCOSYLTRANSFERASE) >gi 1620013 dbj BAA12737\_ (D85186)

UDP-glucose:flavonoid-3-glucosyltransferase [Gentiana

triflora]

205449 Seq. No.



```
LIB3083-089-Q1-L1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1174498
                  464
BLAST score
                  1.0e-46
E value
Match length
                  110
                  78
% identity
                  SYNAPTOBREVIN-RELATED PROTEIN >gi_600710 (M90418) formerly
NCBI Description
                  called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                  205450
Seq. No.
Seq. ID
                  LIB3083-089-Q1-L1-G6
                  BLASTX
Method
                  q1705678
NCBI GI
                  205
BLAST score
                  2.0e-16
E value
                  49
Match length
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                   valosin-containing protein [Glycine max]
                   205451
Seq. No.
                  LIB3083-089-Q1-L1-G8
Seq. ID
                  BLASTN
Method
                  g2695704
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   175
Match length
                   87
% identity
NCBI Description A.thaliana constans gene
                   205452
Seq. No.
                   LIB3083-089-Q1-L1-H10
Seq. ID
Method
                   BLASTX
                   q1702983
NCBI GI
                   354
BLAST score
                   1.0e-33
E value
                   110
Match length
% identity
                   AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850
NCBI Description
                   hypothetical protein - garden strawberry
                   >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria
                   x ananassa] >gi_927034 (L44142) auxin-repressed protein
                   [Fragaria ananassa]
Seq. No.
                   205453
                   LIB3083-089-Q1-L1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4455206
BLAST score
                   434
                   5.0e-43
E value
```

Match length 130 70 % identity

(AL035440) putative beta-1, 3-glucanase [Arabidopsis NCBI Description

thaliana]

NCBI Description



```
205454
Seq. No.
Seq. ID
                  LIB3083-089-Q1-L1-H12
Method
                  BLASTX
NCBI GI
                  g3461831
BLAST score
                  232
                  2.0e-19
E value
                   50
Match length
% identity
                   (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205455
Seq. No.
                  LIB3083-089-Q1-L1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4580398
                   280
BLAST score
                   6.0e-25
E value
                   88
Match length
% identity
                   (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                   thaliana]
                   205456
Seq. No.
                   LIB3083-090-Q1-L1-A11
Seq. ID
                   BLASTX
Method
                   g2129495
NCBI GI
                   284
BLAST score
                   1.0e-25
E value
                   86
Match length
                   69
% identity
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                   (U30508) E6 [Gossypium barbadense]
                   205457
Seq. No.
                                                                                ż
Seq. ID
                   LIB3083-090-Q1-L1-A2
Method
                   BLASTX
                   g3114901
NCBI GI
BLAST score
                   365
                   6.0e-35
E value
                   95
Match length
                   75
% identity
                   (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa]
NCBI Description
                   >qi 3114905 emb CAA06709 (AJ005806) pceberh [Populus
                   balsamifera subsp. trichocarpa]
Seq. No.
                   205458
Seq. ID
                   LIB3083-090-Q1-L1-A3
                   BLASTX
Method
NCBI GI
                   g2160156
BLAST score
                   429
                   1.0e-42
E value
Match length
                   109
                   72
% identity
```

synthetase (gb\_Z73100). [Arabidopsis thaliana]

(AC000132) Strong similarity to S. pombe leucyl-tRNA

Seq. No.

Seq. ID

Method

205464

BLASTX

LIB3083-090-Q1-L1-B1



```
205459
Seq. No.
                  LIB3083-090-Q1-L1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2239091
                  267
BLAST score
                  2.0e-23
E value
                  127
Match length
                  45
% identity
                  (Z84571) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus]
                   205460
Seq. No.
                  LIB3083-090-Q1-L1-A6
Seq. ID
                  BLASTX
Method
                   g2129473
NCBI GI
                   249
BLAST score
                   2.0e-21
E value
                   101
Match length
                   51
% identity
                   arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                   205461
Seq. No.
                   LIB3083-090-Q1-L1-A7
Seq. ID
                   BLASTX
Method
                   g4185511
NCBI GI
                   525
BLAST score
                   1.0e-53
E value
                   113
Match length
                   86
% identity
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                   thaliana]
                   205462
Seq. No.
                   LIB3083-090-Q1-L1-A8
Seq. ID
                   BLASTX
Method
                   g3695388
NCBI GI
                   247
BLAST score
                   4.0e-21
E value
                   78
Match length
% identity
                   (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
                   205463
Seq. No.
Seq. ID
                   LIB3083-090-Q1-L1-A9
Method
                   BLASTX
NCBI GI
                   q3885328
BLAST score
                   431
                   1.0e-42
E value
                   122
Match length
% identity
                   (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
```



```
q585973
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
                  124
Match length
                  89
% identity
                  FRUCTOKINASE >gi 626018 pir S39997 fructokinase (EC
NCBI Description
                  2.7.1.4) - potato >gi 297015 emb CAA78283 (Z12823)
                  fructokinase [Solanum tuberosum] >gi 1095321 prf 2108342A
                  fructokinase [Solanum tuberosum]
                  205465
Seq. No.
                  LIB3083-090-Q1-L1-B12
Seq. ID
                  BLASTX
Method
                  g3702332
NCBI GI
BLAST score
                  160
                  6.0e-11
E value
                  109
Match length
                  28
% identity
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205466
                  LIB3083-090-Q1-L1-B2
Seq. ID
                  BLASTX
Method
                  g4406372
NCBI GI
                  408
BLAST score
                  6.0e-40
E value
Match length
                  123
                  64
% identity
                  (AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                  glomerata]
Seq. No.
                  205467
Seq. ID
                  LIB3083-090-Q1-L1-B3
                  BLASTX
Method
NCBI GI
                  g586076
BLAST score
                  620
E value
                   6.0e-65
Match length
                   116
% identity
                  TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                   tubulin 1 [Lupinus albus]
                   205468
Seq. No.
                   LIB3083-090-Q1-L1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4415992
BLAST score
                   663
                   7.0e-70
E value
```

128 Match length % identity

NCBI Description (AF059288) beta-tubulin 2 [Eleusine indica]

205469 Seq. No.

Seq. ID LIB3083-090-Q1-L1-B5

Method BLASTX NCBI GI g3953458



BLAST score 7.0e-52 E value 120 Match length 85 % identity

(AC002328) F20N2.3 [Arabidopsis thaliana] NCBI Description

205470 Seq. No.

LIB3083-090-Q1-L1-B6 Seq. ID

Method BLASTX g3193303 NCBI GI 417 BLAST score 5.0e-41 E value 124 Match length 61 % identity

(AF069298) similar to several proteins containing a tandem NCBI Description

repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

205471 Seq. No.

LIB3083-090-Q1-L1-C1 Seq. ID

Method BLASTX NCBI GI g70642 616 BLAST score 2.0e-64 E value 126 Match length 22 % identity

ubiquitin precursor - Arabidopsis thaliana NCBI Description

>gi 17678 emb CAA31331 (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi\_987519 (U33014) polyubiquitin

[Arabidopsis thaliana] >gi 226499 prf 1515347A

poly-ubiquitin [Arabidopsis thaliana]

Seq. No. 205472

LIB3083-090-Q1-L1-C10 Seq. ID

BLASTX Method g4193388 NCBI GI 426 BLAST score 4.0e-42 E value 101 Match length 83 % identity

(AF091455) translationally controlled tumor protein [Hevea NCBI Description

brasiliensis]

205473 Seq. No.

LIB3083-090-Q1-L1-C2 Seq. ID

BLASTX Method NCBI GI q1174592 BLAST score 687 1.0e-72 E value 132 Match length 97 % identity

TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin NCBI Description

- garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum

sativum]

205474 Seq. No.



84

% identity

NCBI Description

```
LIB3083-090-Q1-L1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529668
BLAST score
                  244
                   4.0e-21
E value
                  74
Match length
% identity
                   68
NCBI Description
                   (AC002535) putative photolyase/blue-light receptor
                   [Arabidopsis thaliana] >gi 3319288 (AF053366)
                  photolyase/blue light photoreceptor PHR2 [Arabidopsis
                  thaliana]
Seq. No.
                   205475
                  LIB3083-090-Q1-L1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g267082
BLAST score
                   429
E value
                   2.0e-42
Match length
                   105
% identity
                   80
                   TUBULIN BETA-8 CHAIN >qi 320189 pir JQ1592 tubulin beta-8
NCBI Description
                   chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8
                   tubulin [Arabidopsis thaliana]
Seq. No.
                   205476
                   LIB3083-090-Q1-L1-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2583123
BLAST score
                   148
E value
                   2.0e-09
Match length
                   60
                   50
% identity
                   (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                   thaliana]
                   205477
Seq. No.
                   LIB3083-090-Q1-L1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006848
BLAST score
                   339
E value
                   7.0e-32
Match length
                   85
% identity
                   78
                   (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                   bisulcatus]
                   205478
Seq. No.
                   LIB3083-090-Q1-L1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3193316
BLAST score
                   389
E value
                   9.0e-38
Match length
                   88
```

epimerases [Arabidopsis thaliana]

(AF069299) contains similarity to nucleotide sugar

Seq. ID

Method

```
205479
Seq. No.
                  LIB3083-090-Q1-L1-D10
Seq. ID
                  BLASTX
Method
                  g113449
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
                  123
Match length
                  32
% identity
                  PROBABLE ATP-DEPENDENT PERMEASE PRECURSOR
NCBI Description
                  >gi_83202_pir__S19421 ATP-dependent permease ADP1 precursor
                  - yeast (Saccharomyces cerevisiae)
                  >gi 1907154 emb CAA42328 (X59720) YCR011c, len:1049
                   [Saccharomyces cerevisiae]
                  205480
Seq. No.
                  LIB3083-090-Q1-L1-D2
Seq. ID
Method
                  BLASTX
                  g1706958
NCBI GI
                   529
BLAST score
                   3.0e-54
E value
                  103
Match length
% identity
                   96
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   205481
Seq. No.
                  LIB3083-090-Q1-L1-D3
Seq. ID
                  BLASTX
Method
                   g2244816
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
                   42
Match length
                   74
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   205482
Seq. No.
                   LIB3083-090-Q1-L1-D4
Seq. ID
                   BLASTX
Method
                   q4539327
NCBI GI
                   374
BLAST score
                   6.0e-36
E value
                   102
Match length
                   73
% identity
NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana]
                   205483
Seq. No.
                   LIB3083-090-Q1-L1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2149640
                   330
BLAST score
                   2.0e-31
E value
                   70
Match length
                   90
% identity
                   (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                   205484
Seq. No.
```

28119

LIB3083-090-Q1-L1-D6

BLASTX

```
q1706956
NCBI GI
                   660
BLAST score
                  2.0e-69
E value
Match length
                  127
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  205485
Seq. No.
Seq. ID
                  LIB3083-090-Q1-L1-D7
Method
                  BLASTX
                  q1706956
NCBI GI
                   491
BLAST score
                   6.0e-50
E value
                   95
Match length
                   99
% identity
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
                   205486
Seq. No.
                  LIB3083-090-Q1-L1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4098129
                   703
BLAST score
                   1.0e-74
E value
                   130
Match length
                   99
% identity
                  (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   205487
Seq. No.
                   LIB3083-090-Q1-L1-E4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2865522
                   38
BLAST score
                   6.0e-12
E value
                   103
Match length
% identity
                   Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
NCBI Description
                   complete cds
                   205488
Seq. No.
                   LIB3083-090-Q1-L1-E5
Seq. ID
Method
                   BLASTX
                   q3668086
NCBI GI
BLAST score
                   310
                   2.0e-28
E value
Match length
                   128
                   54
% identity
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205489
Seq. No.
                   LIB3083-090-Q1-L1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1707017
BLAST score
                   647
                   5.0e-68
E value
Match length
                   131
% identity
                   93
                  (U78721) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
```



```
205490
Seq. No.
Seq. ID
                  LIB3083-090-Q1-L1-E7
                   BLASTX
Method
                   g1171642
NCBI GI
                   209
BLAST score
                   7.0e-17
E value
                   81
Match length
% identity
                   PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
NCBI Description
                   >gi 481206 pir S38326 protein kinase - Arabidopsis
                   tha\overline{1}iana >\overline{g}i 1\overline{66}809 (L07248) protein kinase [Arabidopsis
                   thaliana]
                   205491
Seq. No.
                   LIB3083-090-Q1-L1-E8
Seq. ID
                   BLASTX
Method
                   g2104691
NCBI GI
                   187
BLAST score
                   5.0e-14
E value
                   111
Match length
% identity
                   34
                  (U92794) alpha glucosidase II, beta subunit [Mus musculus]
NCBI Description
                   205492
Seq. No.
                   LIB3083-090-Q1-L1-F1
Seq. ID
                   BLASTX
Method
                   g135452
NCBI GI
BLAST score
                   365
                   1.0e-48
E value
                   121
Match length
                   74
% identity
                   TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin
NCBI Description
                   [Glycine max]
                   205493
Seq. No.
Seq. ID
                   LIB3083-090-Q1-L1-F10
                   BLASTX
Method
                   g3858935
NCBI GI
                   328
BLAST score
                   1.0e-30
E value
                   92
Match length
                   66
% identity
                   (AL021636) synaptobrevin-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4103357 (AF025332) vesicle-associated
                   membrane protein 7C; synaptobrevin 7C [Arabidopsis
                   thaliana]
                   205494
Seq. No.
Seq. ID
                   LIB3083-090-Q1-L1-F4
                   BLASTX
Method
NCBI GI
                   g3360291
                   261
BLAST score
                   8.0e-23
E value
Match length
                   123
                   34
 % identity
NCBI Description (AF023165) leucine-rich repeat transmembrane protein kinase
```



## 2 [Zea mays]

```
Seq. No.
                  205495
Seq. ID
                  LIB3083-090-Q1-L1-F5
Method
                  BLASTX
NCBI GI
                   g2894612
BLAST score
                   488
                   2.0e-49
E value
Match length
                   125
                   73
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   205496
Seq. No.
Seq. ID
                  LIB3083-090-Q1-L1-F7
                   BLASTX
Method
                   q3080420
NCBI GI
BLAST score
                   384
                   4.0e-37
E value
Match length
                   82
% identity
                   87
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   205497
Seq. No.
Seq. ID
                   LIB3083-090-Q1-L1-F8
Method
                   BLASTX
                   g2576361
NCBI GI
BLAST score
                   159
                   2.0e-24
E value
Match length
                   120
% identity
                   (U39782) lysine and histidine specific transporter
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   205498
Seq. ID
                   LIB3083-090-Q1-L1-G2
Method
                   BLASTX
NCBI GI
                   g3927826
BLAST score
                   157
E value
                   1.0e-10
Match length
                   116
% identity
                   35
                  (AC005727) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205499
Seq. No.
Seq. ID
                   LIB3083-090-Q1-L1-G4
Method
                   BLASTX
NCBI GI
                   g1351974
BLAST score
                   534
                   6.0e-55
E value
Match length
                   104
                   97
% identity
                   ADP-RIBOSYLATION FACTOR >gi 1076788_pir__S49325
NCBI Description
                   ADP-ribosylation factor - maize >gi_1076789_pir_
                                                                     S53486
                   ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
                   (X80042) ADP-ribosylation factor [Zea mays]
```



```
205500
Seq. No.
                  LIB3083-090-Q1-L1-G9
Seq. ID
                  BLASTN
Method
                  g2865522
NCBI GI
BLAST score
                  38
                  6.0e-12
E value
                  103
Match length
                  74
% identity
                  Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
NCBI Description
                  complete cds
                  205501
Seq. No.
                  LIB3083-090-Q1-L1-H1
Seq. ID
                  BLASTN
Method
                  g4406805
NCBI GI
                   40
BLAST score
                   3.0e-13
E value
Match length
                   84
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   205502
                  LIB3083-090-Q1-L1-H10
Seq. ID
                   BLASTX
Method
                   g2970051
NCBI GI
                   271
BLAST score
                   5.0e-24
E value
                   73
Match length
                   71
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
                   205503
Seq. No.
                   LIB3083-090-Q1-L1-H12
Seq. ID
                   BLASTX
Method
                   q3650030
NCBI GI
BLAST score
                   248
                   3.0e-21
E value
                   102
Match length
                   56
% identity
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]
                   205504
Seq. No.
Seq. ID
                   LIB3083-090-Q1-L1-H2
Method
                   BLASTX
NCBI GI
                   q1518540
BLAST score
                   485
                   3.0e-49
E value
                   100
Match length
                   97
% identity
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   205505
Seq. No.
                   LIB3083-090-Q1-L1-H3
```

Seq. ID

Method BLASTX NCBI GI g2244899 BLAST score 459

```
E value
Match length
                  129
% identity
                  69
                  (Z97338) similar to UFD1 protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 205506 LIB3083-090-Q1-L1-H4

Seq. ID BLASTX Method NCBI GI q1103712 BLAST score 525 8.0e-54 E value 110 Match length

% identity

(X83729) inorganic pyrophosphatase [Nicotiana tabacum] NCBI Description

205507 Seq. No.

LIB3083-090-Q1-L1-H5 Seq. ID

Method BLASTX g1706958 NCBI GI BLAST score 370 2.0e-35 E value 129 Match length

% identity 63

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

205508 Seq. No.

Seq. ID LIB3083-090-Q1-L1-H6

Method BLASTX q1800307 NCBI GI BLAST score 220 E value 6.0e-18 125 Match length % identity

(U83883) p105 coactivator [Rattus norvegicus] NCBI Description

Seq. No. 205509

LIB3083-090-Q1-L1-H7 Seq. ID

Method BLASTX NCBI GI g4371290 BLAST score 217 E value 1.0e-17 Match length 93 % identity 47

(AC006260) unknown protein [Arabidopsis thaliana] NCBI Description

205510 Seq. No.

LIB3083-090-Q1-L1-H8 Seq. ID

BLASTX Method g1408471 NCBI GI 390 BLAST score 4.0e-38 E value 94 Match length 76 % identity

(U48938) actin depolymerizing factor 1 [Arabidopsis NCBI Description

thaliana] >gi 3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

```
Seq. No.
                   205511
Seq. ID
                   LIB3083-091-Q1-L1-A12
Method
                   BLASTX
NCBI GI
                   q4098331
BLAST score
                   323
                   3.0e-30
E value
                   74
Match length
                   81
% identity
                   (U76896) beta-tubulin 5 [Triticum aestivum]
NCBI Description
Seq. No.
                   205512
                   LIB3083-091-Q1-L1-A3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2507421
                   353
BLAST score
                   1.0e-33
E value
                   72
Match length
                   93
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                   thaliana] >gi 4490709 emb CAB38843.1 (AL035680)
                   translation initiation factor [Arabidopsis thaliana]
                   205513
Seq. No.
Seq. ID
                   LIB3083-091-Q1-L1-B12
Method
                   BLASTX
                   g3834307
NCBI GI
                   219
BLAST score
                   8.0e-18
E value
Match length
                   46
% identity
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
NCBI Description
                   putative protein from Arabidopsis thaliana BAC gb \overline{\text{A}}\text{L}021712.
                   ESTs gb_N65887 and gb_N65627 come from this gene.
                   [Arabidopsis thaliana]
                   205514
Seq. No.
                   LIB3083-091-Q1-L1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3096939
BLAST score
                   386
                   2.0e-37
E value
Match length
                   115
                   64
% identity
                   (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205515
                   LIB3083-091-Q1-L1-C1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2462929
BLAST score 506
E value 2.0e-51
Match length 133
% identity 70

NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 205516



```
LIB3083-091-Q1-L1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076746
                  485
BLAST score
                   5.0e-49
E value
                  116
Match length
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   205517
Seq. No.
                  LIB3083-091-Q1-L1-C7
Seq. ID
                  BLASTX
Method
                  g1354272
NCBI GI
                   455
BLAST score
                   2.0e-45
E value
                   132
Match length
                   68
% identity
NCBI Description (U51036) aspartic proteinase [Arabidopsis thaliana]
                   205518
Seq. No.
                   LIB3083-091-Q1-L1-D1
Seq. ID
                   BLASTX
Method
                   q4467124
NCBI GI
                   429
BLAST score
                   2.0e-42
E value
                   119
Match length
                   61
% identity
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   205519
                   LIB3083-091-Q1-L1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1402888
BLAST score
                   336
                   2.0e-44
E value
                   122
Match length
% identity
                   (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                   205520
Seq. No.
                   LIB3083-091-Q1-L1-D7
Seq. ID
                   BLASTX
Method
                   q4567251
NCBI GI
BLAST score
                   205
                   3.0e-22
E value
                   77
Match length
% identity
                   70
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205521
```

LIB3083-091-Q1-L1-D9 Seq. ID

Method BLASTX g1332579 NCBI GI 630 BLAST score E value 4.0e-66

28126



```
Match length
                  10
% identity
                   (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  205522
Seq. No.
                  LIB3083-091-Q1-L1-E1
Seq. ID
                  BLASTX
Method
                  g4567251
NCBI GI
                  307
BLAST score
                  3.0e-28
E value
                  79
Match length
                   70
% identity
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205523
Seq. No.
                   LIB3083-091-Q1-L1-E10
Seg. ID
Method
                   BLASTX
NCBI GI
                   g2995990
BLAST score
                   384
E value
                   4.0e-37
Match length
                   117
                   63
% identity
                   (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2995992 (AF053747) dormancy-associated
                   protein [Arabidopsis thaliana]
Seq. No.
                   205524
Seq. ID
                   LIB3083-091-Q1-L1-E11
Method
                   BLASTX
                   g3650032
NCBI GI
                   229
BLAST score
                   5.0e-19
E value
                   49
Match length
                   69
% identity
                   (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
                   205525
Seq. No.
Seq. ID
                   LIB3083-091-Q1-L1-E12
                   BLASTX
Method
                   g2853081
NCBI GI
BLAST score
                   265
                   3.0e-23
E value
Match length
                   78
% identity
                   (ALO21768) ATP binding protein - like [Arabidopsis
NCBI Description
                   thaliana]
                   205526
Seq. No.
Seq. ID
                   LIB3083-091-Q1-L1-E5
Method
                   BLASTX
NCBI GI
                   q112717
BLAST score
                   176
```

NCBI Description 21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911

9.0e-13

63

54

E value Match length

% identity



hypothetical protein precursor - carrot >gi\_18312\_emb\_CAA36642\_ (X52395) precursor polypeptide (AA -22 to 171) [Daucus carota]

 Seq. ID
 LIB3083-091-Q1-L1-E7

 Method
 BLASTN

 NCBI GI
 g3108300

 BLAST score
 131

 E value
 2.0e-67

 Match length
 135

 % identity
 99

Seq. No.

% identity 99
NCBI Description Gossypium barbadense clone pXP195 repetitive DNA sequence

Seq. No. 205528

Seq. ID LIB3083-091-Q1-L1-E9

Method BLASTX
NCBI GI g1854386
BLAST score 511
E value 5.0e-52
Match length 129
% identity 74

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No. 205529

Seq. ID LIB3083-091-Q1-L1-F1

Method BLASTX
NCBI GI g4512659
BLAST score 175
E value 9.0e-13
Match length 70
% identity 49

NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana]

>gi 4544465\_gb\_AAD22372.1\_AC006580\_4 (AC006580) putative

protein kinase [Arabidopsis thaliana]

Seq. No. 205530

Seq. ID LIB3083-091-Q1-L1-F3

Method BLASTX
NCBI GI g2351378
BLAST score 396
E value 1.0e-38
Match length 133
% identity 62

NCBI Description (U54558) translation initiation factor eIF3 p66 subunit

[Homo sapiens] >gi\_4200328\_emb\_CAA18440\_ (AL022313)

EIF3-P66 [Homo sapiens]

>gi\_4503523\_ref\_NP\_003744.1\_pEIF3S7\_ UNKNOWN

Seq. No. 205531

Seq. ID LIB3083-091-Q1-L1-F5

Method BLASTX
NCBI GI g4008006
BLAST score 489
E value 2.0e-49
Match length 130



```
% identity
                  (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  205532
Seq. No.
                  LIB3083-091-Q1-L1-F9
Seq. ID
                  BLASTX
Method
                  q2244970
NCBI GI
                  578
BLAST score
                  6.0e-60
E value
                  131
Match length
                  79
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 2326365_emb_CAA74765_ (Y14423) putative cell wall
                  protein [Arabidopsis thaliana]
                  205533
Seq. No.
                  LIB3083-091-Q1-L1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4490330
BLAST score
                  708
                   4.0e-75
E value
Match length
                   130
% identity
                   98
                   (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   205534
                   LIB3083-091-Q1-L1-G10
Seq. ID
Method
                   BLASTX
                   g1708314
NCBI GI
BLAST score
                   414
E value
                   1.0e-40
                   109
Match length
                   78
% identity
                   HEAT SHOCK PROTEIN 83 >gi 169296 (M99431) heat shock
NCBI Description
                   protein 83 [Pharbitis nil] >gi 445625_prf__1909372A heat
                   shock protein 83 [Ipomoea nil]
                   205535
Seq. No.
                   LIB3083-091-Q1-L1-G11
Seq. ID
                   BLASTX
Method
                   g485742
NCBI GI
BLAST score
                   243
                   4.0e-21
E value
                   74
Match length
                   69
% identity
                   (L32791) pyrophosphatase [Beta vulgaris]
NCBI Description
                   205536
Seq. No.
                   LIB3083-091-Q1-L1-G3
Seq. ID
                   BLASTX
Method
                   g3169065
NCBI GI
BLAST score
                   200
                   7.0e-16
E value
                   116
Match length
```

38

% identity



(AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe]

 Seq. No.
 205537

 Seq. ID
 LIB3083-091-Q1-L1-H10

 Method
 BLASTX

 MCPL CI
 03170531

NCBI GI g3170531 BLAST score 549 E value 2.0e-56 Match length 127 % identity 76

NCBI Description

NCBI Description (AF055635) protein tyrosine phosphatase 1; PTP1;

tyrosine-specific protein phosphatase [Arabidopsis

thaliana]

Seq. No. 205538

Seq. ID LIB3083-091-Q1-L1-H12

Method BLASTX
NCBI GI g3599974
BLAST score 302
E value 1.0e-27
Match length 126
% identity 46

NCBI Description (AF038651) GTP pyrophosphokinase [Corynebacterium

glutamicum]

Seq. No. 205539

Seq. ID LIB3083-091-Q1-L1-H9

Method BLASTX
NCBI GI g2811025
BLAST score 221
E value 5.0e-18
Match length 72
% identity 61

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi\_1944181\_dbj\_BAA19607\_

(AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 205540

Seq. ID LIB3083-092-Q1-L1-A1

Method BLASTX
NCBI GI g2245098
BLAST score 260
E value 2.0e-25
Match length 65
% identity 94

NCBI Description (Z97343) ribosomal protein [Arabidopsis thaliana]

Seq. No. 205541

Seq. ID LIB3083-092-Q1-L1-A10

Method BLASTX
NCBI GI g1707857
BLAST score 371
E value 9.0e-36
Match length 108
% identity 63

NCBI Description (Y09291) obtusifoliol 14-alpha-demethylase [Triticum

aestivum]

Seq. ID



```
205542
Seq. No.
                  LIB3083-092-Q1-L1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g450880
                  491
BLAST score
                  9.0e-50
E value
                  102
Match length
                  92
% identity
                  (X77199) heat shock cognate 70-1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205543
                  LIB3083-092-Q1-L1-A8
Seq. ID
                  BLASTX
Method
                  g4204300
NCBI GI
                  240
BLAST score
                  2.0e-20
E value
                  95
Match length
                  54
% identity
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  205544
                  LIB3083-092-Q1-L1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g123539
BLAST score
                  287
                   4.0e-26
E value
Match length
                   84
% identity
                   65
                  17.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.5-E) >gi 169987
NCBI Description
                   (M11395) small heat shock protein [Glycine max]
Seq. No.
                   205545
                   LIB3083-092-Q1-L1-B2
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
BLAST score
                   598
                   3.0e-62
E value
                   111
Match length
                   99
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   205546
Seq. No.
Seq. ID
                   LIB3083-092-Q1-L1-B3
                   BLASTN
Method
NCBI GI
                   g1143223
BLAST score
                   166
                   2.0e-88
E value
                   363
Match length
                   41
% identity
                  Gossypium barbadense FbLate-2 gene, complete cds
NCBI Description
Seq. No.
                   205547
```

28131

LIB3083-092-Q1-L1-B5

NCBI GI

BLAST score



```
BLASTX
Method
                  g1619602
NCBI GI
                  363
BLAST score
                  8.0e-35
E value
                  100
Match length
                  71
% identity
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                  205548
Seq. No.
                  LIB3083-092-Q1-L1-B9
Seq. ID
                  BLASTN
Method
                  g4220637
NCBI GI
                  50
BLAST score
                   4.0e-19
E value
                  115
Match length
                   91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MIE1, complete sequence [Arabidopsis thaliana]
                   205549
Seq. No.
Seq. ID
                   LIB3083-092-Q1-L1-C8
                  BLASTX
Method
                   g4567232
NCBI GI
                   216
BLAST score
                   5.0e-20
E value
                   65
Match length
                   79
% identity
                   (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
NCBI Description
                   thaliana]
                   205550
Seq. No.
                   LIB3083-092-Q1-L1-D11
Seq. ID
                   BLASTX
Method
                   q4544392
NCBI GI
                   244
BLAST score
                   6.0e-21
E value
                   55
Match length
                   82
% identity
                   (AC007047) dihydrofolate reductase-thymidylate synthase
NCBI Description
                   [Arabidopsis thaliana]
                   205551
Seq. No.
Seq. ID
                   LIB3083-092-Q1-L1-D7
                   BLASTX
Method
NCBI GI
                   q629806
                   529
BLAST score
                   9.0e-57
E value
Match length
                   114
                   93
% identity
                   tubulin beta chain - rice >gi_493725_emb_CAA55912_ (X79367)
NCBI Description
                   beta tubulin [Oryza sativa]
                   205552
Seq. No.
                   LIB3083-092-Q1-L1-D8
Seq. ID
Method
                   BLASTX
```

28132

q4063751

186



```
0e-14
E value
                  99
Match length
                  38
% identity
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4510409_gb AAD21495.1 (AC006929) putative white
                  protein [Arabidopsis thaliana]
                  205553
Seq. No.
Seq. ID
                  LIB3083-092-Q1-L1-E10
                  BLASTX
Method
NCBI GI
                  g547683
                  456
BLAST score
                  7.0e-46
E value
```

90 Match length 96 % identity

HEAT SHOCK COGNATE PROTEIN 80 >gi\_170456 (M96549) heat NCBI Description

shock cognate protein 80 [Solanum lycopersicum] >gi 445601 prf 1909348A heat shock protein hsp80

[Lycopersicon esculentum]

205554 Seq. No. Seq. ID LIB3083-092-Q1-L1-E3 Method BLASTX q2662343 NCBI GI 558

BLAST score 1.0e-57 E value 106 Match length 100 % identity

(D63581) EF-1 alpha [Oryza sativa] NCBI Description

205555 Seq. No.

Seq. ID LIB3083-092-Q1-L1-E7

Method BLASTX g4063752 NCBI GI 237 BLAST score 5.0e-20 E value 92 Match length 55 % identity

(AC005851) unknown protein [Arabidopsis thaliana] NCBI Description >gi 4510410 gb AAD21496.1 (AC006929) unknown protein

[Arabidopsis thaliana]

205556 Seq. No.

LIB3083-092-Q1-L1-E9 Seq. ID

BLASTX Method g2811278 NCBI GI BLAST score 336 8.0e-32 E value 81 Match length 79 % identity

(AF043284) expansin [Gossypium hirsutum] NCBI Description

205557 Seq. No.

Seq. ID LIB3083-092-Q1-L1-F6

Method BLASTX NCBI GI q543867 BLAST score 324

28133



2.0e-30 E value 94 Match length 73 % identity ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description >gi\_1076684\_pir\_\_A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi 303626\_dbj\_BAA03526\_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas] 205558 Seq. No. LIB3083-092-Q1-L1-F7 Seq. ID Method BLASTX g3925363 NCBI GI 344 BLAST score 1.0e-32 E value 87 Match length 90 % identity (AF067961) homeodomain protein [Malus domestica] NCBI Description 205559 Seq. No. LIB3083-092-Q1-L1-F8 Seq. ID Method BLASTX NCBI GI g267069 BLAST score 210 7.0e-17 E value 84 Match length % identity TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] 205560 Seq. No. LIB3083-092-Q1-L1-G4 Seq. ID Method BLASTX q1702983 NCBI GI 281 BLAST score 3.0e-25 E value 96 Match length 55 % identity AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850 NCBI Description hypothetical protein - garden strawberry >gi 22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi 927034 (L44142) auxin-repressed protein [Fragaria ananassa] 205561 Seq. No. LIB3083-092-Q1-L1-G8 Seq. ID BLASTX Method q2244990 NCBI GI 412 BLAST score

4.0e-46 E value 116 Match length 85 % identity

(Z97340) similarity to LIM homeobox protein -NCBI Description

Caenorhabditis [Arabidopsis thaliana]



```
205562
Seq. No.
                  LIB3083-092-Q1-L1-H12
Seq. ID
                  BLASTX
Method
                  q121631
NCBI GI
                  281
BLAST score
                  3.0e-25
E value
                  73
Match length
                  71
% identity
                  GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
NCBI Description
                  >gi_72323_pir__KNNT2S glycine-rich protein 2 - wood tobacco
                  >gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana
                  sylvestris]
                  205563
Seq. No.
                  LIB3083-092-Q1-L1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4544412
                   224
BLAST score
                   2.0e-18
E value
Match length
                   108
                   39
% identity
                   (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205564
                   LIB3083-092-Q1-L1-H9
Seq. ID
Method
                   BLASTX
                   g730583
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
                   97
Match length
                   45
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                   argentatum]
                   205565
Seq. No.
                   LIB3083-094-Q1-L1-A1
Seq. ID
                   BLASTX
Method
                   g2191175
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
                   118
Match length
                   33
 % identity
                   (AF007270) A IG002P16.24 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   205566
 Seq. No.
                   LIB3083-094-Q1-L1-A11
 Seq. ID
                   BLASTX
Method
                   g2995990
NCBI GI
                   193
 BLAST score
                   4.0e-15
 E value
                   85
 Match length
                   54
 % identity
                   (AF053746) dormancy-associated protein [Arabidopsis
 NCBI Description
```

protein [Arabidopsis thaliana]

thaliana] >gi\_2995992 (AF053747) dormancy-associated



```
205567
Seq. No.
Seq. ID
                  LIB3083-094-Q1-L1-A2
Method
                  BLASTX
NCBI GI
                  q4138137
BLAST score
                  478
                  3.0e-48
E value
                  121
Match length
                  75
% identity
NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]
                  205568
Seq. No.
                  LIB3083-094-Q1-L1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1174411
                  377
BLAST score
                  2.0e-36
E value
                  119
Match length
                  65
% identity
                  MICROSOMAL SIGNAL PEPTIDASE 18 KD SUBUNIT (SPC18)
NCBI Description
                  >gi 206978 (L11319) signal peptidase [Rattus norvegicus]
                  205569
Seq. No.
Seq. ID
                  LIB3083-094-Q1-L1-A5
                  BLASTX
Method
                  g4567304
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
                  87
Match length
                  44
% identity
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
                  205570
Seq. No.
Seq. ID
                  LIB3083-094-Q1-L1-A6
Method
                  BLASTX
NCBI GI
                  g1171978
BLAST score
                   508
                   9.0e-52
E value
                   122
Match length
                   22
% identity
                   POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                   205571
Seq. ID
                   LIB3083-094-Q1-L1-A8
                   BLASTX
Method
                   g4263790
NCBI GI
BLAST score
                   499
                   1.0e-50
E value
Match length
                   122
% identity
                   (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
NCBI Description
```

205572

LIB3083-094-Q1-L1-A9

Seq. No.

Seq. ID

```
BLASTX
Method
                  g1209703
NCBI GI
                  195
BLAST score
                  4.0e-15
E value
                  56
Match length
                  70
% identity
                  (U40489) maize gl1 homolog [Arabidopsis thaliana]
NCBI Description
                  205573
Seq. No.
                  LIB3083-094-Q1-L1-B1
Seq. ID
                  BLASTX
Method
                  g1172977
NCBI GI
                  475
BLAST score
                  7.0e-48
E value
                  111
Match length
                  84
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                   205574
Seq. No.
                   LIB3083-094-Q1-L1-B10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2829205
BLAST score
                   48
                   9.0e-19
E value
                   75
Match length
                   93
% identity
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
                   205575
Seq. No.
                   LIB3083-094-Q1-L1-B11
Seq. ID
Method
                   BLASTX
                   g4006876
NCBI GI
BLAST score
                   236
                   1.0e-19
E value
                   86
Match length
                   53
% identity
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205576
Seq. No.
                   LIB3083-094-Q1-L1-B2
Seq. ID
                   BLASTX
Method
                   g2129473
NCBI GI
                   265
BLAST score
                   3.0e-23
E value
                   96
Match length
                   56
% identity
                   arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
```

Seq. No. 205577

Seq. ID LIB3083-094-Q1-L1-B3

Method BLASTX
NCBI GI g2281102
BLAST score 265
E value 3.0e-23

Match length 120

% identity 51
NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No. 205578

Seq. ID LIB3083-094-Q1-L1-B4

Method BLASTX
NCBI GI g2500197
BLAST score 553
E value 4.0e-57
Match length 107
% identity 97

NCBI Description RAC-LIKE GTP BINDING PROTEIN RAC13 >gi\_1361976\_pir\_\_S57325

GTP-binding protein Rac 13 - upland cotton

>gi\_1087111\_bbs\_170156 (S79308) 21.8 kda GTP-binding

protein=Rac13 [Gossypium hirsutum=cotton plants, cv. Acala SJ-2, boll fibers, Peptide, 196 aa] [Gossypium hirsutum]

Seq. No. 205579

Seq. ID LIB3083-094-Q1-L1-B5

Method BLASTX
NCBI GI g730456
BLAST score 503
E value 3.0e-51
Match length 117
% identity 76

NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 205580

Seq. ID LIB3083-094-Q1-L1-C11

Method BLASTX
NCBI GI g4454026
BLAST score 368
E value 3.0e-35
Match length 109
% identity 65

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 205581

Seq. ID LIB3083-094-Q1-L1-C2

Method BLASTX
NCBI GI g3953463
BLAST score 237
E value 5.0e-20
Match length 69
% identity 59

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No. 205582

Seq. ID LIB3083-094-Q1-L1-C3

Method BLASTX
NCBI GI g2961371
BLAST score 230
E value 4.0e-19
Match length 84
% identity 55

NCBI Description (AL022141) hypothetical protein (fragment) [Arabidopsis

Method

BLASTN



## thaliana]

```
Seq. No.
                  205583
Seq. ID
                  LIB3083-094-Q1-L1-C6
                  BLASTX
Method
NCBI GI
                  q3702332
                  311
BLAST score
                  1.0e-28
E value
Match length
                  80
                   70
% identity
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  205584
Seq. No.
Seq. ID
                  LIB3083-094-Q1-L1-C8
                   BLASTN
Method
                   q20419
NCBI GI
                   44
BLAST score
                   1.0e-15
E value
Match length
                   260
                   15
% identity
NCBI Description P.amygdalus mRNA for extensin
                   205585
Seq. No.
                   LIB3083-094-Q1-L1-D11
Seq. ID
                   BLASTX
Method
                   g1351135
NCBI GI
                   591
BLAST score
                   2.0e-61
E value
                   125
Match length
                   85
% identity
                   SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                   >gi_436792_emb_CAA50317_ (X70990) sucrose synthase
                   [Arabidopsis thaliana]
                   205586
Seq. No.
Seq. ID
                   LIB3083-094-Q1-L1-D2
                   BLASTN
Method
NCBI GI
                   g20419
                   40
BLAST score
                   4.0e-13
E value
                   346
Match length
                   16
% identity
                  P.amygdalus mRNA for extensin
NCBI Description
                   205587
Seq. No.
                   LIB3083-094-Q1-L1-D3
Seq. ID
Method
                   BLASTX
                   g3128175
NCBI GI
BLAST score
                   163
                   3.0e-11
E value
                   95
Match length
                   38
% identity
                   (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205588
                   LIB3083-094-Q1-L1-D4
Seq. ID
```

```
q441218
NCBI GI
                  40
BLAST score
                  4.0e-13
E value
Match length
                  63
                  92
% identity
                  Tobacco mRNA for cytokinin binding protein CBP57, complete
NCBI Description
                  cds
                  205589
Seq. No.
                  LIB3083-094-Q1-L1-D5
Seq. ID
                  BLASTX
Method
                  g2829204
NCBI GI
                  378
BLAST score
                  1.0e-36
E value
                  94
Match length
                   84
% identity
                   (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
                   205590
Seq. No.
                  LIB3083-094-Q1-L1-D6
Seq. ID
Method
                  BLASTX
                   g3860008
NCBI GI
                   405
BLAST score
                   1.0e-39
E value
                   120
Match length
                   61
% identity
                  (AF091085) unknown [Homo sapiens]
NCBI Description
                   205591
Seq. No.
                   LIB3083-094-Q1-L1-D7
Seq. ID
                   BLASTX
Method
                   g4510345
NCBI GI
                   287
BLAST score
                   8.0e-26
E value
                   114
Match length
                   50
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                   205592
Seq. No.
Seq. ID
                   LIB3083-094-Q1-L1-D9
                   BLASTX
Method
                   g1915974
NCBI GI
                   539
BLAST score
                   2.0e-55
E value
                   134
Match length
                   76
% identity
                   (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693
NCBI Description
                   (U64818) fructokinase [Lycopersicon esculentum]
                   205593
Seq. No.
Seq. ID
                   LIB3083-094-Q1-L1-E2
                   BLASTX
Method
                   q2832664
NCBI GI
BLAST score
                   162
E value
                   4.0e-11
```

Match length



```
% identity
                  (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                  thaliana]
                  205594
Seq. No.
                  LIB3083-094-Q1-L1-E3
Seq. ID
Method
                  BLASTX
                  q2829899
NCBI GI
                  295
BLAST score
                  9.0e-27
E value
Match length
                  116
% identity
                  (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp AJ001449 2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
                  205595
Seq. No.
                  LIB3083-094-Q1-L1-E4
Seq. ID
                  BLASTX
Method
                  g2497743
NCBI GI
                  145
BLAST score
                   4.0e-09
E value
                   50
Match length
% identity
                  64
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
NCBI Description
                   >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein
                   [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                   [Gossypium hirsutum]
                   205596
Seq. No.
                   LIB3083-094-Q1-L1-E5
Seq. ID
                   BLASTX
Method
                   q2827649
NCBI GI
BLAST score
                   418
                   3.0e-41
E value
Match length
                   122
% identity
                   (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205597
                   LIB3083-094-Q1-L1-E6
Seq. ID
Method
                   BLASTN
                   g2244901
NCBI GI
BLAST score
                   51
                   1.0e-19
E value
Match length
                   95
                   88
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   205598
Seq. No.
                   LIB3083-094-Q1-L1-E7
```

Seq. ID LIB3083-094-Q1-L1-E3
Method BLASTX

Method BLASTX
NCBI GI g2494174
BLAST score 609
E value 1.0e-63
Match length 122



% identity GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi\_497979 (U10034) NCBI Description glutamate decarboxylase [Arabidopsis thaliana]

205599 Seq. No. LIB3083-094-Q1-L1-E8 Seq. ID BLASTX Method

g3924848 NCBI GI 177 BLAST score 6.0e-13 E value 121 Match length 38 % identity

(Z81586) cDNA EST yk335d8.5 comes from this gene; cDNA EST NCBI Description yk335d8.3 comes from this gene [Caenorhabditis elegans]

205600 Seq. No.

LIB3083-094-Q1-L1-E9 Seq. ID

BLASTX Method g543867 NCBI GI 362 BLAST score 1.0e-34 E value 103 Match length 78 % identity

ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi\_1076684\_pir\_\_A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi 303626\_dbj\_BAA03526\_ (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

205601 Seq. No.

LIB3083-094-Q1-L1-F1 Seq. ID

BLASTX Method NCBI GI g1843628 263 BLAST score 5.0e-23 E value 76 Match length

68 % identity

(U88061) SNF5 homolog BSH [Arabidopsis thaliana] NCBI Description

205602 Seq. No.

Seq. ID LIB3083-094-Q1-L1-F11

BLASTX Method g135406 NCBI GI BLAST score 572 3.0e-59 E value 113 Match length 92 % identity

TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi\_99768\_pir\_\_A32712 tubulin NCBI Description

alpha-5 chain - Arabidopsis thaliana >gi\_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi\_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

205603 Seq. No.

Seq. ID LIB3083-094-Q1-L1-F2

BLASTX Method NCBI GI q3927825 447 BLAST score



```
E value
Match length
                  116
% identity
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                  [Arabidopsis thaliana]
                  205604
Seq. No.
                  LIB3083-094-Q1-L1-F4
Seq. ID
                  BLASTX
Method
                  g2642648
NCBI GI
                  596
BLAST score
                  4.0e-62
E value
                  121
Match length
% identity
                   (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                   [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                   shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
                   cytosolic heat shock 70 protein [Spinacia oleracea]
                  205605
Seq. No.
                  LIB3083-094-Q1-L1-F7
Seq. ID
                  BLASTX
Method
                   g3757515
NCBI GI
                   198
BLAST score
                   2.0e-15
E value
                   46
Match length
                   78
% identity
                  (AC005167) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205606
Seq. No.
                   LIB3083-094-Q1-L1-G2
Seq. ID
                   BLASTN
Method
                   g1143223
NCBI GI
                   226
BLAST score
                   1.0e-124
E value
                   336
Match length
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   205607
Seq. No.
                   LIB3083-094-Q1-L1-G4
Seq. ID
                   BLASTX
Method
                   g3201554
NCBI GI
                   519
BLAST score
                   5.0e-53
E value
                   124
Match length
% identity
                   (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
 Seq. No.
                   205608
                   LIB3083-094-Q1-L1-G6
```

Seq. ID

BLASTX Method g4234774 NCBI GI 144 BLAST score 5.0e-09 E value 91 Match length 43 % identity

28143



```
(AF073926) cis-Golgi SNARE p28 [Homo sapiens]
NCBI Description
                  205609
Seq. No.
                  LIB3083-094-Q1-L1-G7
Seq. ID
                  BLASTX
Method
                  g3522938
NCBI GI
                  318
BLAST score
                  1.0e-29
E value
                  104
Match length
                  59
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                  205610
Seq. No.
                  LIB3083-094-Q1-L1-G8
Seq. ID
                  {\tt BLASTX}
Method
                   g1352440
NCBI GI
                   265
BLAST score
                   3.0e-23
E value
                   59
Match length
                   76
% identity
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                   (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)
                   (EIF-4F P26 SUBUNIT) >gi_1002915 (U34597) p26 [Oryza
                   sativa]
                   205611
Seq. No.
                   LIB3083-094-Q1-L1-G9
Seq. ID
Method
                   BLASTX
                   g2584806
NCBI GI
                   144
BLAST score
                   2.0e-09
E value
                   30
Match length
% identity
                   97
                   (Y15253) phospholipase C [Pisum sativum]
NCBI Description
                   205612
Seq. No.
                   LIB3083-094-Q1-L1-H1
Seq. ID
                   BLASTX
Method
                   g2129950
NCBI GI
                   514
BLAST score
                   2.0e-52
E value
                   124
Match length
                   83
% identity
                   inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) -
NCBI Description
                   common tobacco
                   205613
Seq. No.
                   LIB3083-094-Q1-L1-H2
Seq. ID
```

BLASTX Method q3334138 NCBI GI 454 BLAST score 2.0e-45 E value 98 Match length 83 % identity

CALNEXIN HOMOLOG PRECURSOR >gi\_669003 (U20502) calnexin NCBI Description

[Glycine max]



```
Seq. No.
                  LIB3083-094-Q1-L1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4337027
                  428
BLAST score
                  2.0e-42
E value
Match length
                  122
% identity
NCBI Description (AF123254) MFP2 [Arabidopsis thaliana]
Seq. No.
                  205615
Seq. ID
                  LIB3083-094-Q1-L1-H5
Method
                  BLASTX
                   q3367522
NCBI GI
                   358
BLAST score
                   4.0e-34
E value
                   127
Match length
% identity
                  (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   205616
Seq. No.
                   LIB3083-094-Q1-L1-H6
Seq. ID
Method
                   BLASTX
                   g1843527
NCBI GI
                   586
BLAST score
                   7.0e-61
E value
                   117
Match length
                   56
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
                   205617
Seq. No.
                   LIB3083-094-Q1-L1-H7
Seq. ID
Method
                   BLASTX
                   g4263787
NCBI GI
BLAST score
                   185
                   7.0e-14
E value
Match length
                   71
                   58
% identity
NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
                   205618
Seq. No.
Seq. ID
                   LIB3083-094-Q1-L1-H8
Method
                   BLASTX
                   g3983663
NCBI GI
BLAST score
                   345
                   1.0e-32
E value
Match length
                   121
 % identity
                   60
                   (AB011270) importin-betal [Oryza sativa]
NCBI Description
                   205619
 Seq. No.
                   LIB3083-095-Q1-L1-A10
 Seq. ID
                   BLASTX
Method
                   g2262177
NCBI GI
                   343
BLAST score
```

2.0e-32

E value



108

65

4.0e-37

BLAST score

Match length

NCBI Description

% identity

E value

```
Match length
                   64
% identity
                   (AC002329) hypothetical protein similar to T18A10.3
NCBI Description
                   [Arabidopsis thaliana]
                  205620
Seq. No.
                  LIB3083-095-Q1-L1-A11
Seq. ID
                  BLASTX
Method
                  q2832686
NCBI GI
BLAST score
                  186
                   4.0e-14
E value
Match length
                   57
% identity
                   58
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                   205621
Seq. No.
                  LIB3083-095-Q1-L1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244736
                   437
BLAST score
                   1.0e-43
E value
                   81
Match length
% identity
                   100
                  (D88415) expansin [Gossypium hirsutum]
NCBI Description
                   205622
Seq. No.
                   LIB3083-095-Q1-L1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3421094
                   338
BLAST score
                   7.0e-32
E value
Match length
                   72
                   90
% identity
                   (AF043527) 20S proteasome subunit PAF2 [Arabidopsis
NCBI Description
                   thaliana]
                   205623
Seq. No.
                   LIB3083-095-Q1-L1-A6
Seq. ID
Method
                   BLASTX
                   g1172632
NCBI GI
BLAST score
                   241
                   1.0e-20
E value
                   99
Match length
                   52
% identity
                   PROFILIN >gi_557660_emb_CAA57632_ (X82120) profilin
NCBI Description
                   [Nicotiana tabacum]
                   205624
Seq. No.
Seq. ID
                   LIB3083-095-Q1-L1-A7
                   BLASTX
Method
                   g2661840
NCBI GI
```

28146

(Y15430) adenosine kinase [Physcomitrella patens]



```
205625
Seq. No.
                  LIB3083-095-Q1-L1-A8
Seq. ID
Method
                  BLASTX
                  g2829865
NCBI GI
                  471
BLAST score
E value
                  2.0e-47
Match length
                  108
% identity
                  85
                   (ACO02396) N-terminal region similar to DNA-J proteins
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  205626
                  LIB3083-095-Q1-L1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2811278
BLAST score
                  364
E value
                   6.0e-35
Match length
                  100
% identity
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                  205627
Seq. No.
Seq. ID
                  LIB3083-095-Q1-L1-B12
Method
                  BLASTX
NCBI GI
                  g1914683
                   358
BLAST score
                   3.0e-34
E value
Match length
                   107
% identity
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
                   205628
Seq. No.
Seq. ID
                   LIB3083-095-Q1-L1-B3
Method
                  BLASTX
NCBI GI
                   g2493146
BLAST score
                   203
                   2.0e-16
E value
                   48
Match length
                   90
% identity
                   VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 755148
NCBI Description
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                   [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275)
                   vacuolar H+-ATPase c subunit [Citrus unshiu]
                   205629
Seq. No.
Seq. ID
                   LIB3083-095-Q1-L1-B4
                   BLASTN
Method
                   g1143223
NCBI GI
                   128
BLAST score
                   9.0e-66
E value
                   332
Match length
```

47 % identity

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

205630 Seq. No.

Seq. ID LIB3083-095-Q1-L1-B5

Method BLASTX

Method

NCBI GI

BLASTX g1706956



```
g3914237
NCBI GI
                  167
BLAST score
                  7.0e-12
E value
                  94
Match length
                  35
% identity
                  COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (P24A)
NCBI Description
                   (RNP24) >gi_1212965_emb_CAA63069_ (X92098) transmembrane
                  protein [Homo sapiens]
Seq. No.
                  205631
                  LIB3083-095-Q1-L1-B6
Seq. ID
Method
                  BLASTX
                  q3482933
NCBI GI
                  414
BLAST score
                  8.0e-41
E value
                  107
Match length
% identity
                   72
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                  thaliana]
                   205632
Seq. No.
                   LIB3083-095-Q1-L1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1706956
BLAST score
                   441
                   6.0e-44
E value
Match length
                   82
                   95
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   205633
Seq. No.
                   LIB3083-095-Q1-L1-B8
Seq. ID
Method
                   BLASTX
                   g100226
NCBI GI
                   424
BLAST score
                   5.0e-42
E value
                   109
Match length
                   77
% identity
                  hypothetical protein - tomato >gi_19275 emb CAA78112
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   205634
Seq. No.
                   LIB3083-095-Q1-L1-C10
Seq. ID
                   BLASTX
Method
                   g2979553
NCBI GI
BLAST score
                   354
                   9.0e-34
E value
                   109
Match length
% identity
                   (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205635
Seq. No.
Seq. ID
                   LIB3083-095-Q1-L1-C2
```

NCBI Description



```
BLAST score
                  4.0e-49
E value
                  110
Match length
                  78
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  205636
Seq. No.
                  LIB3083-095-Q1-L1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244801
BLAST score
                  140
E value
                  1.0e-08
Match length
                  53
                   58
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   205637
Seq. No.
                   LIB3083-095-Q1-L1-C4
Seq. ID
Method
                   BLASTX
                   g2760837
NCBI GI
BLAST score
                   152
                   4.0e-10
E value
Match length
                   106
% identity
                   33
                  (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   205638
Seq. No.
                   LIB3083-095-Q1-L1-C8
Seq. ID
Method
                   BLASTX
                   g3935167
NCBI GI
                   447
BLAST score
                   1.0e-44
E value
                   95
Match length
% identity
                   92
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
NCBI Description
                   205639
Seq. No.
                   LIB3083-095-Q1-L1-D1
Seq. ID
Method
                   BLASTX
                   g3763926
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
                   57
Match length
% identity
                   72
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205640
                   LIB3083-095-Q1-L1-D11
Seq. ID
                   BLASTX
Method
                   g267079
NCBI GI
                   491
BLAST score
                   7.0e-50
E value
                   107
Match length
                   86
% identity
                   TUBULIN BETA-6 CHAIN >gi 320187 pir JQ1590 tubulin beta-6
```

tubulin [Arabidopsis thaliana]

chain - Arabidopsis thalīana >gi\_166904 (M84703) beta-6



```
205641
Seq. No.
Seq. ID
                  LIB3083-095-Q1-L1-D3
Method
                  BLASTX
NCBI GI
                  g135452
                  389
BLAST score
                  6.0e-38
E value
Match length
                  84
% identity
                  86
                  TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin
NCBI Description
                  [Glycine max]
                  205642
Seq. No.
Seq. ID
                  LIB3083-095-Q1-L1-D4
                  BLASTX
Method
NCBI GI
                  g1171978
BLAST score
                  275
                  2.0e-24
E value
                  71
Match length
                  24
% identity
NCBI Description
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
                  205643
Seq. No.
Seq. ID
                  LIB3083-095-Q1-L1-D9
                  BLASTN
Method
NCBI GI
                  g1143223
BLAST score
                  123
E value
                  9.0e-63
Match length
                  319
                  62
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                  205644
Seq. No.
Seq. ID
                  LIB3083-095-Q1-L1-E1
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                   462
E value
                  2.0e-46
Match length
                  94
                  10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  205645
Seq. No.
Seq. ID
                  LIB3083-095-Q1-L1-E11
Method
                  BLASTX
NCBI GI
                  g3549666
BLAST score
                  357
                   4.0e-34
E value
Match length
                  87
                  78
% identity
```

Seq. No. 205646

NCBI Description

Seq. ID LIB3083-095-Q1-L1-E2

(AL031394) putative protein [Arabidopsis thaliana]



```
Method
NCBI GI
                   g1076746
BLAST score
                   385
E value
                   2.0e-37
Match length
                   97
% identity
                   79
NCBI Description
                   heat shock protein 70 - rice (fragment)
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   205647
Seq. ID
                   LIB3083-095-Q1-L1-E5
Method
                   BLASTX
NCBI GI
                   g3914002
BLAST score
                   423
E value
                   6.0e-42
Match length
                   101
% identity
                   81
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279
                   (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.
                   205648
Seq. ID
                   LIB3083-095-Q1-L1-E6
Method
                   BLASTX
NCBI GI
                   g4204261
BLAST score
                   172
E value
                   2.0e-12
Match length
                   108
% identity
                   43
NCBI Description
                  (AC005223) 27887 [Arabidopsis thaliana]
Seq. No.
                   205649
                  LIB3083-095-Q1-L1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2996096
BLAST score
                   569
E value
                   5.0e-59
Match length
                   108
% identity
NCBI Description
                  (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
Seq. No.
                  205650
Seq. ID
                  LIB3083-095-Q1-L1-F11
Method
                  BLASTX
                  q1657382
                  447
                  1.0e-44
                  83
                  95
NCBI Description
                  (Y09101) cholinephosphate cytidylyltransferase [Pisum
```

NCBI GI BLAST score E value Match length % identity

sativum]

Seq. No. 205651

Seq. ID LIB3083-095-Q1-L1-F3

Method BLASTX NCBI GI g123906



BLAST score E value 9.0e-23 Match length 109 % identity 48 HYOSCYAMINE 6-DIOXYGENASE (HYOSCYAMINE 6-BETA-HYDROXYLASE) NCBI Description >gi\_100173\_pir\_\_A40005 hyoscyamine (6S)-dioxygenase (EC 1.14.11.11) - henbane >gi 168268 (M62719) hyoscyamine 6 beta-hydroxylase [Hyoscyamus niger] >gi 511931 dbj BAA05630 (D26583) Hyoscyamine 6 beta-hydroxylase [Hyoscyamus niger] 205652 Seq. No. Seq. ID LIB3083-095-Q1-L1-F5 Method BLASTX NCBI GI g4115377 506 BLAST score 1.0e-51 E value 107 Match length 85 % identity NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] Seq. No. 205653 LIB3083-095-Q1-L1-F6 Seq. ID Method BLASTX NCBI GI q3402713 BLAST score 339 E value 5.0e-32 Match length 106 % identity 60 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana] Seq. No. 205654 Seq. ID LIB3083-095-Q1-L1-F7 Method BLASTX NCBI GI g2570047 BLAST score Ī76 E value 7.0e-1377 Match length 38 % identity NCBI Description (Y09234) MSTK2S kinase-like protein [Mus musculus] Seq. No. 205655 Seq. ID LIB3083-095-Q1-L1-F8 Method BLASTX NCBI GI g1045614 BLAST score 198

2.0e-15 E value 44 Match length % identity 68

NCBI Description (U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]

205656 Seq. No.

Seq. ID LIB3083-095-Q1-L1-G11

Method BLASTX NCBI GI g2559012 BLAST score 446 E value 1.0e-44

28152



Match length % identity

(AF026293) chaperonin containing t-complex polypeptide 1, NCBI Description

beta subunit; CCT-beta [Homo sapiens] >gi\_4090929

(AF026166) chaperonin-containing TCP-1 beta subunit homolog

[Homo sapiens]

205657 Seq. No.

LIB3083-095-Q1-L1-G3 Seq. ID

Method BLASTX NCBI GI q606942 BLAST score 478 3.0e-48E value 94 Match length % identity

(U13760) unknown [Gossypium hirsutum] NCBI Description

205658 Seq. No.

LIB3083-095-Q1-L1-G6 Seq. ID

BLASTX Method q4415996 NCBI GI 475 BLAST score 6.0e-48 E value 88 Match length 97 % identity

(AF059290) beta-tubulin 4 [Eleusine indica] NCBI Description

205659 Seq. No.

LIB3083-095-Q1-L1-G7 Seq. ID

BLASTX Method q3513727 NCBI GI 440 BLAST score 7.0e-44E value 106 Match length 82 % identity

(AF080118) contains similarity to TPR domains (Pfam: NCBI Description TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi\_4539358\_emb\_CAB40052.1\_ (AL049525) putative

protein [Arabidopsis thaliana]

205660 Seq. No.

Seq. ID LIB3083-095-Q1-L1-G9

Method BLASTX q1174592 NCBI GI BLAST score 563 3.0e-58 E value 108 Match length % identity 99

TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin NCBI Description

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 205661

Seq. ID LIB3083-095-Q1-L1-H1

Method BLASTX g2252830 NCBI GI



BLAST score 350 3.0e-33 E value Match length 109 % identity 66 (AF013293) weak similarity to receptor protein kinase NCBI Description [Arabidopsis thaliana] 205662 Seq. No. LIB3083-095-Q1-L1-H11 Seq. ID Method BLASTX g2117937 NCBI GI 194 BLAST score 5.0e-15 E value Match length 75 % identity 52 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -NCBI Description barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare] 205663 Seq. No. LIB3083-095-Q1-L1-H3 Seq. ID BLASTX Method . g4206209 NCBI GI BLAST score 525 8.0e-54 E value Match length 104 % identity 95 (AF071527) putative glucan synthase component [Arabidopsis NCBI Description thaliana] >gi\_4263042\_gb\_AAD15311\_ (AC005142) putative glucan synthase component [Arabidopsis thaliana] Seq. No. 205664 LIB3083-095-Q1-L1-H4 Seq. ID BLASTX Method g2065531 NCBI GI 211 BLAST score 4.0e-17 E value 91 Match length 49 % identity (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] NCBI Description Seq. No. 205665 LIB3083-095-Q1-L1-H6 Seq. ID BLASTX Method g3789911 NCBI GI 241 BLAST score 1.0e-20 E value 98 Match length % identity

(AF081802) developmental protein DG1118 [Dictyostelium NCBI Description

discoideum]

205666 Seq. No.

LIB3083-095-Q1-L1-H7 Seq. ID

BLASTX Method q4185511 NCBI GI BLAST score 437



```
2.0e-43
E value
                   110
Match length
% identity
                   75
NCBI Description
                   thaliana]
```

(AF102822) actin depolymerizing factor 4 [Arabidopsis

Seq. No. Seq. ID

205667 LIB3083-097-Q1-L1-A2

Method BLASTN NCBI GI BLAST score 32

g4510392

E value 1.0e-08 Match length 68 87 % identity

Arabidopsis thaliana chromosome II BAC T17D12 genomic NCBI Description

sequence, complete sequence

Seq. No.

205668

Seq. ID

LIB3083-097-Q1-L1-A4

Method BLASTN NCBI GI g2264304 BLAST score 42 2.0e-14 E value Match length 142 % identity 86

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.

205669

Seq. ID LIB3083-097-Q1-L1-A5

Method BLASTX NCBI GI q1418127 BLAST score 545 E value 5.0e-56 Match length 115 87 % identity

NCBI Description (D63166) CTP:phosphocholine cytidylyltransferase [Brassica

napus]

Seq. No.

205670

Seq. ID

LIB3083-097-Q1-L1-A8

Method BLASTX NCBI GI q418507 BLAST score 233 E value 1.0e-19 Match length 102 % identity

NCBI Description S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE

METHYLTRANSFERASE >gi 541097 pir S40872 hypothetical protein f161 - Escherichia coli >gi 305032 (L19201) ORF f161 [Escherichia coli] >gi 1336002 (U56082)

S-adenosylmethionine: 2-demethylmenaquinone

methyltransferase [Escherichia coli] >gi\_1790364 (AE000467)

menaquinone biosynthesis, unknown [Escherichia coli]

205671 Seq. No.

LIB3083-097-Q1-L1-A9 Seq. ID



```
BLASTX
Method
                  q4371292
NCBI GI
                   491
BLAST score
                   9.0e-50
E value
                  118
Match length
                  75
% identity
NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]
                  205672
Seq. No.
                  LIB3083-097-Q1-L1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1706956
BLAST score
                   586
                   7.0e-61
E value
Match length
                   124
                   90
% identity
NCBI Description
                  (U58283) cellulose synthase [Gossypium hirsutum]
                   205673
Seq. No.
                   LIB3083-097-Q1-L1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2668505
BLAST score
                   194
E value
                   7.0e-15
Match length
                   104
% identity
                   44
                   (U61837) putative cyclin G1 interacting protein [Homo
NCBI Description
                   sapiens]
                   205674
Seq. No.
                   LIB3083-097-Q1-L1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2653446
                   621
BLAST score
E value
                   6.0e-65
                   129
Match length
% identity
                  (AB009077) proton pyrophosphatase [Vigna radiata]
NCBI Description
                   205675
Seq. No.
                   LIB3083-097-Q1-L1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g231660
                   331
BLAST score
                   6.0e-31
E value
Match length
                   121
                   55
% identity
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.
                   205676
Seq. ID
                   LIB3083-097-Q1-L1-B6
Method
                   BLASTX
NCBI GI
                   g2129499
BLAST score
                   418
```

28156

2.0e-41

93

85

E value

Match length % identity



```
fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  205677
Seq. No.
Seq. ID
                  LIB3083-097-Q1-L1-B7
Method
                  BLASTX
NCBI GI
                  q4467145
                  268
BLAST score
                  1.0e-23
E value
                  72
Match length
% identity
                  (AL035540) farnesylated protein (ATFP6) [Arabidopsis
NCBI Description
                  thaliana]
                  205678
Seq. No.
                  LIB3083-097-Q1-L1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g136636
                  310
BLAST score
                  1.0e-28
E value
Match length
                  62
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                  >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                  Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin
                  Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894_pdb_2AAK
                  Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                  >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                  thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                  [Arabidopsis Thaliana]
                  205679
Seq. No.
                  LIB3083-097-Q1-L1-C1
Seq. ID
                  BLASTX
Method
                  q1001263
NCBI GI
                  227
BLAST score
                  9.0e-19
E value
                  129
Match length
                   39
% identity
                  (D64003) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   205680
                   LIB3083-097-Q1-L1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   a1346172
                   326
```

BLAST score 2.0e-35 E value 106 Match length 77 % identity

78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) NCBI Description (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)

>gi\_170384 (L08830) glucose-regulated protein 78

[Lycopersicon esculentum]

205681 Seq. No.

LIB3083-097-Q1-L1-C4 Seq. ID

BLAST score

E value

209 1.0e-16

```
BLASTX
Method
                   q3169182
NCBI GI
                   313
BLAST score
                   8.0e-29
E value
                   78
Match length
% identity
                   76
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]
                   205682
Seq. No.
                   LIB3083-097-Q1-L1-C5
Seq. ID
Method
                   BLASTX
                   g2160191
NCBI GI
BLAST score
                   666
                   3.0e-70
E value
Match length
                   126
                   95
% identity
                   (AC000132) Identical to A. thaliana AtK-1 (gb_X79279).
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   205683
                   LIB3083-097-Q1-L1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q131772
BLAST score
                   473
                   1.0e-47
E value
                   111
Match length
                   86
% identity
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                   maize
                   205684
Seq. No.
                   LIB3083-097-Q1-L1-C7
Seq. ID
                   BLASTX
Method
                   g3928083
NCBI GI
                   475
BLAST score
                   7.0e-48
E value
                   128
Match length
% identity
                   70
                   (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205685
Seq. No.
                   LIB3083-097-Q1-L1-C8
Seq. ID
Method
                   BLASTX
                   g3548804
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
                   78
Match length
                   67
 % identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   205686
 Seq. No.
                   LIB3083-097-Q1-L1-D1
Seq. ID
                   BLASTX
Method
                   g2129703
NCBI GI
```



Match length 98 % identity 44

NCBI Description receptor kinase - Arabidopsis thaliana

>gi\_2129704\_pir\_\_S71184 receptor kinase - Arabidopsis
thaliana >qi 166692 (M80238) receptor kinase [Arabidopsis

thaliana] >gi 445123 prf 1908429A receptor kinase

[Arabidopsis thaliana]

Seq. No. 205687

Seq. ID LIB3083-097-Q1-L1-D2

Method BLASTX
NCBI GI g124226
BLAST score 632
E value 3.0e-66
Match length 128
% identity 93

NCBI Description INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)

>gi\_100278\_pir\_\_S21059 translation initiation factor
eIF-5A.2 - curled-leaved tobacco >gi\_19702\_emb\_CAA45104\_
(X63542) eukaryotic initiation factor 5A (2) [Nicotiana

plumbaginifolia]

Seq. No. 205688

Seq. ID LIB3083-097-Q1-L1-D3

Method BLASTX
NCBI GI g1702983
BLAST score 331
E value 6.0e-31
Match length 111
% identity 57

NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi\_99855\_pir\_\_S11850

hypothetical protein - garden strawberry

>gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria
x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 205689

Seq. ID LIB3083-097-Q1-L1-D4

Method BLASTX
NCBI GI g218157
BLAST score 217
E value 1.0e-17
Match length 49
% identity 86

NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 205690

Seg. ID LIB3083-097-Q1-L1-D6

Method BLASTX
NCBI GI g1663706
BLAST score 194
E value 7.0e-15
Match length 110
% identity 40

NCBI Description (D87685) similar to human transcription factor TFIIS

(S34159). [Homo sapiens]



```
Seq. No.
                   205691
                  LIB3083-097-Q1-L1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132944
                  472
BLAST score
                  7.0e-50
E value
                  101
Match length
                   91
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi 806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
                   205692
Seq. No.
                  LIB3083-097-Q1-L1-E1
Seq. ID
Method
                  BLASTX
                   g1706956
NCBI GI
BLAST score
                   492
                   3.0e-58
E value
Match length
                   129
                   91
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   205693
Seq. ID
                   LIB3083-097-Q1-L1-E2
Method
                   BLASTX
NCBI GI
                   g1351365
BLAST score
                   185
                   8.0e-14
E value
Match length
                   56
% identity
                   62
                   UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN
NCBI Description
                   (CR6) >gi 2130002 pir_S68969 ubiquinol--cytochrome-c
                   reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768
                   (X82325) cytochrome c reductase subunit [Solanum tuberosum]
                   205694
Seq. No.
                   LIB3083-097-Q1-L1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1934730
BLAST score
                   306
                   5.0e-28
E value
                   90
Match length
                   60
% identity
                   (U95036) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   205695
Seq. No.
                   LIB3083-097-Q1-L1-E6
Seq. ID
                   BLASTN
Method
                   g2980787
NCBI GI
                   33
BLAST score
                   5.0e-09
E value
                   53
Match length
                   91
% identity
                   Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
NCBI Description
                   (ESSAII project)
```

28160

205696

Seq. No.

 $\{y_i\}_{i=1}^n$ 



```
LIB3083-097-Q1-L1-E7
Seq. ID
                  BLASTX
Method
                  g4097579
NCBI GI
                  476
BLAST score
                  6.0e-48
E value
                  98
Match length
% identity
                  90
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
                  205697
Seq. No.
                  LIB3083-097-Q1-L1-E8
Seq. ID
Method
                  BLASTX
                  q1169782
NCBI GI
                  468
BLAST score
                  5.0e-47
E value
                  122
Match length
                  76
% identity
                  FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis
NCBI Description
                  thaliana]
                  205698
Seq. No.
                  LIB3083-097-Q1-L1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1531758
                   606
BLAST score
                   3.0e-63
E value
                   128
Match length
                   84
% identity
                  (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   205699
Seq. No.
                   LIB3083-097-Q1-L1-F2
Seq. ID
                   BLASTX
Method
                   g1935000
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
                   67
Match length
% identity
                   43
NCBI Description (Y12314) GTPase [Schizosaccharomyces pombe]
                   205700
Seq. No.
                   LIB3083-097-Q1-L1-F3
Seq. ID
                   BLASTX
Method
                   g3540207
NCBI GI
                   213
BLAST score
                   4.0e-17
 E value
                   116
Match length
                   41
 % identity
 NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]
                   205701
 Seq. No.
                   LIB3083-097-Q1-L1-F5
 Seq. ID
                   BLASTX
 Method
                   g505100
 NCBI GI
```

28161

142

7.0e-09

BLAST score

E value



Match length 81 % identity 42

NCBI Description (D31886) KIAA0066 [Homo sapiens]

Seq. No.

205702

Seq. ID

LIB3083-097-Q1-L1-G3

Method NCBI GI BLASTX g1488647

6.0e-16

BLAST score

200

E value Match length

67 64

% identity NCBI Description

(X99937) RNA helicase [Spinacia oleracea]

Seq. No.

205703

Seq. ID

LIB3083-097-Q1-L1-G4

Method NCBI GI BLAST score E value BLASTX g267069 531 2.0e-54

Match length 98 % identity 99

NCBI Description

TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi 166914

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.

205704

Seq. ID

LIB3083-097-Q1-L1-G5

Method BLASTX
NCBI GI g3868853
BLAST score 203
E value 6.0e-16
Match length 68

% identity

60

205705

NCBI Description

(AB013853) GPI-anchored protein [Vigna radiata]

Seq. No.

Seq. ID

LIB3083-097-Q1-L1-G6

Method BLASTX
NCBI GI g1352077
BLAST score 533
E value 1.0e-54
Match length 125

% identity

74

NCBI Description

BETA-GALACTOSIDASE PRECURSOR (LACTASE)

(EXO-(1-->4)-BETA-D-GALACTANASE) >gi\_971485\_emb\_CAA58734\_

(X83854) putative beta-galactosidase/galactanase [Lycopersicon esculentum] >gi\_4138139\_emb\_CAA10174\_ (AJ012797) ss-galactosidase [Lycopersicon esculentum]

Seq. No.

205706

Seq. ID

LIB3083-097-Q1-L1-G7

Method BLASTX
NCBI GI g2662343
BLAST score 512
E value 3.0e-52

% identity

NCBI Description

thaliana]



```
Match length
                  100
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  205707
Seq. No.
Seq. ID
                  LIB3083-097-Q1-L1-H3
                  BLASTX
Method
                  g1703375
NCBI GI
                   496
BLAST score
                   3.0e-50
E value
                   96
Match length
                   100
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
                   205708
Seq. No.
                   LIB3083-097-Q1-L1-H4
Seq. ID
                   BLASTX
Method
                   g2129473
NCBI GI
                   285
BLAST score
                   2.0e-25
E value
Match length
                   105
                   53
% identity
                   arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                   205709
Seq. No.
                   LIB3083-097-Q1-L1-H6
Seq. ID
                   BLASTX
Method
                   g799177
NCBI GI
                   144
BLAST score
                   5.0e-09
E value
Match length
                   122
                   33
% identity
NCBI Description (U22055) 100 kDa coactivator [Homo sapiens]
                   205710
Seq. No.
                   LIB3083-097-Q1-L1-H7
Seq. ID
                   BLASTX
Method
                   g2541876
NCBI GI
                   306
BLAST score
                   5.0e-28
E value
                   109
Match length
                   57
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                   205711
Seq. No.
                   LIB3083-097-Q1-L1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4185511
BLAST score
                   293
                   1.0e-26
E value
Match length
                   68
```

28163

(AF102822) actin depolymerizing factor 4 [Arabidopsis

NCBI GI



```
205712
Seq. No.
Seq. ID
                  LIB3083-099-Q1-L1-A1
Method
                  BLASTX
NCBI GI
                  g2580499
BLAST score
                  296
                  4.0e-27
E value
                  90
Match length
                   64
% identity
                   (U67186) NADPH: ferrihemoprotein oxidoreductase
NCBI Description
                   [Eschscholzia californica]
                  205713
Seq. No.
Seq. ID
                  LIB3083-099-Q1-L1-A10
                  BLASTX
Method
                  g1209655
NCBI GI
                  239
BLAST score
                  2.0e-20
E value
                  80
Match length
                   54
% identity
NCBI Description (U37428) gl1 [Zea mays]
                   205714
Seq. No.
                  LIB3083-099-Q1-L1-A12
Seq. ID
Method
                  BLASTX
                   g2440044
NCBI GI
BLAST score
                   316
                   2.0e-29
E value
                   78
Match length
                   79
% identity
                  (AJ001293) major intrinsic protein PIPB [Craterostigma
NCBI Description
                   plantagineum]
                   205715
Seq. No.
                   LIB3083-099-Q1-L1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1350956
                   440
BLAST score
                   5.0e-44
E value
                   91
Match length
                   95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
Seq. No.
                   205716
                   LIB3083-099-Q1-L1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1843527
                   428
BLAST score
                   1.0e-42
E value
                   87
Match length
                   98
% identity
NCBI Description
                   (U73747) annexin [Gossypium hirsutum]
                   205717
Seq. No.
Seq. ID
                   LIB3083-099-Q1-L1-A4
Method
                   BLASTX
```

28164

q3757514

Match length

84



```
BLAST score
                  1.0e-37
E value
                  87
Match length
% identity
                  84
                  (AC005167) putative plasma membrane intrinsic protein
NCBI Description
                  [Arabidopsis thaliana]
                  205718
Seq. No.
                  LIB3083-099-Q1-L1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3005931
BLAST score
                  283
                  8.0e-26
E value
Match length
                  75
% identity
                  35
NCBI Description (AJ005016) ABC transporter [Homo sapiens]
Seq. No.
                  205719
                  LIB3083-099-Q1-L1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2208988
BLAST score
                  323
E value
                  3.0e-30
Match length
                  72
                  82
% identity
NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays]
Seq. No.
                  205720
                  LIB3083-099-Q1-L1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706956
                  474
BLAST score
E value
                  5.0e-48
                  91
Match length
% identity
                  100
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  205721
Seq. ID
                  LIB3083-099-Q1-L1-B3
                  BLASTN
Method
                  g4567193
NCBI GI
BLAST score
                  61
                  6.0e-26
E value
                  181
Match length
                  83
% identity
                  Arabidopsis thaliana chromosome II BAC T26C19 genomic
NCBI Description
                  sequence, complete sequence
                  205722
Seq. No.
Seq. ID
                  LIB3083-099-Q1-L1-B4
Method
                  BLASTX
NCBI GI
                   g466160
BLAST score
                   373
                   4.0e-36
E value
```

% identity 85
NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III



>gi\_630771\_pir\_\_S44903 ZK652.3 protein - Caenorhabditis
elegans >gi\_289769 (L14429) putative [Caenorhabditis
elegans]

205723 Seq. No. Seq. ID LIB3083-099-Q1-L1-B8 BLASTN Method g2558943 NCBI GI 151 BLAST score 1.0e-79 E value 242 Match length 95 % identity NCBI Description Gossypium hirsutum histone 3 mRNA, complete cds 205724 Seq. No.

Seq. ID LIB3083-099-Q1-L1-B9 Method BLASTN

Method BLASIN NCBI GI g4567193

BLAST score 71 E value 8.0e-32 Match length 223 % identity 83

NCBI Description Arabidopsis thaliana chromosome II BAC T26C19 genomic

sequence, complete sequence

Seq. No. 205725

Seq. ID LIB3083-099-Q1-L1-C10

Method BLASTX
NCBI GI g3080427
BLAST score 424
E value 4.0e-42
Match length 92
% identity 84

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 205726

Seq. ID LIB3083-099-Q1-L1-C11

Method BLASTN
NCBI GI g1143223
BLAST score 134
E value 2.0e-69
Match length 236
% identity 51

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205727

Seq. ID LIB3083-099-Q1-L1-C12

Method BLASTX
NCBI GI g2661840
BLAST score 161
E value 3.0e-11
Match length 53
% identity 53

NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 205728

Seq. ID LIB3083-099-Q1-L1-C2



```
Method
                   q401142
NCBI GI
                   424
BLAST score
                   4.0e-42
E value
                   90
Match length
% identity
                   91
                   SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                   >gi 322721 pir S31479 sucrose synthase (EC 2.4.1.13) -
                   fava bean >gi 22038 emb_CAA49428_ (X69773) sucrose synthase
                   [Vicia faba] >gi_295426 (M97551)
                   UDP-glucose:D-fructose-2-glucosyltransferase [Vicia faba]
Seq. No.
                   205729
                   LIB3083-099-Q1-L1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q120673
BLAST score
                   367
E value
                   2.0e-35
Match length
                   91
                   78
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - garden petunia
                   >qi 20551 emb CAA42904 (X60346) glyceraldehyde
                   3-phosphate dehydrogenase [Petunia x hybrida]
Seq. No.
                   205730
Seq. ID
                   LIB3083-099-Q1-L1-D10
Method
                   BLASTX
                   g4262157
NCBI GI
                   227
BLAST score
                   5.0e-19
E value
                   77
Match length
                   29
% identity
                   (AC005275) putative calmodulin [Arabidopsis thaliana]
NCBI Description
                   205731
Seq. No.
                   LIB3083-099-Q1-L1-D11
Seq. ID
                   BLASTX
Method
                   g3834314
NCBI GI
                    423
BLAST score
                    5.0e-42
E value
                   87
Match length
                    90
% identity
                   (AC005679) Similar to gene pi010 glycosyltransferase
NCBI Description
                    gi_2257490 from S. pombe clone 1750 gb AB004534. ESTs
                    gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis
                    thaliana]
                    205732
Seq. No.
Seq. ID
                   LIB3083-099-Q1-L1-D12
Method
                   BLASTX
NCBI GI
                    q3860277
```

Method BLASTX
NCBI GI g3860277
BLAST score 437
E value 1.0e-43
Match length 92
% identity 93





(AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi 4314394 gb AAD15604\_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana] 205733 Seq. No. LIB3083-099-Q1-L1-D2 Seq. ID BLASTX Method q1706956 NCBI GI BLAST score 481 8.0e-49 E value 91 Match length % identity 100 (U58283) cellulose synthase [Gossypium hirsutum] NCBI Description 205734 Seq. No. LIB3083-099-Q1-L1-D3 Seq. ID Method BLASTX g2129770 NCBI GI 307 BLAST score 2.0e-28 E value Match length 73 71 % identity xyloglucan endotransglycosylase-related protein XTR-2 -NCBI Description Arabidopsis thaliana >gi\_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >qi 2154611 dbj BAA20290 (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana] 205735 Seq. No. LIB3083-099-Q1-L1-D4 Seq. ID BLASTX Method g730456 NCBI GI BLAST score 354 6.0e-34 E value 78 Match length 81 % identity 40S RIBOSOMAL PROTEIN S19 NCBI Description 205736 Seq. No. LIB3083-099-Q1-L1-D5 Seq. ID BLASTX Method g4185499 NCBI GI 248 BLAST score 2.0e-21 E value 71 Match length 61 % identity (AF096095) fertilization-independent seed 2 protein NCBI Description [Arabidopsis thaliana] >gi 4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.

LIB3083-099-Q1-L1-D7 Seq. ID

205737

Method BLASTX NCBI GI g3776011 BLAST score 310 8.0e-29 E value



Match length 92 % identity 62

NCBI Description (AJ010469) RNA helicase [Arabidopsis thaliana]

Seq. No. 205738

Seq. ID LIB3083-099-Q1-L1-D9

Method BLASTX
NCBI GI g267076
BLAST score 485
E value 3.0e-49
Match length 92
% identity 100

NCBI Description TUBULIN BETA-3 CHAIN >gi\_81953\_pir\_\_S20870 tubulin beta-3

chain - garden pea (fragment) >gi 388255\_emb\_CAA38615\_

(X54846) beta-tubulin 3 [Pisum sativum]

Seq. No. 205739

Seq. ID LIB3083-099-Q1-L1-E10

Method BLASTX
NCBI GI g2213590
BLAST score 186
E value 3.0e-14
Match length 67
% identity 49

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 205740

Seq. ID LIB3083-099-Q1-L1-E11

Method BLASTX
NCBI GI g3377820
BLAST score 293
E value 1.0e-26
Match length 70
% identity 80

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 205741

Seq. ID LIB3083-099-Q1-L1-E2

Method BLASTX
NCBI GI g232024
BLAST score 412
E value 7.0e-41
Match length 79
% identity 99

NCBI Description PROTEIN E6 >gi\_421806\_pir\_\_A46130 fiber protein - upland

cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi\_1000084

(U30505) E6 [Gossypium hirsutum]

Seq. No. 205742

Seq. ID LIB3083-099-Q1-L1-E5

Method BLASTX
NCBI GI g2495365
BLAST score 302
E value 7.0e-28



Match length 90 % identity 69

NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi\_445127\_prf\_\_1908431B

heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No. 205743

Seq. ID LIB3083-099-Q1-L1-E7

Method BLASTX
NCBI GI g3451071
BLAST score 399
E value 3.0e-39
Match length 92
% identity 88

NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis

thaliana]

Seq. No. 205744

Seq. ID LIB3083-099-Q1-L1-F10

Method BLASTX
NCBI GI g1778051
BLAST score 198
E value 1.0e-15
Match length 86
% identity 42

NCBI Description (U62583) Prt1 homolog [Homo sapiens]

>gi\_4503527\_ref\_NP\_003742.1\_pEIF3S9\_ UNKNOWN

Seq. No. 205745

Seq. ID LIB3083-099-Q1-L1-F12

Method BLASTX
NCBI GI g2335100
BLAST score 415
E value 4.0e-41
Match length 92
% identity 84

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 205746

Seq. ID LIB3083-099-Q1-L1-F2

Method BLASTX
NCBI GI g2827555
BLAST score 348
E value 3.0e-33
Match length 89
% identity 74

NCBI Description (AL021635) Translation factor EF-1 alpha - like protein

[Arabidopsis thaliana]

Seq. No. 205747

Seq. ID LIB3083-099-Q1-L1-F5

Method BLASTX
NCBI GI g1171978
BLAST score 389
E value 5.0e-38
Match length 93
% identity 23

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)



(PABP 2) >qi 304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi 2911051 emb\_CAA17561\_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

```
205748
Seq. No.
Seq. ID
                  LIB3083-099-Q1-L1-F6
                  BLASTX
Method
                  g2501850
NCBI GI
                  459
BLAST score
                  3.0e-46
E value
                  94
Match length
                  89
% identity
                  (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
NCBI Description
                  205749
Seq. No.
                  LIB3083-099-Q1-L1-F8
Seq. ID
                  BLASTX
Method
                  g3668097
NCBI GI
                  372
BLAST score
                   6.0e-36
E value
                   95
Match length
% identity
                  81
                   (AC004667) putative glycine cleavage system protein H
NCBI Description
                  precursor [Arabidopsis thaliana]
                   205750
Seq. No.
                  LIB3083-099-Q1-L1-G10
Seq. ID
Method
                  BLASTX
                  g1420936
NCBI GI
                   415
BLAST score
                   4.0e-41
E value
                   89
Match length
% identity
                   87
                   (U61396) Vigna unguiculata aspartic proteinase mRNA,
NCBI Description
                   complete cds. [Vigna unguiculata]
                   205751
Seq. No.
Seq. ID
                   LIB3083-099-Q1-L1-G11
                   BLASTX
Method
                   g586076
NCBI GI
                   434
BLAST score
                   3.0e-43
E value
                   81
Match length
                   98
% identity
                   TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                   tubulin 1 [Lupinus albus]
                   205752
Seq. No.
Seq. ID
                   LIB3083-099-Q1-L1-G2
                   BLASTN
Method
NCBI GI
                   g4104241
                   116
BLAST score
```

% identity NCBI Description Gossypium hirsutum palmitoyl-acyl carrier protein

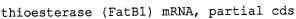
1.0e-58

120

99

E value Match length





```
Seq. No.
                  205753
                  LIB3083-099-Q1-L1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3068809
BLAST score
                  309
                   1.0e-28
E value
Match length
                   65
                   92
% identity
                   (AF059295) Skp1 homolog [Arabidopsis thaliana]
NCBI Description
                   205754
Seq. No.
Seq. ID
                  LIB3083-099-Q1-L1-G6
                  BLASTX
Method
                   q3023713
NCBI GI
                   144
BLAST score
                   3.0e-09
E value
                   37
Match length
                   86
% identity
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
                   (U09450) enolase [Oryza sativa]
                   205755
Seq. No.
                   LIB3083-099-Q1-L1-G7
Seq. ID
                   BLASTX
Method
                   g4103342
NCBI GI
                   408
BLAST score
                   3.0e-40
E value
Match length
                   92
                   87
% identity
                   (AF022377) agamous-like putative transcription factor
NCBI Description
                   [Cucumis sativus]
Seq. No.
                   205756
                   LIB3083-099-Q1-L1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3860247
BLAST score
                   443
E value
                   2.0e-44
Match length
                   92
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205757
Seq. ID
                   LIB3083-099-Q1-L1-H1
                   BLASTX
Method
NCBI GI
                   g464846
BLAST score
                   324
                   2.0e-30
E value
Match length
                   63
                   92
% identity
                   TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin
NCBI Description
                   alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178)
```

alpha-tubulin #6 [Zea mays]



```
205758
Seq. No.
                  LIB3083-099-Q1-L1-H10
Seq. ID
Method
                  BLASTX
                  q3738257
NCBI GI
BLAST score
                   419
                  1.0e-41
E value
                   92
Match length
% identity
                   (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
                   205759
Seq. No.
Seq. ID
                  LIB3083-099-Q1-L1-H5
                   BLASTX
Method
                   g2689720
NCBI GI
BLAST score
                   384
                   2.0e-37
E value
                   92
Match length
                   77
% identity
                  (AF037168) DnaJ homologue [Arabidopsis thaliana]
NCBI Description
                   205760
Seq. No.
                   LIB3083-099-Q1-L1-H6
Seq. ID
                   BLASTX
Method
                   g1946369
NCBI GI
                   207
BLAST score
                   1.0e-16
E value
                   93
Match length
                   30
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                   205761
Seq. ID
                   LIB3083-100-Q1-L1-A10
Method
                   BLASTX
                   q4098321
NCBI GI
BLAST score
                   686
                   1.0e-72
E value
                   132
Match length
                   100
% identity
                   (U76745) beta-tubulin 2 [Triticum aestivum]
NCBI Description
                   205762
Seq. No.
Seq. ID
                   LIB3083-100-Q1-L1-A11
Method
                   BLASTX
                   q3513727
NCBI GI
                   477
BLAST score
E value
                   4.0e-48
Match length
                   119
% identity
                   (AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                   TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                   kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                   thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
```

protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

205763 LIB3083-100-Q1-L1-A2



```
BLASTX
Method
                  q2275215
NCBI GI
BLAST score
                  403
                  2.0e-39
E value
                  122
Match length
                   63
% identity
                  (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  205764
Seq. No.
                  LIB3083-100-Q1-L1-A3
Seq. ID
                  BLASTX
Method
                  g2342719
NCBI GI
                   252
BLAST score
                  1.0e-21
E value
                   91
Match length
                   55
% identity
NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]
                   205765
Seq. No.
                   LIB3083-100-Q1-L1-A4
Seq. ID
                   BLASTX
Method
                   g2739376
NCBI GI
                   395
BLAST score
                   2.0e-38
E value
                   108
Match length
                   69
% identity
                  (AC002505) putative permease [Arabidopsis thaliana]
NCBI Description
                   205766
Seq. No.
                   LIB3083-100-Q1-L1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q112717
                   147
BLAST score
                   2.0e-09
E value
                   46
Match length
                   59
% identity
                   21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911
NCBI Description
                   hypothetical protein precursor - carrot
                   >qi 18312 emb CAA36642 (X52395) precursor polypeptide (AA
                   -22 to 171) [Daucus carota]
                   205767
Seq. No.
Seq. ID
                   LIB3083-100-Q1-L1-A6
                   BLASTX
Method
                   q2342719
NCBI GI
BLAST score
                   296
E value
                   8.0e-27
                   101
Match length
 % identity
                   57
                   (AC002341) SF16 protein isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   205768
                   LIB3083-100-Q1-L1-A7
```

Seq. ID

BLASTX Method NCBI GI g3513727 BLAST score 498 E value 1.0e-50



Match length 118 % identity 36

NCBI Description (AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi\_4539358\_emb\_CAB40052.1\_ (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 205769

Seq. ID LIB3083-100-Q1-L1-A8

Method BLASTX
NCBI GI g1174600
BLAST score 621
E value 5.0e-65
Match length 119
% identity 97

NCBI Description TUBULIN BETA CHAIN >gi 493710 dbj BAA06382 (D30717)

beta-tubulin [Oryza sativa]

Seq. No. 205770

Seq. ID LIB3083-100-Q1-L1-A9

Method BLASTN
NCBI GI g1743353
BLAST score 42
E value 4.0e-15
Match length 78

% identity 88

NCBI Description N.tabacum mRNA for aldehyde dehydrogenase

Seq. No. 205771

Seq. ID LIB3083-100-Q1-L1-B11

Method BLASTN
NCBI GI g256119
BLAST score 33
E value 4.0e-09
Match length 65
% identity 88

NCBI Description triose phosphate isomerase [Lactuca sativa=lettuce, mRNA

Partial, 785 nt]

Seq. No. 205772

Seq. ID LIB3083-100-Q1-L1-B3

Method BLASTX
NCBI GI g2811278
BLAST score 525
E value 1.0e-53
Match length 108
% identity 91

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 205773

Seq. ID LIB3083-100-Q1-L1-B4

Method BLASTX
NCBI GI 94234768
BLAST score 669
E value 1.0e-70
Match length 122

28175

n.



% identity (AF069468) sterol-C5-desaturase [Arabidopsis thaliana] NCBI Description Seq. No. 205774 LIB3083-100-Q1-L1-B6 Seq. ID Method BLASTX NCBI GI q4455192 BLAST score 344 E value 2.0e-32 121 Match length 31 % identity (AL035440) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 205775 LIB3083-100-Q1-L1-B7 Seq. ID BLASTX Method q1709535 NCBI GI BLAST score 544 6.0e-56 E value Match length 130 % identity DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) NCBI Description [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi 887388 emb CAA60447 (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi 1669658 emb CAA70527 (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana] Seq. No. 205776 LIB3083-100-Q1-L1-C10 Seq. ID BLASTX Method NCBI GI q82512 BLAST score 568 9.0e-59 E value Match length 114 43 % identity ubiquitin precursor - rice (fragment) NCBI Description >gi\_218189\_dbj\_BAA02241\_ (D12776) poly-ubiquitin [Oryza sativa] Seq. No. 205777 Seq. ID LIB3083-100-Q1-L1-C11 BLASTX Method NCBI GI g217909 BLAST score 140 1.0e-08 E value Match length 62 % identity 50 NCBI Description (D14044) glycolate oxidase [Cucurbita sp.] 205778

Seq. No.

LIB3083-100-Q1-L1-C2 Seq. ID

BLASTX Method g3337361 NCBI GI 502 BLAST score



E value 5.0e-51
Match length 120
% identity 72

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 205779

Seq. ID LIB3083-100-Q1-L1-C3

Method BLASTX
NCBI GI g1170507
BLAST score 493
E value 5.0e-50
Match length 121
% identity 82

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)

>gi\_100276\_pir\_\_S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi\_19699\_emb\_CAA43514\_ (X61206)
nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 205780

Seq. ID LIB3083-100-Q1-L1-C4

Method BLASTX
NCBI GI g586076
BLAST score 498
E value 2.0e-50
Match length 97
% identity 97

NCBI Description TUBULIN BETA-1 CHAIN >gi\_486734\_pir\_\_S35142 tubulin beta

chain - white lupine >gi\_402636\_emb\_CAA49736\_ (X70184) Beta

tubulin 1 [Lupinus albus]

Seq. No. 205781

Seq. ID LIB3083-100-Q1-L1-C6

Method BLASTX
NCBI GI g123650
BLAST score 572
E value 3.0e-59
Match length 114
% identity 98

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN >gi\_82245\_pir\_\_S03250 heat

shock protein 70 (clone pMON9743) - garden petunia >gi 20557 emb CAA30018 (X06932) heat shock protein 70

[Petunia x hybrida]

Seq. No. 205782

Seq. ID LIB3083-100-Q1-L1-C7

Method BLASTX
NCBI GI g2760317
BLAST score 439
E value 1.0e-43
Match length 131
% identity 66

NCBI Description (AC002130) F1N21.1 [Arabidopsis thaliana]

Seq. No. 205783

Seq. ID LIB3083-100-Q1-L1-C8

Method BLASTX



```
q2911042
NCBI GI
                  536
BLAST score
                  5.0e-55
E value
                  123
Match length
                  86
% identity
                  (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  205784
Seq. No.
                  LIB3083-100-Q1-L1-C9
Seq. ID
                  BLASTX
Method
                  g2244734
NCBI GI
                  417
BLAST score
                  5.0e-41
E value
                  82
Match length
                   99
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
                   205785
Seq. No.
                  LIB3083-100-Q1-L1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3121849
BLAST score
                   658
                   3.0e-69
E value
                   132
Match length
                   50
% identity
                  CALMODULIN >gi 1773321 (U79736) calmodulin [Helianthus
NCBI Description
                   annuus]
                   205786
Seq. No.
Seq. ID
                   LIB3083-100-Q1-L1-D4
                   BLASTX
Method
                   g3426039
NCBI GI
                   212
BLAST score
                   5.0e-17
E value
                   112
Match length
                   71
% identity
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
                   205787
Seq. No.
                   LIB3083-100-Q1-L1-D5
Seq. ID
                   BLASTN
Method
                   g1143223
NCBI GI
BLAST score
                   115
                   6.0e-58
E value
                   328
Match length
                   51
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
                   205788
Seq. No.
Seq. ID
                   LIB3083-100-Q1-L1-D6
Method
                   BLASTX
                   q2815246
NCBI GI
                   218
BLAST score
E value
                   8.0e-18
Match length
                   55
```

28178

71

% identity

Seq. ID

Method

NCBI GI



(X95709) class I type 2 metallothionein [Cicer arietinum] NCBI Description 205789 Seq. No. LIB3083-100-Q1-L1-D7 Seq. ID Method BLASTX g2129758 NCBI GI 390 BLAST score 7.0e-38 E value 78 Match length 87 % identity ubiquitin conjugating enzyme E2 protein - Arabidopsis NCBI Description thaliana >gi\_992704 (U33757) UBC7 [Arabidopsis thaliana] 205790 Seq. No. Seq. ID LIB3083-100-Q1-L1-D8 Method BLASTX g2160169 NCBI GI 261 BLAST score 9.0e-23 E value 91 Match length 59 % identity (AC000132) No definition line found [Arabidopsis thaliana] NCBI Description 205791 Seq. No. LIB3083-100-Q1-L1-D9 Seq. ID BLASTX Method q3128192 NCBI GI 524 BLAST score 1.0e-53 E value 117 Match length 89 % identity (AC004521) axi 1-like protein [Arabidopsis thaliana] NCBI Description 205792 Seq. No. LIB3083-100-Q1-L1-E11 Seq. ID BLASTX Method g3983665 NCBI GI 497 BLAST score 2.0e-50 E value 121 Match length 80 % identity (AB011271) importin-beta2 [Oryza sativa] NCBI Description Seq. No. 205793 Seq. ID LIB3083-100-Q1-L1-E12 BLASTX Method NCBI GI g1354272 222 BLAST score 3.0e-18 E value 46 Match length 87 % identity NCBI Description (U51036) aspartic proteinase [Arabidopsis thaliana] 205794 Seq. No.

28179

LIB3083-100-Q1-L1-E2

BLASTX

g1619297



BLAST score 592
E value 1.0e-61
Match length 110
% identity 99
NCBI Description (Y08490) alpha-tubulin 2 [Hordeum vulgare]
Seq. No. 205795

Seq. ID LIB3083-100-Q1-L1-E3
Method BLASTX
NCBI GI g4510428
BLAST score 357
E value 5.0e-34

E value 5.0e
Match length 126
% identity 56

NCBI Description (AC006929) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 205796

Seq. ID LIB3083-100-Q1-L1-E4

Method BLASTX
NCBI GI g2244975
BLAST score 480
E value 2.0e-48
Match length 128
% identity 70

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 205797

Seq. ID LIB3083-100-Q1-L1-E5

Method BLASTX
NCBI GI g4098272
BLAST score 234
E value 9.0e-20
Match length 44
% identity 98

NCBI Description (U76558) alpha-tubulin [Triticum aestivum]

Seq. No. 205798

Seq. ID LIB3083-100-Q1-L1-E6

Method BLASTX
NCBI GI g267131
BLAST score 246
E value 4.0e-21
Match length 102
% identity 23

NCBI Description NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)

>gi\_423120\_pir\_\_A46174 RNA-binding protein TIAR - human
>gi\_189310 (M96954) nucleolysin TIAR [Homo sapiens]
>gi\_4507499 ref NP 003243.1\_pTIAL1\_ TIA1 cytotoxic

granule-associated RNA-binding protein-like

Seq. No. 205799

Seq. ID LIB3083-100-Q1-L1-E8

Method BLASTX
NCBI GI g3880320
BLAST score 203
E value 6.0e-16



Match length 38
% identity 100
NCBI Description (Z81134) predicted using Genefinder; similar to tubulin alpha subunit [Caenorhabditis elegans]

 Seq. No.
 205800

 Seq. ID
 LIB3083-100-Q1-L1-E9

 Method
 BLASTX

 NCBI GI
 g606942

 BLAST score
 569

 E value
 7.0e-59

E value 7.0e-59
Match length 123
% identity 92

NCBI Description (U13760) unknown [Gossypium hirsutum]

Seq. No. 205801

Seq. ID LIB3083-100-Q1-L1-F1

Method BLASTX
NCBI GI g267069
BLAST score 509
E value 6.0e-52
Match length 94
% identity 99

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 205802

Seq. ID LIB3083-100-Q1-L1-F10

Method BLASTX
NCBI GI g1706956
BLAST score 494
E value 3.0e-50
Match length 110
% identity 88

NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 205803

Seq. ID LIB3083-100-Q1-L1-F12

Method BLASTX
NCBI GI g3236248
BLAST score 517
E value 1.0e-52
Match length 127
% identity 78

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 205804

Seq. ID LIB3083-100-Q1-L1-F4

Method BLASTX
NCBI GI g4510421
BLAST score 166
E value 1.0e-11
Match length 105
% identity 34

NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                  205805
Seq. ID
                  LIB3083-100-Q1-L1-F5
Method
                  BLASTX
NCBI GI
                  g3327868
BLAST score
                  159
                  8.0e-11
E value
Match length
                  112
% identity
                  (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
NCBI Description
                  thaliana]
                  205806
Seq. No.
Seq. ID
                  LIB3083-100-Q1-L1-F6
Method
                  BLASTX
NCBI GI
                  g2760349
BLAST score
                  606
                  3.0e-63
E value
Match length
                  123
                  20
% identity
                 (U84969) ubiquitin [Arabidopsis thaliana]
NCBI Description
                  205807
Seq. No.
Seq. ID
                  LIB3083-100-Q1-L1-F9
Method
                  BLASTX
NCBI GI
                  g4098331
BLAST score
                  586
                  7.0e-61
E value
                  129
Match length
                  83
% identity
NCBI Description (U76896) beta-tubulin 5 [Triticum aestivum]
                  205808
Seq. No.
                  LIB3083-100-Q1-L1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1717967
BLAST score
                  223
                  3.0e-18
E value
Match length
                  98
                   48
% identity
NCBI Description
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID
                   3-O-GLUCOSYLTRANSFERASE) >gi 1345584 emb CAA53582 (X75968)
                   3-O-glucsyltransferase [Vitis vinifera]
                  205809
Seq. No.
                  LIB3083-100-Q1-L1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702332
BLAST score
                   177
E value
                   6.0e-13
```

Match length 69 % identity 48

(AC005397) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 205810

LIB3083-100-Q1-L1-G11 Seq. ID

Method BLASTN



```
NCBI GI
                  q2154714
BLAST score
                  46
E value
                  9.0e-17
                  90
Match length
                  88
% identity
NCBI Description A.thaliana mRNA for CDPK-related protein kinase
Seq. No.
                  205811
Seq. ID
                  LIB3083-100-Q1-L1-G12
Method
                  BLASTX
NCBI GI
                  q2098709
BLAST score
                  634
E value
                  2.0e-66
Match length
                  134
% identity
                  86
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
                  205812
Seq. No.
Seq. ID
                  LIB3083-100-Q1-L1-G2
Method
                  BLASTX
NCBI GI
                  g3540195
BLAST score
                  462
                  2.0e-46
E value
Match length
                  107
% identity
                  41
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  205813
                  LIB3083-100-Q1-L1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128175
BLAST score
                  144
                  4.0e-09
E value
Match length
                  90
% identity
                  37
NCBI Description
                  (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  205814
Seq. ID
                  LIB3083-100-Q1-L1-G4
Method
                  BLASTX
NCBI GI
                  g1532165
BLAST score
                  154
E value
                  3.0e-10
Match length
                  41
% identity
                  73
NCBI Description
                  (U63815) similar to dehydrogenase encoded by GenBank
                  Accession Number S39508; localized according to blastn
                  similarity to EST sequences; therefore, the coding span
                  corresponds only to an area of similarity since the
                  initation codon and stop
Seq. No.
                  205815
Seq. ID
                  LIB3083-100-Q1-L1-G5
```

Method BLASTX NCBI GI g2541876 BLAST score 291 E value 3.0e-26



Match length 127 % identity 53

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 205816

Seq. ID LIB3083-100-Q1-L1-G7

Method BLASTX
NCBI GI g1706958
BLAST score 696
E value 9.0e-74
Match length 129
% identity 99

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 205817

Seq. ID LIB3083-100-Q1-L1-G9

Method BLASTN
NCBI GI g1143223
BLAST score 238
E value 1.0e-131
Match length 399
% identity 30

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205818

Seq. ID LIB3083-100-Q1-L1-H12

Method BLASTX
NCBI GI g1170938
BLAST score 471
E value 2.0e-47
Match length 93
% identity 92

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>qi 481566 pir S38875 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi\_429106\_emb\_CAA80866\_ (Z24742) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 205819

Seq. ID LIB3083-100-Q1-L1-H2

Method BLASTX
NCBI GI g1777921
BLAST score 576
E value 1.0e-59
Match length 113
% identity 96

NCBI Description (U54774) glutamate decarboxylase [Nicotiana tabacum]

Seq. No. 205820

Seq. ID LIB3083-100-Q1-L1-H3

Method BLASTX
NCBI GI g2245136
BLAST score 387
E value 1.0e-37
Match length 107



% identity 71

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 205821

Seq. ID LIB3083-100-Q1-L1-H4

Method BLASTX
NCBI GI g4455275
BLAST score 202
E value 8.0e-16
Match length 125
% identity 39

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 205822

Seq. ID LIB3083-100-Q1-L1-H5

Method BLASTN
NCBI GI g1480456
BLAST score 39
E value 1.0e-12
Match length 55

% identity 93
NCBI Description Hevea brasiliensis latex allergen Hev b 5 mRNA, complete

cds

Seq. No. 205823

Seq. ID LIB3083-100-Q1-L1-H7

Method BLASTX
NCBI GI g3935138
BLAST score 140
E value 1.0e-08
Match length 97
% identity 37

NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No. 205824

Seq. ID LIB3083-101-Q1-L1-A1

Method BLASTX
NCBI GI g4105772
BLAST score 425
E value 5.0e-42
Match length 101
% identity 40

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 205825

Seq. ID LIB3083-101-Q1-L1-A12

Method BLASTX
NCBI GI g3377797
BLAST score 286
E value 5.0e-26
Match length 66
% identity 85

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA



## R90691 [Ara

205826 Seq. No. Seq. ID LIB3083-101-Q1-L1-A3 Method BLASTX NCBI GI g4115377 257 BLAST score E value 1.0e-22 Match length 81 % identity 65 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 205827 Seq. ID

LIB3083-101-Q1-L1-A6 Method BLASTX NCBI GI q2146731 BLAST score 225

E value 4.0e-19 Match length 69 % identity 62

FK506-binding protein - Arabidopsis thaliana >qi 1354207 NCBI Description

?^,

(U49453) rof1 [Arabidopsis thaliana]

Seq. No. 205828

Seq. ID LIB3083-101-Q1-L1-A7

Method BLASTX NCBI GI q3582436 BLAST score 328 1.0e-30 E value Match length 107 % identity 59

NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 205829

Seq. ID LIB3083-101-Q1-L1-A8

Method BLASTX NCBI GI g4104242 BLAST score 379 9.0e-37 E value Match length 98 % identity 80

NCBI Description (AF034266) palmitoyl-acyl carrier protein thioesterase

[Gossypium hirsutum]

Seq. No. 205830

Seq. ID LIB3083-101-Q1-L1-A9

Method BLASTX NCBI GI g3297823 BLAST score 262 7.0e-23 E value Match length 76 72 % identity

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 205831

LIB3083-101-Q1-L1-B10 Seq. ID

Method BLASTN



```
q1706957
NCBI GI
                  112
BLAST score
                  2.0e-56
E value
                  160
Match length
                  93
% identity
                  Gossypium hirsutum cellulose synthase (celA2) mRNA, partial
NCBI Description
                  205832
Seq. No.
                  LIB3083-101-Q1-L1-B11
Seq. ID
                  BLASTX
Method
                  q2306917
NCBI GI
BLAST score
                  356
                  5.0e-34
E value
Match length
                  90
                  78
% identity
                   (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   205833
                  LIB3083-101-Q1-L1-B12
Seq. ID
Method
                   BLASTX
                   q3850148
NCBI GI
BLAST score
                   161
                   3.0e-11
E value
                   94
Match length
                   14
% identity
                   (AL033396) regulator of chromosome condensation [Candida
NCBI Description
                   albicans]
                   205834
Seq. No.
Seq. ID
                   LIB3083-101-Q1-L1-B4
                   BLASTX
Method
                   q1928981
NCBI GI
                   422
BLAST score
                   1.0e-41
E value
                   114
Match length
                   75
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   205835
Seq. No.
Seq. ID
                   LIB3083-101-Q1-L1-B6
                   BLASTX
Method
                   q1946355
NCBI GI
BLAST score
                   408
E value
                   5.0e-40
```

Match length 126 59 % identity

(U93215) maize transposon MuDR mudrA protein isolog NCBI Description [Arabidopsis thaliana] >gi 2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 205836

LIB3083-101-Q1-L1-B7 Seq. ID

Method BLASTX NCBI GI q4097094



```
BLAST score
                  2.0e-33
E value
Match length
                  107
% identity
                  64
                  (U45447) vacuolar proton-ATPase subunit D [Oryctolagus
NCBI Description
                  cuniculus]
                  205837
Seq. No.
Seq. ID
                  LIB3083-101-Q1-L1-B8
Method
                  BLASTX
NCBI GI
                  g2493146
BLAST score
                  325
                  3.0e-30
E value
                  94
Match length
                  71
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148
NCBI Description
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                  [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275)
                  vacuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.
                  205838
                  LIB3083-101-Q1-L1-B9
Seq. ID
Method
                  BLASTX
                  g100490
NCBI GI
                  419
BLAST score
                  3.0e-41
E value
                  84
Match length
                  26
% identity
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                  >gi 16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                  majus]
                  205839
Seq. No.
                  LIB3083-101-Q1-L1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4100433
                  283
BLAST score
                   3.0e-25
E value
                  72
Match length
                  75
% identity
NCBI Description
                  (AF000378) beta-glucosidase [Glycine max]
                  205840
Seq. No.
Seq. ID
                  LIB3083-101-Q1-L1-C11
Method
                   BLASTX
                   a2655037
NCBI GI
BLAST score
                   234
                   1.0e-19
E value
                   128
Match length
                   40
% identity
                   (AF019952) tumor suppressing STF cDNA 1 [Homo sapiens]
NCBI Description
```

>qi 4507703 ref NP 003301.1 pTSSC1 tumor suppressing

subtransferable candidate

Seq. No. 205841

LIB3083-101-Q1-L1-C12 Seq. ID

Method BLASTN



NCBI GI g2829205 BLAST score 378 E value 0.0e+00 Match length 390 % identity 18

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 205842

Seq. ID LIB3083-101-Q1-L1-C4

Method BLASTX
NCBI GI g136636
BLAST score 276
E value 1.0e-24
Match length 50
% identity 100

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ #biquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 205843

Seq. ID LIB3083-101-Q1-L1-C6

Method BLASTX
NCBI GI g3582436
BLAST score 520
E value 4.0e-53
Match length 124
% identity 80

NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 205844

Seq. ID LIB3083-101-Q1-L1-C7

Method BLASTX
NCBI GI g2154715
BLAST score 327
E value 6.0e-31
Match length 73
% identity 84

NCBI Description (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No. 205845

Seq. ID LIB3083-101-Q1-L1-C9

Method BLASTX
NCBI GI g3695388
BLAST score 271
E value 6.0e-24
Match length 91
% identity 54

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

Seq. No. 205846

NCBI GI

E value

BLAST score

q1172835

448 8.0e-45



```
LIB3083-101-Q1-L1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980806
BLAST score
                  418
E value
                  4.0e-41
Match length
                  129
                  63
% identity
NCBI Description
                  (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  205847
Seq. ID
                  LIB3083-101-Q1-L1-D2
Method
                  BLASTX
NCBI GI
                  q807698
BLAST score
                  299
                  2.0e-27
E value
Match length
                  96
% identity
                  61
                  (D32206) prepro-cucumisin [Cucumis melo]
NCBI Description
Seq. No.
                  205848
Seq. ID
                  LIB3083-101-Q1-L1-D4
Method
                  BLASTX
NCBI GI
                  q2306917
BLAST score
                  449
E value
                  7.0e-45
Match length
                  96
% identity
                  91
NCBI Description
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
                  thaliana]
Seq. No.
                  205849
Seq. ID
                  LIB3083-101-Q1-L1-D6
Method
                  BLASTX
NCBI GI
                  q2245109
BLAST score
                  344
E value
                  2.0e-32
Match length
                  94
% identity
                  71
NCBI Description
                  (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis
                  thaliana]
Seq. No.
                  205850
                  LIB3083-101-Q1-L1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2252630
BLAST score
                  177
E value
                  5.0e-13
Match length
                  50
% identity
                  (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205851
                  LIB3083-101-Q1-L1-E1
Seq. ID
Method
                  BLASTX
```



Match length 87 % identity 97

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-A1 >gi\_496268 (L16767)

GTP-binding protein [Nicotiana tabacum]

Seq. No. 205852

Seq. ID LIB3083-101-Q1-L1-E12

Method BLASTX
NCBI GI g4490336
BLAST score 206
E value 3.0e-16
Match length 94
% identity 48

% identity 48
NCBI Description (AL035656) auxin-induced protein-like [Arabidopsis

thaliana]

Seq. No. 205853

Seq. ID LIB3083-101-Q1-L1-E2

Method BLASTX
NCBI GI g4454307
BLAST score 418
E value 2.0e-41
Match length 88
% identity 85

NCBI Description (AJ132763) cyclophilin [Pseudotsuga menziesii]

Seq. No. 205854

Seq. ID LIB3083-101-Q1-L1-E3

Method BLASTX
NCBI GI g464707
BLAST score 469
E value 4.0e-47
Match length 97
% identity 94

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910 emb\_CAB39647.1 (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 205855

Seq. ID LIB3083-101-Q1-L1-E4

Method BLASTX
NCBI GI g4185511
BLAST score 455
E value 2.0e-45
Match length 99



% identity 84
NCBI Description (AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No. 205856

Seq. ID LIB3083-101-Q1-L1-E6

Method BLASTX
NCBI GI 93327868
BLAST score 142
E value 6.0e-09
Match length 87
% identity 41

NCBI Description (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis

thaliana]

Seq. No. 205857

Seq. ID LIB3083-101-Q1-L1-E7

Method BLASTX
NCBI GI 94510383
BLAST score 172
E value 2.0e-12
Match length 60
% identity 60

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 205858

Seq. ID LIB3083-101-Q1-L1-F2

Method BLASTX
NCBI GI g3642014
BLAST score 174
E value 2.0e-12
Match length 49
% identity 61

NCBI Description (AL031620) similar to Zinc finger, C3HC4 type (RING finger)

[Caenorhabditis elegans]

Seq. No. 205859

Seq. ID LIB3083-101-Q1-L1-F6

Method BLASTN
NCBI GI g3869087
BLAST score 50
E value 3.0e-19
Match length 212
% identity 87

NCBI Description Nicotiana paniculata mRNA for elongation factor-1 alpha,

complete cds

Seq. No. 205860

Seq. ID LIB3083-101-Q1-L1-G10

Method BLASTX
NCBI GI g3402701
BLAST score 197
E value 3.0e-15
Match length 56
% identity 71

NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]



Seq. No. 205861

Seq. ID LIB3083-101-Q1-L1-G2

Method BLASTX
NCBI GI g4056462
BLAST score 421
E value 2.0e-41
Match length 126
% identity 63

NCBI Description (AC005990) Strong similarity to gb\_Y09876 aldehyde

dehydrogenase (NAD+) from Nicotiana tabacum and a member of

the aldehyde dehydrogenase family PF\_00171. ESTs gb\_F15117, gb\_R83958 and gb\_586262 come from this gene.

[Arabidopsis thaliana]

Seq. No. 205862

Seq. ID LIB3083-101-Q1-L1-G4

Method BLASTX
NCBI GI g547683
BLAST score 330
E value 2.0e-31
Match length 70
% identity 90

NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi\_170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum]
>gi\_445601\_prf\_\_1909348A heat shock protein hsp80

[Lycopersicon esculentum]

Seq. No. 205863

Seq. ID LIB3083-101-Q1-L1-G5

Method BLASTX
NCBI GI g1082054
BLAST score 201
E value 8.0e-16
Match length 80
% identity 49

NCBI Description (Z49859) copper transporter protein [Arabidopsis thaliana]

Seq. No. 205864

Seq. ID LIB3083-101-Q1-L1-G6

Method BLASTX
NCBI GI g1174592
BLAST score 518
E value 5.0e-53
Match length 104
% identity 98

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin

- garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 205865

Seq. ID LIB3083-101-Q1-L1-G7

Method BLASTX
NCBI GI g2288986
BLAST score 516
E value 1.0e-52
Match length 126
% identity 74

```
NCBI Description
                  (AC002335) glyoxalase II isolog [Arabidopsis thaliana]
Seq. No.
                  205866
                  LIB3083-101-Q1-L1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q644492
                  33
BLAST score
                  6.0e-09
E value
Match length
                  49
                  92
% identity
NCBI Description
                  Corn elongation factor lalpha gene, complete cds
Seq. No.
                  205867
Seq. ID
                  LIB3083-101-Q1-L1-H1
Method
                  BLASTX
NCBI GI
                  g3201613
BLAST score
                  297
                  5.0e-27
E value
Match length
                  120
                  59
% identity
NCBI Description
                  (AC004669) glutathione S-transferase [Arabidopsis thaliana]
                  205868
Seq. No.
Seq. ID
                  LIB3083-101-Q1-L1-H10
                  BLASTX
Method
NCBI GI
                  g2244835
BLAST score
                  144
                  5.0e-09
E value
                  73
Match length
                  48
% identity
                  (Z97337) protein kinase homolog [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB3083-101-Q1-L1-H11
Method BLASTX
NCBI GI g4539292
BLAST score 431
E value 8.0e-43
Match length 106

Seq. No.

% identity 76
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

205869

Seq. No. 205870

Seq. ID LIB3083-101-Q1-L1-H12

Method BLASTX
NCBI GI g1483218
BLAST score 237
E value 6.0e-20
Match length 119
% identity 45

NCBI Description (X99793) induced upon wounding stress [Arabidopsis

thaliana]

Seq. No. 205871

Seq. ID LIB3083-101-Q1-L1-H2

Method BLASTX



```
NCBI GI
                   g1079251
BLAST score
                   95
E value
                   4.0e-12
Match length
                   63
% identity
                   66
NCBI Description
                  alpha-tubulin brain-specific isotype (clone pTUB5) - chum
                  salmon
Seq. No.
                  205872
Seq. ID
                  LIB3083-101-Q1-L1-H3
Method
                  BLASTX
NCBI GI
                  g4567283
BLAST score
                  277
E value
                  1.0e-24
Match length
                  89
% identity
                  65
NCBI Description
                  (AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.
                  205873
Seq. ID
                  LIB3083-101-Q1-L1-H5
Method
                  BLASTX
NCBI GI
                  g3757522
BLAST score
                  341
E value
                  4.0e-32
Match length
                  124
% identity
                  65
NCBI Description
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.
                  205874
Seq. ID
                  LIB3083-101-Q1-L1-H9
Method
                  BLASTN
NCBI GI
                  q451543
BLAST score
                  173
                  1.0e-92
E value
Match length
                  232
% identity
                  94
                  Gossypium barbadense Sea Island proline-rich cell wall
NCBI Description
                  protein gene complete cds. >gi_1598725_gb_I18370_I18370
                  Sequence 25 from patent US
Seq. No.
                  205875
Seq. ID
                  LIB3083-102-Q1-L1-A3
Method
                  BLASTX
NCBI GI
                  q1707959
BLAST score
                  473
E value
                  6.0e-55
Match length
                  112
% identity
                  96
                  GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 2
NCBI Description
                   (GLUTAMATE--AMMONIA LIGASE) >gi 1134898 emb CAA63982
                   (X94321) glutamine synthetase [Vitis vinifera]
```

Seq. No. 205876

 Seq. ID
 LIB3083-102-Q1-L1-A5

 Method
 BLASTN

 NCBI GI
 g2244733

 BLAST score
 210



E value 1.0e-114 Match length 307 % identity 97

NCBI Description Cotton mRNA for actin, clone CF456, partial cds

Seq. No. 205877

Seq. ID LIB3083-102-Q1-L1-A6

Method BLASTX
NCBI GI g1076696
BLAST score 307
E value 4.0e-28
Match length 68
% identity 78

NCBI Description cyprosin - cardoon >gi\_556819\_emb\_CAA57510\_ (X81984)

cyprosin [Cynara cardunculus]

Seq. No. 205878

Seq. ID LIB3083-102-Q1-L1-A7

Method BLASTX
NCBI GI g3702368
BLAST score .515
E value 2.0e-52
Match length 131
% identity 74

NCBI Description (AJ001855) alpha subunit of F-actin capping protein

[Arabidopsis thaliana]

Seq. No. 205879

Seq. ID LIB3083-102-Q1-L1-B1

Method BLASTX
NCBI GI g464849
BLAST score 649
E value 3.0e-68
Match length 131
% identity 98

NCBI Description TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha

chain - almond >gi\_2041 $\overline{3}$ \_emb\_C $\overline{A}$ A47 $\overline{63}$ 5\_ (X67162)

alpha-tubulin [Prunus dulcis]

Seq. No. 205880

Seq. ID LIB3083-102-Q1-L1-B2

Method BLASTX
NCBI GI g267073
BLAST score 416
E value 1.0e-52
Match length 110
% identity 97

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin

beta chain - Arabidopsis thaliana >gi\_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 205881

Seq. ID LIB3083-102-Q1-L1-B6

Method BLASTX NCBI GI g1561774 BLAST score 387



.0e-38 E value Match length 92 % identity 82

NCBI Description (U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.

205882 Seq. ID LIB3083-102-Q1-L1-C3

Method BLASTX NCBI GI q4185511 BLAST score 314 6.0e-29 E value Match length 88 68 % identity

NCBI Description (AF102822) actin depolymerizing factor 4 [Arabidopsis

thaliana]

205883

Seq. No.

Seq. ID LIB3083-102-Q1-L1-C4

Method BLASTN NCBI GI g2829205 189 BLAST score 1.0e-102 E value 269 Match length 74

% identity NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

205884 Seq. No.

LIB3083-102-Q1-L1-C6 Seq. ID

Method BLASTX NCBI GI q1173104 BLAST score 394 1.0e-38 E value Match length 91 71 % identity

RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease NCBI Description

[Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease,

RNS2 [Arabidopsis thaliana]

Seq. No. 205885

Seq. ID LIB3083-102-Q1-L1-C7

Method BLASTX NCBI GI q2224695 BLAST score 196 E value 4.0e-15 Match length 111 % identity 45

(AB002375) KIAA0377 [Homo sapiens] NCBI Description

205886 Seq. No.

Seq. ID LIB3083-102-Q1-L1-C8

Method BLASTX NCBI GI g1345970 BLAST score 489 E value 1.0e-49 Match length 93 89 % identity





NCBI Description OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi\_870784 (U25817) omega-3 fatty acid desaturase [Sesamum indicum]

Seq. No. 205887

Seq. ID LIB3083-102-Q1-L1-D1

Method BLASTX
NCBI GI g1702983
BLAST score 243
E value 9.0e-31
Match length 108
% identity 64

NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855\_pir\_\_S11850

hypothetical protein - garden strawberry

>gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria
x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 205888

Seq. ID LIB3083-102-Q1-L1-D3

Method BLASTN
NCBI GI g1143223
BLAST score 173
E value 2.0e-92
Match length 356
% identity 51

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205889

Seq. ID LIB3083-102-Q1-L1-D5

Method BLASTX
NCBI GI g2129473
BLAST score 205
E value 4.0e-16
Match length 76
% identity 51

NCBI Description arabinogalactan-like protein - loblolly pine >gi\_607774

(U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 205890

Seq. ID LIB3083-102-Q1-L1-D6

Method BLASTN
NCBI GI g4104241
BLAST score 184
E value 3.0e-99
Match length 208
% identity 97

NCBI Description Gossypium hirsutum palmitoyl-acyl carrier protein

thioesterase (FatB1) mRNA, partial cds

Seq. No. 205891

Seq. ID LIB3083-102-Q1-L1-D7

Method BLASTX
NCBI GI g2982451
BLAST score 158
E value 1.0e-14
Match length 56



% identity

(AL022223) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 205892

LIB3083-102-Q1-L1-E1 Seq. ID

Method BLASTX NCBI GI q3935147 BLAST score 392 E value 1.0e-45 Match length 123 % identity 69

NCBI Description (AC005106) T25N20.11 [Arabidopsis thaliana]

Seq. No. 205893

LIB3083-102-Q1-L1-E2 Seq. ID

BLASTN Method NCBI GI g1143223 BLAST score 74 1.0e-33 E value

Match length 225 % identity 89

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205894

Seq. ID LIB3083-102-Q1-L1-E4

Method BLASTX NCBI GI q1388078 BLAST score 276 9.0e-25 E value Match length 72

% identity

NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]

Seq. No. 205895

Seq. ID LIB3083-102-Q1-L1-E8

Method BLASTX NCBI GI g1169238 BLAST score 477 2.0e-48 E value Match length 94 % identity 89

NCBI Description GLUTAMATE DECARBOXYLASE (GAD) >gi 1076648 pir A48767

> glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding garden petunia >gi 294112 (L16797) glutamate decarboxylase

[Petunia hybrida] >gi 309680 (L16977) glutamate

decarboxylase [Petunia hybrida]

Seq. No. 205896

Seq. ID LIB3083-102-Q1-L1-F3

Method BLASTX NCBI GI g4415992 BLAST score 286 1.0e-36 E value Match length 88 93 % identity

(AF059288) beta-tubulin 2 [Eleusine indica] NCBI Description

```
205897
Seq. No.
Seq. ID
                  LIB3083-102-Q1-L1-F7
                  BLASTX
Method
NCBI GI
                  g3121748
BLAST score
                  141
                  1.0e-08
E value
Match length
                  75
                  35
% identity
                  PUTATIVE ALLANTOINASE >qi 2635738 emb CAB15231 (Z99120)
NCBI Description
                  similar to allantoinase [Bacillus subtilis]
                  205898
Seq. No.
                  LIB3083-102-Q1-L1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334138
BLAST score
                  403
                  2.0e-39
E value
                  109
Match length
% identity
                  71
                  CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
NCBI Description
                   [Glycine max]
                  205899
Seq. No.
Seq. ID
                  LIB3083-102-Q1-L1-G2
                  BLASTN
Method
                  g2970050
NCBI GI
                  45
BLAST score
                  3.0e-16
E value
                  109
Match length
                  85
% identity
NCBI Description Vigna radiata mRNA for ARG10, complete cds
                  205900
Seq. No.
                  LIB3083-102-Q1-L1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4097579
                   455
BLAST score
                   2.0e-45
E value
                  130
Match length
% identity
                   71
NCBI Description
                  (U64922) NTGP1 [Nicotiana tabacum]
Seq. No.
                  205901
                  LIB3083-102-Q1-L1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                   q231757
BLAST score
                   288
                   7.0e-26
E value
Match length
                   92
                   59
% identity
```

NCBI Description CAFFEIC ACID 3-0-METHYLTRANSFERASE

3-O-METHYLTRANSFERASE) (COMT) >gi\_99653\_pir\_\_S18568 lignin-bispecific O-methyltransferase (EC 2.1.1.-) quaking aspen >gi\_20951\_emb\_CAA44006\_ (X62096) lignin bispecific acid/5-hydroxyferulic acid methyltransferase

[Populus tremuloides] >gi\_2226267 (U13171) caffeic

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID





## acid/5-hydroxyferulic acid O-methyltransferase [Populus tremuloides]

Seq. No. 205902 Seq. ID LIB3083-102-Q1-L1-H2 Method BLASTX NCBI GI q2982301 BLAST score 188 E value 2.0e-14 Match length 91 % identity 46 (AF051235) YGL010w-like protein [Picea mariana] NCBI Description Seq. No. 205903 Seq. ID LIB3083-102-Q1-L1-H3 Method BLASTX NCBI GI g3033397 BLAST score 378 2.0e-36 E value Match length 125 % identity 64 NCBI Description (AC004238) unknown protein [Arabidopsis thaliana] Seq. No. 205904 Seq. ID LIB3083-102-Q1-L1-H6 Method BLASTX NCBI GI g2065531 BLAST score 365 4.0e-35 E value Match length 94 % identity 71 NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] Seq. No. 205905 Seq. ID LIB3083-102-Q1-L1-H7 Method BLASTX NCBI GI g3193306 BLAST score 283 E value 3.0e-25 Match length 94 % identity 60 NCBI Description (AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana] Seq. No. 205906 Seq. ID LIB3083-103-Q1-L1-A10 Method BLASTX NCBI GI g3395440 BLAST score 179 E value 2.0e-13 Match length 76 % identity 41 NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 205907

Seq. ID LIB3083-103-Q1-L1-A11

BLAST score

343

```
Method
NCBI GI
                  g2154715
BLAST score
                  605
                  4.0e-63
E value
Match length
                  130
% identity
                  90
                  (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
NCBI Description
                  205908
Seq. No.
Seq. ID
                  LIB3083-103-Q1-L1-A12
Method
                  BLASTX
NCBI GI
                  g1703380
BLAST score
                  510
                  6.0e-52
E value
                  109
Match length
                  89
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
Seq. No.
                  205909
Seq. ID
                  LIB3083-103-Q1-L1-B11
Method
                  BLASTX
NCBI GI
                  g3269288
BLAST score
                  447
                  1.0e-44
E value
Match length
                  103
% identity
                  82
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                  205910
Seq. No.
Seq. ID
                  LIB3083-103-Q1-L1-B12
Method
                  BLASTX
NCBI GI
                  q586076
BLAST score
                  313
E value
                  3.0e-29
Match length
                  61
% identity
                  92
                  TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                  tubulin 1 [Lupinus albus]
                  205911
Seq. No.
Seq. ID
                  LIB3083-103-Q1-L1-B9
Method
                  BLASTX
NCBI GI
                  q166949
BLAST score
                  412
E value
                  2.0e-40
Match length
                  126
% identity
NCBI Description
                  (M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea
                  americana]
                  205912
Seq. No.
Seq. ID
                  LIB3083-103-Q1-L1-C10
Method
                  BLASTX
                  q4468990
NCBI GI
```



E value 2.0e-32 Match length 106 % identity 67

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 205913

Seq. ID LIB3083-103-Q1-L1-C11

Method BLASTX
NCBI GI g2459446
BLAST score 421
E value 2.0e-41
Match length 128
% identity 63

NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Seq. No. 205914

Seq. ID LIB3083-103-Q1-L1-C12

Method BLASTX
NCBI GI g2494320
BLAST score 285
E value 7.0e-26
Match length 63
% identity 89

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)

>gi 1806575 emb CAA67868 (X99517) Eukaryotic initiation

factor-5 [Zea mays]

Seq. No. 205915

Seq. ID LIB3083-103-Q1-L1-D11

Method BLASTX
NCBI GI g4006886
BLAST score 557
E value 2.0e-57
Match length 122
% identity 81

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 205916

Seq. ID LIB3083-103-Q1-L1-E10

Method BLASTX
NCBI GI g2493852
BLAST score 291
E value 3.0e-26
Match length 63
% identity 84

NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE VC

>gi\_1070356\_emb\_CAA92107\_ (Z68091) cytochrome c oxidase, Vc

subunit [Hordeum vulgare]

Seq. No. 205917

Seq. ID LIB3083-103-Q1-L1-E9

Method BLASTX
NCBI GI g1174595
BLAST score 660
E value 2.0e-69
Match length 128



% identity 98
NCBI Description TUBULIN BETA-1 CHAIN >gi\_1076658\_pir\_\_S50747 beta-tubulin -

potato >gi 609268\_emb\_CAA83847\_ (Z33382) beta-tubulin

[Solanum tuberosum]

Seq. No. 205918

Seq. ID LIB3083-103-Q1-L1-F10

Method BLASTX
NCBI GI g1732511
BLAST score 417
E value 5.0e-41
Match length 93
% identity 85

NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis

thaliana]

Seq. No. 205919

Seq. ID LIB3083-103-Q1-L1-F9

Method BLASTX
NCBI GI g2271477
BLAST score 305
E value 5.0e-28
Match length 62
% identity 94

NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No. 205920

Seq. ID LIB3083-103-Q1-L1-G10

Method BLASTX
NCBI GI g3123271
BLAST score 506
E value 2.0e-51
Match length 118
% identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi\_2224751\_emb\_CAA74381\_ (Y14052)

ribosomal protein S6 [Arabidopsis thaliana]

Seq. No. 205921

Seq. ID LIB3083-103-Q1-L1-G12

Method BLASTX
NCBI GI g1737492
BLAST score 402
E value 3.0e-39
Match length 122
% identity 20

NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 205922

Seq. ID LIB3083-103-Q1-L1-G9

Method BLASTX
NCBI GI g2829895
BLAST score 264
E value 4.0e-23
Match length 69
% identity 72

NCBI Description (AC002311) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                  205923
Seq. ID
                  LIB3083-103-Q1-L1-H12
Method
                  BLASTX
NCBI GI
                  g2791896
BLAST score
                  615
E value
                  3.0e-64
                  127
Match length
% identity
                  95
NCBI Description
                  (Y08997) 146kDa nuclear protein [Xenopus laevis]
                  205924
Seq. No.
                  LIB3083-103-Q1-L1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2706450
BLAST score
                  281
                  3.0e-25
E value
Match length
                  72
% identity
                  79
NCBI Description
                  (AJ225172) magnesium dependent soluble inorganic
                  pyrophosphatase [Solanum tuberosum]
                  205925
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-A2
Method
                  BLASTN
NCBI GI
                  g3046851
BLAST score
                  35
E value
                  3.0e-10
                  138
Match length
                  39
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIJ24, complete sequence [Arabidopsis thaliana]
                  205926
Seq. No.
                  LIB3083-104-Q1-L1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334138
BLAST score
                  542
                  1.0e-55
E value
Match length
                  130
                  77
% identity
NCBI Description
                  CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
                  [Glycine max]
Seq. No.
                  205927
Seq. ID
                  LIB3083-104-Q1-L1-A4
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                  530
E value
                  3.0e-54
Match length
                  130
% identity
```

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 205928

Seq. ID LIB3083-104-Q1-L1-A5

Method BLASTX



```
NCBI GI
                  q3080420
BLAST score
                  610
E value
                  1.0e-63
Match length
                  134
                  87
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  205929
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-A6
Method
                  BLASTX
NCBI GI
                  q4567273
BLAST score
                  360
                  2.0e-34
E value
Match length
                  97
% identity
                  71
                  (AC006841) putative vacuolar proton ATPase subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  205930
Seq. ID
                  LIB3083-104-Q1-L1-B1
Method
                  BLASTX
NCBI GI
                  g266567
BLAST score
                  187
                  5.0e-14
E value
Match length
                  101
                  45
% identity
                  MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
NCBI Description
                  (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
                  >gi 421956 pir S23558 mitochondrial processing peptidase
                  (EC 3.4.99.41) alpha chain precursor - potato
                  >gi_21493_emb_CAA46990 (X66284) mitochondrial processing
                  peptidase [Solanum tuberosum]
                  205931
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-B2
Method
                  BLASTX
NCBI GI
                  g231496
BLAST score
                  592
E value
                  1.0e-61
Match length
                  116
% identity
                  98
                  ACTIN 58 >gi_100421_pir__ S20094 actin - potato
NCBI Description
                  >gi_21536_emb_CAA39278 (X55749) actin [Solanum tuberosum]
                  205932
Seq. No.
                  LIB3083-104-Q1-L1-B3
Seq. ID
Method
                  BLASTX
                  q4204315
NCBI GI
BLAST score
                  265
E value
```

3.0e-23 Match length 67 70 % identity

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 205933

Seq. ID LIB3083-104-Q1-L1-B7



```
Method
NCBI GI
                  g2791806
BLAST score
                  295
E value
                  1.0e-26
                  82
Match length
                  66
% identity
NCBI Description
                  (AF041433) bet3 [Mus musculus]
                  205934
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-B8
Method
                  BLASTX
NCBI GI
                  q4539335
BLAST score
                  304
                  9.0e-28
E value
Match length
                  126
                  49
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205935
Seq. ID
                  LIB3083-104-Q1-L1-C1
Method
                  BLASTX
NCBI GI
                  g547867
BLAST score
                  556
                  2.0e-57
E value
                  131
Match length
                  79
% identity
NCBI Description
                  LIPOXYGENASE 1 >gi 541878 pir JQ2267 lipoxygenase (EC
                  1.13.11.12) AtLox1 - Arabidopsis thaliana >gi_289203
                  (L04637) lipoxygenase [Arabidopsis thaliana] >gi_436920
                  (U01843) lipoxygenase 1 [Arabidopsis thaliana]
Seq. No.
                  205936
Seq. ID
                  LIB3083-104-Q1-L1-C3
Method
                  BLASTN
NCBI GI
                  g1143223
BLAST score
                  125
                  7.0e-64
E value
Match length
                  363
% identity
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                  205937
Seq. ID
                  LIB3083-104-Q1-L1-C8
Method
                  BLASTX
NCBI GI
                  q2506139
BLAST score
                  413
E value
                  1.0e-40
Match length
                  107
% identity
                  75
NCBI Description
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                  (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                  archain/delta-COP [Oryza sativa]
```

Seq. No. 205938

LIB3083-104-Q1-L1-D1 Seq. ID

Method BLASTX NCBI GI g1174870



```
BLAST score
                  3.0e-23
E value
Match length
                  73
                  74
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN
NCBI Description
                  >gi 633685 emb CAA55861 (X79274) ubiquinol--cytochrome c
                  reductase [Solanum tuberosum]
                  205939
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-D2
Method
                  BLASTX
                  g1706958
NCBI GI
BLAST score
                  305
                  4.0e-28
E value
Match length
                  87
                  70
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  205940
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-D4
Method
                  BLASTX
                  q1143322
NCBI GI
                                                               £.7
                  185
BLAST score
                  7.0e-14
E value
                  109
Match length
                   39
% identity
                  (U40979) alfa-carboxyltransferase precursor [Glycine max]
NCBI Description
                   205941
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-D5
Method
                  BLASTX
NCBI GI
                   q1076315
BLAST score
                   225
                   2.0e-18
E value
                   125
Match length
                   41
% identity
                  cytochrome P450 - Arabidopsis thaliana
NCBI Description
                   >gi 853719 emb CAA60793 (X87367) CYP90 protein
                   [Arabidopsis thaliana] >gi 871988 emb CAA60794 (X87368)
                   CYP90 protein [Arabidopsis thaliana]
                   205942
Seq. No.
Seq. ID
                   LIB3083-104-Q1-L1-D6
                   BLASTX
Method
NCBI GI
                   q3126963
BLAST score
                   283
```

E value 2.0e-25 95 Match length % identity

(AF061805) acidic chitinase [Elaeagnus umbellata] NCBI Description

Seq. No. 205943

LIB3083-104-Q1-L1-D8 Seq. ID

Method BLASTX NCBI GI g3582333 BLAST score 618 1.0e-64 E value



Match length 127 % identity 93

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 205944

Seq. ID LIB3083-104-Q1-L1-E1

Method BLASTX
NCBI GI g2244799
BLAST score 346
E value 1.0e-32
Match length 124
% identity 53

NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No. 205945

Seq. ID LIB3083-104-Q1-L1-E2

Method BLASTX
NCBI GI g1706958
BLAST score 449
E value 8.0e-45
Match length 123
% identity 64

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 205946

Seq. ID LIB3083-104-Q1-L1-E7

Method BLASTX
NCBI GI g3511285
BLAST score 644
E value 1.0e-67
Match length 128
% identity 91

NCBI Description (AF081534) cellulose synthase [Populus alba x Populus

tremula]

Seq. No. 205947

Seq. ID LIB3083-104-Q1-L1-E8

Method BLASTX
NCBI GI g2982451
BLAST score 207
E value 1.0e-21
Match length 92
% identity 74

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 205948

Seg. ID LIB3083-104-Q1-L1-F2

Method BLASTX
NCBI GI g3915031
BLAST score 566
E value 7.0e-66
Match length 126
% identity 99

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi\_1217628\_emb\_CAA65232\_

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

```
205949
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-F3
Method
                  BLASTX
NCBI GI
                  g4325367
BLAST score
                  177
                  7.0e-13
E value
                  37
Match length
                  78
% identity
                  (AF128396) contains similarity to Nicotiana tabacum B-type
NCBI Description
                  cyclin (GB:D50737) [Arabidopsis thaliana]
                  205950
Seq. No.
Seq. ID
                  LIB3083-104-Q1-L1-F5
                  BLASTX
Method
                  g4455158
NCBI GI
BLAST score
                  577
                  8.0e-60
E value
Match length
                  128
                  82
% identity
NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana]
                  205951
Seq. No.
                  LIB3083-104-Q1-L1-F6
Seq. ID
Method
                  BLASTX
                  g1170747
NCBI GI
BLAST score
                  343
                  2.0e-32
E value
                  80
Match length
                  84
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
NCBI Description
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  205952
                  LIB3083-104-Q1-L1-F8
Seq. ID
Method
                  BLASTN
                  g2829205
NCBI GI
BLAST score
                  357
E value
                  0.0e+00
                  398
Match length
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
Seq. No.
                  205953
Seq. ID
                  LIB3083-104-Q1-L1-G2
                  BLASTX
Method
NCBI GI
                  q1706956
BLAST score
                  554
```

E value 4.0e-57 Match length 103 98 % identity

(U58283) cellulose synthase [Gossypium hirsutum] NCBI Description

Seq. No. 205954



Seq. ID LIB3083-104-Q1-L1-G6

Method BLASTX
NCBI GI g4218011
BLAST score 272
E value 5.0e-24
Match length 85
% identity 60

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi\_4309721\_gb\_AAD15491\_ (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 205955

Seq. ID LIB3083-104-Q1-L1-G7

Method BLASTX
NCBI GI g1076800
BLAST score 620
E value 8.0e-65
Match length 130
% identity 85

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -

maize >gi\_600116\_emb\_CAA84406\_ (Z34934) cytosolic ascorbate
peroxidase [Zea mays] >gi\_1096503\_prf\_\_2111423A ascorbate

peroxidase [Zea mays]

Seq. No. 205956

Seq. ID LIB3083-104-Q1-L1-H1

Method BLASTX
NCBI GI g119640
BLAST score 293
E value 1.0e-26
Match length 113
% identity 54

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN

E8) >gi\_82109\_pir\_\_S01642 ripening protein E8 - tomato >gi\_19199\_emb\_CAA31789\_ (X13437) E8 protein [Lycopersicon

esculentum]

Seq. No. 205957

Seq. ID LIB3083-104-Q1-L1-H2

Method BLASTX
NCBI GI g1169009
BLAST score 341
E value 4.0e-32
Match length 123
% identity 52

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi\_542009\_pir\_\_S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi\_437777\_emb\_CAA52814\_ (X74814) O-Methyltransferase

[Eucalyptus gunnii]

Seq. No. 205958

Seq. ID LIB3083-104-Q1-L1-H3

Method BLASTX NCBI GI g136636 BLAST score 399



E value 6.0e-39
Match length 76
% identity 96

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi\_1076424\_pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin

Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis Thaliana]

Seq. No. 205959

Seq. ID LIB3083-104-Q1-L1-H5

Method BLASTX
NCBI GI g2088646
BLAST score 428
E value 2.0e-42
Match length 86
% identity 87

NCBI Description (AF002109) Sulp isolog [Arabidopsis thaliana]

Seq. No. 205960

Seq. ID LIB3083-104-Q1-L1-H6

Method BLASTX
NCBI GI g1706958
BLAST score 456
E value 1.0e-45
Match length 84
% identity 94

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 205961

Seq. ID LIB3083-104-Q1-L1-H7

Method BLASTX
NCBI GI g2129473
BLAST score 214
E value 3.0e-17
Match length 108
% identity 43

NCBI Description arabinogalactan-like protein - loblolly pine >gi\_607774

(U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 205962

Seq. ID LIB3083-105-Q1-L1-A1

Method BLASTX
NCBI GI g3540207
BLAST score 394
E value 2.0e-38
Match length 100
% identity 73

NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 205963

Seq. ID LIB3083-105-Q1-L1-A11

Method BLASTX



```
NCBI GI
                   q4455198
BLAST score
                  386
                  1.0e-37
E value
Match length
                  95
% identity
                  77
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205964
                  LIB3083-105-Q1-L1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2865522
BLAST score
                  33
                  4.0e-09
E value
Match length
                  49
                  60
% identity
                  Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  205965
Seq. ID
                  LIB3083-105-Q1-L1-A6
Method
                  BLASTX
NCBI GI
                  q4103152
BLAST score
                  150
                  6.0e-10
E value
Match length
                  52
                  54
% identity
                  (AF020716) histidyl-tRNA synthetase [Triticum aestivum]
NCBI Description
Seq. No.
                  205966
Seq. ID
                  LIB3083-105-Q1-L1-A8
Method
                  BLASTX
NCBI GI
                  q81816
BLAST score
                  435
E value
                  2.0e-43
Match length
                  81
                   95
% identity
                  tubulin beta-1 chain - soybean
NCBI Description
                  205967
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-A9
Method
                  BLASTX
NCBI GI
                  g1762309
BLAST score
                  169
                   4.0e-12
E value
Match length
                   60
% identity
                   70
                   (U53345) AP-1 Golgi-related complex component; clathrin
NCBI Description
                   coated vesicles; clathrin assembly protein [Camptotheca
                  acuminata]
                   205968
Seq. No.
```

LIB3083-105-Q1-L1-B2 Seq. ID

Method BLASTX NCBI GI g2129495 BLAST score 476 E value 3.0e-48 99 Match length

% identity 88

NCBI Description fiber protein E6 (clone SIE6-2A) - sea-island cotton

>gi 1000088 (U30507) E6 [Gossypium barbadense] >gi\_1000090

(U30508) E6 [Gossypium barbadense]

Seq. No. 205969

Seq. ID LIB3083-105-Q1-L1-B5

Method BLASTN
NCBI GI g1143223
BLAST score 124
E value 2.0e-63
Match length 253
% identity 90

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 205970

Seq. ID LIB3083-105-Q1-L1-B6

Method BLASTX
NCBI GI g3831470
BLAST score 297
E value 4.0e-27
Match length 100
% identity 59

NCBI Description (AC005700) unknown protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 205971

Seq. ID LIB3083-105-Q1-L1-B9

Method BLASTX
NCBI GI g3136048
BLAST score 246
E value 3.0e-21
Match length 64
% identity 72

NCBI Description (AL023592) putative helicase [Schizosaccharomyces pombe]

Seq. No. 205972

Seq. ID LIB3083-105-Q1-L1-C1

Method BLASTX
NCBI GI g464981
BLAST score 295
E value 6.0e-27
Match length 57
% identity 95

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >qi 388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 205973

Seq. ID LIB3083-105-Q1-L1-C10

Method BLASTX
NCBI GI g120669
BLAST score 382
E value 4.0e-37
Match length 75
% identity 96

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

% identity

30

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

```
Seq. No.
                  205974
                  LIB3083-105-Q1-L1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544399
BLAST score
                  428
                  1.0e-42
E value
                  96
Match length
                  79
% identity
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  205975
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-C2
Method
                  BLASTX
NCBI GI
                  q2119927
                  222
BLAST score
                  2.0e-18
E value
                   48
Match length
                   92
% identity
NCBI Description translation elongation factor G, chloroplast - soybean
                   205976
Seq. No.
                  LIB3083-105-Q1-L1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1518540
BLAST score
                   442
                   3.0e-44
E value
                   96
Match length
                   88
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   205977
Seq. No.
                   LIB3083-105-Q1-L1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4105772
BLAST score
                   222
E value
                   2.0e-18
Match length
                   72
                   28
% identity
                  (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
Seq. No.
                   205978
                   LIB3083-105-Q1-L1-C5
Seq. ID
Method
                   BLASTN
                   g2829205
NCBI GI
BLAST score
                   79
                   1.0e-36
E value
                   208
Match length
```

precursor (PRP) mRNA, complete cds

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein



```
205979
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-C6
Method
                  BLASTX
NCBI GI
                  g3738283
BLAST score
                  395
                  1.0e-38
E value
Match length
                  82
                  84
% identity
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  205980
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-C8
Method
                  BLASTX
NCBI GI
                  g2129473
BLAST score
                  213
E value
                  2.0e-17
Match length
                  72
                  58
% identity
NCBI Description
                  arabinogalactan-like protein - loblolly pine >gi_607774
                  (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                  205981
Seq. ID
                  LIB3083-105-Q1-L1-C9
Method
                  BLASTX
NCBI GI
                  g3386597
BLAST score
                  182
E value
                  1.0e-13
                  57
Match length
                  67
% identity
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
                  >gi_3702347 (AC005397) putative permease [Arabidopsis
                  thaliana]
Seq. No.
                  205982
Seq. ID
                  LIB3083-105-Q1-L1-D10
Method
                  BLASTN
NCBI GI
                  g2995991
BLAST score
                  43
E value
                  5.0e-15
Match length
                  87
% identity
                  87
NCBI Description
                  Arabidopsis thaliana dormancy-associated protein (DRM1)
                  gene, complete cds
                  205983
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-D11
Method
                  BLASTX
                  q584825
NCBI GI
BLAST score
                  280
                  3.0e-25
E value
```

Match length 59 % identity 86

B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot NCBI Description

>gi 297889 emb CAA51078 (X72385) B2 protein [Daucus

carota]

Seq. No. 205984

```
LIB3083-105-Q1-L1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g541951
BLAST score
                   203
E value
                   4.0e-16
Match length
                   86
% identity
                   49
NCBI Description
                  SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
                   [Glycine max]
Seq. No.
                  205985
Seq. ID
                  LIB3083-105-Q1-L1-D3
Method
                  BLASTX
NCBI GI
                  q2632252
BLAST score
                   362
                  8.0e-35
E value
Match length
                  94
% identity
                  76
                  (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                  205986
Seq. No.
                  LIB3083-105-Q1-L1-D4
Seq. ID
Method
                  BLASTX
                  q4406819
NCBI GI
BLAST score
                  174
                  1.0e-12
E value
Match length
                  76
                  49
% identity
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  205987
Seq. ID
                  LIB3083-105-Q1-L1-D7
Method
                  BLASTX
NCBI GI
                  q464849
BLAST score
                   479
E value
                  1.0e-48
Match length
                  97
% identity
                   99
NCBI Description
                  TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
                  chain - almond >gi_20413_emb_CAA47635_ (X67162)
                  alpha-tubulin [Prunus dulcis]
                  205988
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-D8
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  256
                  2.0e-22
E value
Match length
                  81
                  74
% identity
NCBI Description
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                  thaliana]
```

Seq. No. 205989

Seq. ID LIB3083-105-Q1-L1-D9

Method BLASTX NCBI GI g4531443



BLAST score 172 E value 2.0e-12 Match length 65 % identity 60 NCBI Description (AC0062

NCBI Description (AC006224) putative 50s ribosomal protein L3 [Arabidopsis

thaliana]

Seq. No. 205990

Seq. ID LIB3083-105-Q1-L1-E10

Method BLASTX
NCBI GI g2811278
BLAST score 291
E value 2.0e-26
Match length 89
% identity 65

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No.

205991

Seq. ID LIB3083-105-Q1-L1-E12

Method BLASTX
NCBI GI g2129825
BLAST score 436
E value 2.0e-43
Match length 98
% identity 85

NCBI Description dynamin-like protein phragmoplastin 12 - soybean

>gi\_1217994 (U25547) SDL [Glycine max]

Seq. No. 205992

Seq. ID LIB3083-105-Q1-L1-E2

Method BLASTX
NCBI GI g3738332
BLAST score 329
E value 6.0e-31
Match length 93
% identity 68

NCBI Description (AC005170) putative eukaryotic initiation factor

[Arabidopsis thaliana]

Seq. No. 205993

Seq. ID LIB3083-105-Q1-L1-E6

Method BLASTX
NCBI GI g4115377
BLAST score 293
E value 1.0e-26
Match length 100
% identity 52

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 205994

Seq. ID LIB3083-105-Q1-L1-E8

Method BLASTX
NCBI GI g4098331
BLAST score 495
E value 2.0e-50
Match length 92
% identity 96





```
NCBI Description
                  (U76896) beta-tubulin 5 [Triticum aestivum]
                  205995
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-E9
Method
                  BLASTX
NCBI GI
                  g1743277
BLAST score
                  488
E value
                  1.0e-49
                  95
Match length
                  . 96
% identity
                  (Y09741) beta-tubulin 1 [Hordeum vulgare]
NCBI Description
                  205996
Seq. No.
                  LIB3083-105-Q1-L1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746062
                  277
BLAST score
                  8.0e-25
E value
                  96
Match length
                  53
% identity
NCBI Description
                  (AC005311) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  205997
Seq. ID
                  LIB3083-105-Q1-L1-F10
Method
                  BLASTX
NCBI GI
                  q3334320
BLAST score
                  403
                  1.0e-39
E value
                  77
Match length
                  96
% identity
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  205998
Seq. ID
                  LIB3083-105-Q1-L1-F11
Method
                  BLASTX
NCBI GI
                  ~g2244971
BLAST score
                  269
                  6.0e-24
E value
Match length
                  92
                  60
% identity
NCBI Description
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
                  205999
Seq. No.
                  LIB3083-105-Q1-L1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q466160
                  373
BLAST score
                  4.0e-36
E value
Match length
                  84
```

% identity

NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III

> >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis elegans >gi 289769 (L14429) putative [Caenorhabditis

elegans]

Seq. No. 206000



```
LIB3083-105-Q1-L1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706956
BLAST score
                  518
                  4.0e-53
E value
                  98
Match length
                  99
% identity
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  206001
Seq. ID
                  LIB3083-105-Q1-L1-F3
                  BLASTX
Method
NCBI GI
                  q4263695
                  146
BLAST score
                  2.0e-09
E value
                  97
Match length
                  34
% identity
                  (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  206002
Seq. ID
                  LIB3083-105-Q1-L1-F4
                  BLASTX
Method
                  g4454032
NCBI GI
BLAST score
                  234
                  9.0e-20
E value
                  97
Match length
                  48
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  206003
Seq. ID
                  LIB3083-105-Q1-L1-F5
                  BLASTX
Method
                  g1486472
NCBI GI
BLAST score
                  449
                  5.0e-45
E value
Match length
                  96
                  93
% identity
                  (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                  tuberosum]
                  206004
Seq. No.
Seq. ID
                  LIB3083-105-Q1-L1-F8
Method
                  BLASTX
NCBI GI
                  g3184281
                  224
BLAST score
E value
                  1.0e-18
                  95
Match length
% identity
                  47
                  (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206005
Seq. ID
                  LIB3083-105-Q1-L1-F9
Method
                  BLASTX
NCBI GI
                  g2129770
BLAST score
                  459
```

28220

3.0e-46

E value



Match length 96 % identity 83

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -

Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 206006

Seq. ID LIB3083-105-Q1-L1-G12

Method BLASTX
NCBI GI g4098331
BLAST score 529
E value 2.0e-54
Match length 98
% identity 97

NCBI Description (U76896) beta-tubulin 5 [Triticum aestivum]

Seq. No. 206007

Seq. ID LIB3083-105-Q1-L1-G2

Method BLASTX
NCBI GI g4204300
BLAST score 204
E value 3.0e-16
Match length 74

% identity 61

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 206008

Seq. ID LIB3083-105-Q1-L1-G5

Method BLASTX
NCBI GI g3176690
BLAST score 424
E value 5.0e-42
Match length 98
% identity 84

NCBI Description (AC003671) Similar to ubiquitin ligase gb\_D63905 from S.

cerevisiae. EST gb\_R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 206009

Seq. ID LIB3083-105-Q1-L1-G6

Method BLASTX
NCBI GI g3775993
BLAST score 293
E value 1.0e-26
Match length 58
% identity 95

NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No. 206010

Seq. ID LIB3083-105-Q1-L1-G9

Method BLASTX
NCBI GI g267069
BLAST score 415
E value 5.0e-41
Match length 77



% identity TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] 206011 Seq. No. میں شہ LIB3083-105-Q1-L1-H1 Seq. ID BLASTX Method q3461821 NCBI GI 224 BLAST score 2.0e-18 E value 69 Match length 65 % identity (AC004138) putative nucleoside triphosphatase [Arabidopsis NCBI Description thaliana] 206012 Seq. No. LIB3083-105-Q1-L1-H10 Seq. ID Method BLASTX NCBI GI g320556 181 BLAST score 1.0e-13 E value 76 Match length 45 % identity chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis NCBI Description thaliana >gi\_166666 (M38240) basic chitinase [Arabidopsis thaliana] 206013 Seq. No. Seq. ID LIB3083-105-Q1-L1-H11 Method BLASTX NCBI GI q4056457 370 BLAST score 1.0e-35 E value 99 Match length 70 % identity (AC005990) ESTs gb 234051 and gb F13722 come from this NCBI Description gene. [Arabidopsis thaliana] 206014 Seq. No. LIB3083-105-Q1-L1-H12 Seq. ID Method BLASTX q4510344 NCBI GI 175 BLAST score 7.0e-13 E value Match length 69 % identity 54 (AC006921) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 206015

LIB3083-105-Q1-L1-H2 Seq. ID

Method BLASTX NCBI GI g2129651 BLAST score 197 E value 2.0e-15 Match length 81



% identity 49

NCBI Description myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi 499045 emb CAA84065 (Z34292) myosin [Arabidopsis

thaliana]

Seq. No. 206016

Seq. ID LIB3083-105-Q1-L1-H4

Method BLASTX
NCBI GI g2829204
BLAST score 387
E value 1.0e-37
Match length 97
% identity 84

NCBI Description (AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

Seq. No. 206017

Seq. ID LIB3083-105-Q1-L1-H5

Method BLASTX
NCBI GI g4235430
BLAST score 384
E value 2.0e-37
Match length 100
% identity 77

NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No. 206018

Seq. ID LIB3083-105-Q1-L1-H7

Method BLASTX
NCBI GI g3608171
BLAST score 253
E value 5.0e-22
Match length 69
% identity 74

NCBI Description (D86306) proton-translocating inorganic pyrophosphatase

[Cucurbita moschata]

Seq. No. 206019

Seq. ID LIB3083-105-Q1-L1-H8

Method BLASTX
NCBI GI 94008159
BLAST score 401
E value 2.0e-39
Match length 96
% identity 78

NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]

Seq. No. 206020

Seq. ID LIB3083-106-Q1-L1-A10

Method BLASTX
NCBI GI g3059140
BLAST score 336
E value 1.0e-31
Match length 99
% identity 70

NCBI Description (AJ001706) NAD-dependent glyceraldehyde-3-phosphate

dehydrogenase [Pinus sylvestris]

Seq. ID Method

NCBI GI



```
206021
Seq. No.
Seq. ID
                  LIB3083-106-Q1-L1-A11
                  BLASTX
Method
NCBI GI
                  g3413170
BLAST score
                  258
                  2.0e-23
E value
                  96
Match length
% identity
                  69
                  (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]
NCBI Description
                  206022
Seq. No.
                  LIB3083-106-Q1-L1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760537
BLAST score
                  315
                  1.0e-29
E value
Match length
                  65
% identity
                  89
NCBI Description
                  (Y16088) cytosolic form of cyclophilin [Lupinus luteus]
                  206023
Seq. No.
Seq. ID
                  LIB3083-106-Q1-L1-B11
Method
                  BLASTX
NCBI GI
                  g2462733
BLAST score
                  251
E value
                  1.0e-21
Match length
                  69
                  68
% identity
NCBI Description
                  (AC002292) Putative enoyl-CoA hydratase/isomerase
                  [Arabidopsis thaliana]
                  206024
Seq. No.
Seq. ID
                  LIB3083-106-Q1-L1-B12
Method
                  BLASTX
NCBI GI
                  q2388580
BLAST score
                  279
                  2.0e-25
E value
Match length
                  62
                  84
% identity
NCBI Description
                  (AC000098) Similar to Sequence 10 from patent 5477002
                   (gb_1253956). [Arabidopsis thaliana]
Seq. No.
                  206025
Seq. ID
                  LIB3083-106-Q1-L1-B9
Method
                  BLASTX
NCBI GI
                  q4490332
BLAST score
                  276
                  6.0e-25
E value
Match length
                  79
% identity
                  68
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206026
```

28224

LIB3083-106-Q1-L1-C11

BLASTX

q462187



BLAST score 311 E value 1.0e-28 Match length 100 % identity 69

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi 282928 pir A42906 serine

hydroxymethyltransferase - garden pea >gi\_169158 (M87649)

serine hydroxymethyltransferase [Pisum sativum]

Seq. No. 206027

Seq. ID LIB3083-106-Q1-L1-C9

Method BLASTX
NCBI GI g3063396
BLAST score 481
E value 1.0e-48
Match length 115
% identity 80

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 206028

Seq. ID LIB3083-106-Q1-L1-D12

Method BLASTX
NCBI GI g421843
BLAST score 491
E value 9.0e-50
Match length 119
% identity 79

NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana

>gi 217861 dbj BAA01715 (D10909) serine/threonine protein

kinase [Arabidopsis thaliana]

Seq. No. 206029

Seq. ID LIB3083-106-Q1-L1-E11

Method BLASTX
NCBI GI 94105772
BLAST score 450
E value 6.0e-45
Match length 107
% identity 43

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 206030

Seq. ID LIB3083-106-Q1-L1-F10

Method BLASTN
NCBI GI g1143223
BLAST score 100
E value 4.0e-49
Match length 248
% identity 88

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 206031

Seq. ID LIB3083-106-Q1-L1-F12

Method BLASTX NCBI GI g3337361 BLAST score 243



```
0e-20
E value
Match length
                  85
% identity
                  54
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206032
                  LIB3083-106-Q1-L1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4415992
                   602
BLAST score
                   9.0e-63
E value
                  119
Match length
                   97
% identity
                  (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
                   206033
Seq. No.
                  LIB3083-107-Q1-L1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123271
BLAST score
                   375
                   2.0e-36
E value
                   71
Match length
                   97
% identity
                  40S RIBOSOMAL PROTEIN S6 >qi 2224751 emb CAA74381 (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
                   206034
Seq. No.
Seq. ID
                  LIB3083-107-Q1-L1-A2
                  BLASTX
Method
NCBI GI
                   g1814403
BLAST score
                   412
                   1.0e-40
E value
                   96
Match length
                   81
% identity
                   (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   206035
Seq. ID
                   LIB3083-107-Q1-L1-A4
Method
                   BLASTX
NCBI GI
                   g3650032
BLAST score
                   237
E value
                   4.0e-20
Match length
                   49
% identity
                   (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   206036
Seq. ID
                   LIB3083-107-Q1-L1-A6
                   BLASTX
Method
NCBI GI
                   g1009712
BLAST score
                   490
```

8.0e-50 E value Match length 98 90 % identity

(U27698) calreticulin [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  206037
                  LIB3083-107-Q1-L1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3355463
BLAST score
                   44
                  1.0e-15
E value
Match length
                  76
% identity
                   89
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   206038
Seq. No.
Seq. ID
                  LIB3083-107-Q1-L1-A8
                  BLASTX
Method
                   q1352664
NCBI GI
BLAST score
                   270
E value
                   5.0e-24
                   59
Match length
% identity
                   90
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
NCBI Description
                   SUBUNIT >qi 2117984 pir S52660 phosphoprotein phosphatase
                   (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana
                   >gi 473259 (U08047) Ser/Thr protein phosphatase
                   [Arabidopsis thaliana] >gi 4204949 (U60136)
                   serine/threonine protein phosphatase 2A-4 catalytic subunit
                   [Arabidopsis thaliana]
                   206039
Seq. No.
Seq. ID
                   LIB3083-107-Q1-L1-A9
Method
                   BLASTX
                   q1495273
NCBI GI
BLAST score
                   259
                   9.0e-23
E value
Match length
                   65
% identity
                   82
                  (Z50752) sugar transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206040
Seq. ID
                   LIB3083-107-Q1-L1-B1
Method
                   BLASTX
NCBI GI
                   q4115384
BLAST score
                   443
E value
                   3.0e-44
Match length
                   96
% identity
                   84
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206041
                   LIB3083-107-Q1-L1-B10
Seq. ID
Method
                   BLASTN
```

g2829205

NCBI GI BLAST score 149 E value 2.0e-78 209 Match length 93 % identity

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

-,2

Method

NCBI GI

BLASTX

q1477428



## precursor (PRP) mRNA, complete cds

```
206042
Seq. No.
                  LIB3083-107-Q1-L1-B3
Seq. ID
Method
                  BLASTN
                  g496494
NCBI GI
                  32
BLAST score
                  1.0e-08
E value
                  56
Match length
                  89
% identity
NCBI Description P.vulgata alpha tub 2 mRNA
                  206043
Seq. No.
                  LIB3083-107-Q1-L1-B4
Seq. ID
                  BLASTX
Method
                  g2341034
NCBI GI
                   457
BLAST score
                  5.0e-46
E value
                   94
Match length
                   96
% identity
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206044
                  LIB3083-107-Q1-L1-B5
Seq. ID
                  BLASTX
Method
                   q4204315
NCBI GI
                   230
BLAST score
                   2.0e-19
E value
                   78
Match length
                   58
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206045
Seq. ID
                   LIB3083-107-Q1-L1-B7
                   BLASTX
Method
NCBI GI
                   q870794
BLAST score
                   170
                   1.0e-12
E value
                   66
Match length
                   10
% identity
                  (L05917) polyubiquitin [Arabidopsis thaliana]
NCBI Description
                   206046
Seq. No.
                   LIB3083-107-Q1-L1-B8
Seq. ID
                   BLASTX
Method
                   g2462746
NCBI GI
BLAST score
                   353
                   9.0e-34
E value
                   81
Match length
                   83
% identity
                   (ACO02292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   206047
Seq. No.
Seq. ID
                   LIB3083-107-Q1-L1-B9
```



BLAST score 231
E value 2.0e-19
Match length 43
% identity 100
NCBI Description (X99623) alpha-tub

NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 206048

Seq. ID LIB3083-107-Q1-L1-C1

Method BLASTN
NCBI GI g4165340
BLAST score 34
E value 1.0e-09
Match length 90
% identity 84

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 206049

Seq. ID LIB3083-107-Q1-L1-C10

Method BLASTX
NCBI GI g1524370
BLAST score 229
E value 3.0e-19
Match length 62
% identity 71

NCBI Description (X92491) TOM20 [Solanum tuberosum]

Seq. No. 206050

Seq. ID LIB3083-107-Q1-L1-C2

Method BLASTX
NCBI GI g2191150
BLAST score 431
E value 6.0e-43
Match length 94
% identity 39

NCBI Description (AF007269) similar to mitochondrial carrier family

[Arabidopsis thaliana]

Seq. No. 206051

Seq. ID LIB3083-107-Q1-L1-C3

Method BLASTX
NCBI GI g2760362
BLAST score 447
E value 8.0e-45
Match length 94
% identity 90

NCBI Description (AF016511) 15.9 kDa subunit of RNA polymerase II

[Arabidopsis thaliana]

Seq. No. 206052

Seq. ID LIB3083-107-Q1-L1-C8

Method BLASTN
NCBI GI g1143223
BLAST score 268
E value 1.0e-149
Match length 288
% identity 40





# NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

 Seq. No.
 206053

 Seq. ID
 LIB3083-107-Q1-L1-C9

 Method
 BLASTN

 NCBI GI
 g2829205

 BLAST score
 262

 E value
 1.0e-146

 Match length
 274

% identity 27
NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 206054

Seq. ID LIB3083-107-Q1-L1-D12

Method BLASTX
NCBI GI g1742951
BLAST score 468
E value 3.0e-47
Match length 92
% identity 96

NCBI Description (Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 206055

Seq. ID LIB3083-107-Q1-L1-D2

Method BLASTX
NCBI GI g3046703
BLAST score 299
E value 1.0e-27
Match length 74
% identity 76

NCBI Description (AL021749) protein kinase ADK1-like protein [Arabidopsis

thaliana]

Seq. No. 206056

Seq. ID LIB3083-107-Q1-L1-D4

Method BLASTX
NCBI GI g1352664
BLAST score 308
E value 2.0e-28
Match length 65
% identity 92

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC

SUBUNIT >gi 2117984\_pir\_\_S52660 phosphoprotein phosphatase

(EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi\_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi\_4204949 (U60136)

serine/threonine protein phosphatase 2A-4 catalytic subunit

[Arabidopsis thaliana]

Seq. No. 206057

Seq. ID LIB3083-107-Q1-L1-D6

Method BLASTX
NCBI GI g1743277
BLAST score 429
E value 9.0e-43
Match length 89

% identity

NCBI Description



% identity (Y09741) beta-tubulin 1 [Hordeum vulgare] NCBI Description 206058 Seq. No. LIB3083-107-Q1-L1-D7 Seq. ID BLASTX Method g1335862 NCBI GI 460 BLAST score 3.0e-46 E value 95 Match length 94 % identity (U42608) clathrin heavy chain [Glycine max] NCBI Description 206059 Seq. No. LIB3083-107-Q1-L1-E1 Seq. ID Method BLASTX NCBI GI g1174718 158 BLAST score 3.0e-11 E value 66 Match length 58 % identity PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR NCBI Description >gi 322579\_pir\_\_JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi\_166888 (L00670) protein kinase [Arabidopsis thaliana] 206060 Seq. No. LIB3083-107-Q1-L1-E10 Seq. ID BLASTX Method g4558556 NCBI GI 148 BLAST score 6.0e-10 E value 56 Match length 45 % identity (AC007138) predicted protein of unknown function NCBI Description [Arabidopsis thaliana] 206061 Seq. No. LIB3083-107-Q1-L1-E3 Seq. ID BLASTN Method NCBI GI g516853 39 BLAST score 1.0e-12 E value 73 Match length % identity Soybean SUBI-2 gene for ubiquitin, complete cds NCBI Description 206062 Seq. No. Seq. ID LIB3083-107-Q1-L1-E8 BLASTX Method q1706958 NCBI GI BLAST score 178 3.0e-13 E value 53 Match length

(U58284) cellulose synthase [Gossypium hirsutum]

Method

NCBI GI

BLASTX

g1854386



```
Seq. No.
                  LIB3083-107-Q1-L1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1703380
BLAST score
                  364
                  4.0e-35
E value
                  73
Match length
                   99
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
                  206064
Seq. No.
                  LIB3083-107-Q1-L1-F1
Seq. ID
                  BLASTX
Method
                  g1707642
NCBI GI
                  180
BLAST score
                   8.0e-14
E value
                   66
Match length
                   62
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
                   206065
Seq. No.
                  LIB3083-107-Q1-L1-F10
Seq. ID
                  BLASTX
Method
                   g4006876
NCBI GI
BLAST score
                   167
                   6.0e-12
E value
                   85
Match length
                   46
% identity
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   206066
Seq. No.
                   LIB3083-107-Q1-L1-F12
Seq. ID
Method
                   BLASTX
                   q3935145
NCBI GI
BLAST score
                   188
                   2.0e-14
E value
                   62
Match length
                   56
% identity
                   (AC005106) T25N20.9 [Arabidopsis thaliana]
NCBI Description
                   206067
Seq. No.
Seq. ID
                   LIB3083-107-Q1-L1-F2
                   BLASTX
Method
                   q549975
NCBI GI
BLAST score
                   184
E value
                   6.0e-14
Match length
                   78
                   53
% identity
                   (U12858) nucleosome assembly protein I-like protein;
NCBI Description
                   similar to mouse nap I, PIR Accession Number JS0707
                   [Arabidopsis thaliana]
Seq. No.
                   206068
                   LIB3083-107-Q1-L1-F4
Seq. ID
```

Seq. No.

Seq. ID

206073

LIB3083-107-Q1-L1-G11



```
BLAST score
                  5.0e-25
E value
                  86
Match length
                  66
% identity
                  (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                  vinifera]
                  206069
Seq. No.
                  LIB3083-107-Q1-L1-F6
Seq. ID
Method
                  BLASTX
                  g2499488
NCBI GI
                  432
BLAST score
                  5.0e-43
E value
                  93
Match length
                  84
% identity
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi 483547_emb_CAA83682_ (Z32849)
                  pyrophosphate-dependent phosphofructokinase alpha subunit
                   [Ricinus communis]
                  206070
Seq. No.
                  LIB3083-107-Q1-L1-F9
Seq. ID
Method
                  BLASTX
                  g1903034
NCBI GI
                  247
BLAST score
                  3.0e-21
E value
                  97
Match length
                  51
% identity
NCBI Description (X94625) amp-binding protein [Brassica napus]
Seq. No.
                  206071
                  LIB3083-107-Q1-L1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2194132
BLAST score
                   348
                   4.0e-33
E value
                   94
Match length
                   73
% identity
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                   206072
Seq. No.
                  LIB3083-107-Q1-L1-G10
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
BLAST score
                   491
                   4.0e-50
E value
Match length
                   93
                   98
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

```
BLASTX
Method
NCBI GI
                   g3860317
                   200
BLAST score
                   8.0e-16
E value
                   41
Match length
                   95
% identity
                   (AJ012685) actin [Cicer arietinum]
NCBI Description
                   206074
Seq. No.
                   LIB3083-107-Q1-L1-G3
Seq. ID
                   BLASTX
```

Method NCBI GI q4539401 BLAST score 159 4.0e-11 E value Match length 87 48 % identity

(AL035526) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. LIB3083-107-Q1-L1-G6 Seq. ID BLASTN Method q4098126 NCBI GI BLAST score 55 E value 3.0e-22

75 Match length 100 % identity

Gossypium hirsutum sucrose synthase mRNA, partial cds NCBI Description

206076 Seq. No.

LIB3083-107-Q1-L1-G9 Seq. ID

BLASTX Method g1076627 NCBI GI BLAST score 354 6.0e - 34E value Match length 94 78 % identity

inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco NCBI Description

>gi 790479\_emb\_CAA58701\_ (X83730) inorganic pyrophosphatase

[Nicotiana tabacum]

206077 Seq. No.

LIB3083-107-Q1-L1-H5 Seq. ID

BLASTX Method g3135265 NCBI GI 342 BLAST score 1.0e-32 E value 85 Match length 73 % identity

(AC003058) unknown protein [Arabidopsis thaliana] NCBI Description

206078 Seq. No.

LIB3083-107-Q1-L1-H7 Seq. ID

BLASTX Method g4309738 NCBI GI 283 BLAST score 1.0e-25 E value 73 Match length

% identity (AC006439) putative tubby protein [Arabidopsis thaliana] NCBI Description 206079 Seq. No. LIB3083-107-Q1-L1-H8 Seq. ID BLASTN Method g2828278 NCBI GI 51 BLAST score 7.0e-20 E value 119 Match length 86 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 NCBI Description (ESSAII project) 206080 Seq. No. Seq. ID LIB3083-107-Q1-L1-H9 BLASTX Method g3023751 NCBI GI 386 BLAST score 1.0e-37 E value 95 Match length % identity 81 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS NCBI Description ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772 pir S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase [Trīticum aestīvum] 206081 Seq. No. Seq. ID LIB3083-108-Q1-L1-A1 BLASTX Method NCBI GI g4510342 BLAST score 201 3.0e-16 E value 75 Match length 52 % identity (AC006921) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana]

206082 Seq. No.

Seq. ID LIB3083-108-Q1-L1-A11

Method BLASTX NCBI GI q4490301 191 BLAST score 1.0e-14 E value 77 Match length 55 % identity

(AL035678) hypothetical protein [Arabidopsis thaliana] NCBI Description

206083 Seq. No.

Seq. ID LIB3083-108-Q1-L1-A12

Method BLASTX NCBI GI q2129473 BLAST score 319 E value 1.0e-29 Match length 125 % identity 49



```
NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774
                  (U09556) arabinogalactan-like protein [Pinus taeda]
                  206084
Seq. No.
                  LIB3083-108-Q1-L1-A2
Seq. ID
                  BLASTX
Method
                  g3548818
NCBI GI
                  249
BLAST score
                   2.0e-21
E value
                   70
Match length
                   67
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206085
Seq. No.
                   LIB3083-108-Q1-L1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2065531
BLAST score
                   434
                   4.0e-43
E value
                   113
Match length
                   68
% identity
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
                   206086
Seq. No.
                   LIB3083-108-Q1-L1-A6
Seq. ID
                   BLASTX
Method
                   q4519417
NCBI GI
                   385
BLAST score
                   3.0e-37
E value
                   112
Match length
% identity
                   62
                   (AB024327) WD-40 repeat protein [Homo sapiens]
NCBI Description
                   206087
Seq. No.
                   LIB3083-108-Q1-L1-A7
Seq. ID
                   BLASTX
Method
                   g3264759
NCBI GI
                   394
BLAST score
                   3.0e-41
E value
                   124
Match length
                   74
 % identity
                   (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
NCBI Description
                   206088
 Seq. No.
                   LIB3083-108-Q1-L1-A9
 Seq. ID
                   BLASTX
Method
                   g4539351
 NCBI GI
                   439
 BLAST score
                   1.0e-43
 E value
                   113
 Match length
 % identity
                   (AL035539) putative protein [Arabidopsis thaliana]
```

206089 Seq. No.

NCBI Description

LIB3083-108-Q1-L1-B10 Seq. ID

BLASTX Method NCBI GI g2281102



```
BLAST score
                   5.0e-10
E value
                   32
Match length
                   88
% identity
                   (AC002333) SF16 isolog [Arabidopsis thaliana]
NCBI Description
                   206090
Seq. No.
                  LIB3083-108-Q1-L1-B11
Seq. ID
                  BLASTX
Method
                   g2832642
NCBI GI
                   147
BLAST score
                   2.0e-09
E value
                   83
Match length
                   22
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
                   206091
Seq. No.
                   LIB3083-108-Q1-L1-B2
Seq. ID
                   BLASTN
Method
                   g1706955
NCBI GI
BLAST score
                   290
E value
                   1.0e-162
                   290
Match length
                   100
% identity
                   Gossypium hirsutum cellulose synthase (celA1) mRNA,
NCBI Description
                   complete cds
                   206092
Seq. No.
Seq. ID
                   LIB3083-108-Q1-L1-B3
                   BLASTX
Method
NCBI GI
                   g1173327
BLAST score
                   419
                   3.0e-41
E value
                   86
Match length
                   92
% identity
                   U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')
NCBI Description
                   >gi 322619 pir S30580 U2 snRNP protein A' - Arabidopsis
                   thaliana >gi 17669 emb CAA48890 (X69137) U2 small nuclear
                   ribonucleoprotein A' [Arabidopsis thaliana]
                   206093
Seq. No.
                   LIB3083-108-Q1-L1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2661840
BLAST score
                   353
                   1.0e-33
E value
Match length
                   100
% identity
                   66
                   (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
                   206094
Seq. No.
Seq. ID
                   LIB3083-108-Q1-L1-B5
                   BLASTX
Method
```

NCBI GI g4417283
BLAST score 237
E value 7.0e-20
Match length 108



```
% identity
                  (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                  206095
Seq. No.
Seq. ID
                  LIB3083-108-Q1-L1-B6
                  BLASTX
Method
                  g4097579
NCBI GI
                  592
BLAST score
                  1.0e-61
E value
                  126
Match length
% identity
                 (U64922) NTGP1 [Nicotiana tabacum]
NCBI Description
                   206096
Seq. No.
                  LIB3083-108-Q1-L1-B8
Seq. ID
                   BLASTX
Method
                   g602076
NCBI GI
                   251
BLAST score
                   1.0e-21
E value
                   55
Match length
                   22
% identity
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                   206097
Seq. No.
                   LIB3083-108-Q1-L1-C11
Seq. ID
                   BLASTX
Method
                   q1743277
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   72
Match length
                   92
% identity
                  (Y09741) beta-tubulin 1 [Hordeum vulgare]
NCBI Description
                   206098
Seq. No.
                   LIB3083-108-Q1-L1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2894534
                   527
BLAST score
                   6.0e-54
E value
                   124
Match length
                   84
% identity
                   (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                   206099
Seq. No.
Seq. ID
                   LIB3083-108-Q1-L1-C3
                   BLASTX
Method
NCBI GI
                   q4249382
                   522
BLAST score
```

2.0e-53 E value 119 Match length % identity

(AC005966) Strong similarity to gi\_3337350 F13P17.3 NCBI Description

putative permease from Arabidopsis thaliana BAC

gb\_AC004481. [Arabidopsis thaliana]

206100 Seq. No.

LIB3083-108-Q1-L1-C4 Seq. ID



```
BLASTX
Method
                   q1421730
NCBI GI
BLAST score
                   337
                   1.0e-31
E value
                   87
Match length
                   75
% identity
                   (U43082) RF2 [Zea mays]
NCBI Description
                   206101
Seq. No.
                   LIB3083-108-Q1-L1-C5
Seq. ID
                   BLASTX
Method
                   g2661840
NCBI GI
                   252
BLAST score
                   1.0e-21
E value
                   64
Match length
                   75
% identity
                   (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
                   206102
Seq. No.
                   LIB3083-108-Q1-L1-C6
Seq. ID
                   BLASTX
Method
                   g4558672
NCBI GI
                   204
BLAST score
                   4.0e-16
E value
                   106
Match length
                   45
% identity
                   (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
                   thaliana]
                   206103
Seq. No.
Seq. ID
                   LIB3083-108-Q1-L1-C7
Method
                   BLASTX
                   q3212869
NCBI GI
                   604
BLAST score
                   6.0e-63
E value
Match length
                   129
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206104
Seq. No.
Seq. ID
                   LIB3083-108-Q1-L1-C8
                   BLASTN
Method
NCBI GI
                   q2980787
BLAST score
                   39
                   1.0e-12
E value
Match length
                   75
 % identity
                   88
                   Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2
NCBI Description
                   (ESSAII project)
                   206105
 Seq. No.
                   LIB3083-108-Q1-L1-C9
 Seq. ID
Method
                   BLASTX
```

NCBI GI g2642448 BLAST score 250 2.0e-21 E value Match length 106



% identity 27

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 206106

Seq. ID LIB3083-108-Q1-L1-D1

Method BLASTX
NCBI GI g1402878
BLAST score 360
E value 2.0e-34
Match length 113

Match length 11: 8 identity 59

NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 206107

Seq. ID LIB3083-108-Q1-L1-D10

Method BLASTX
NCBI GI g3201615
BLAST score 442
E value 5.0e-44
Match length 108

% identity 81

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 206108

Seq. ID LIB3083-108-Q1-L1-D3

Method BLASTN
NCBI GI g1143223
BLAST score 359
E value 0.0e+00
Match length 397
% identity 57

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 206109

Seq. ID LIB3083-108-Q1-L1-D8

Method BLASTX
NCBI GI g3024501
BLAST score 614
E value 4.0e-64
Match length 122
% identity 98

NCBI Description RAS-RELATED PROTEIN RAB11C >gi\_1370146\_emb\_CAA98179\_

(Z73951) RAB11C [Lotus japonicus]

Seq. No. 206110

Seq. ID LIB3083-108-Q1-L1-D9

Method BLASTX
NCBI GI g1730635
BLAST score 160
E value 7.0e-11
Match length 102
% identity 37

NCBI Description HYPOTHETICAL 40.7 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION

>gi\_2132777\_pir\_\_S60917 probable membrane protein YNL264c yeast (Saccharomyces cerevisiae) >gi\_1045245\_emb\_CAA63233\_

E value

Match length

% identity

4.0e-35 112

NCBI Description heat shock protein 17.7 - garden pea

65



(X92494) ORF N0815 [Saccharomyces cerevisiae]
>gi\_1302321\_emb\_CAA96171\_ (Z71540) ORF YNL264c
[Saccharomyces cerevisiae]

```
206111
Seq. No.
Seq. ID
                  LIB3083-108-Q1-L1-E1
Method
                  BLASTX
                  q4558664
NCBI GI
BLAST score
                  390
E value
                  8.0e-38
                  136
Match length
                  13
% identity
                  (AC007063) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  206112
Seq. No.
Seq. ID
                  LIB3083-108-Q1-L1-E11
                  BLASTX
Method
NCBI GI
                  g2829911
BLAST score
                  266
E value
                  2.0e-23
Match length
                  82
                   61
% identity
                  (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  206113
Seq. No.
                  LIB3083-108-Q1-L1-E2
Seq. ID
                  BLASTX
Method
                  g2213643
NCBI GI
                  146
BLAST score
                   2.0e-09
E value
Match length
                   49
% identity
                   61
                  (U57338) glossyl homolog [Oryza sativa]
NCBI Description
                   206114
Seq. No.
Seq. ID
                  LIB3083-108-Q1-L1-E7
                   BLASTX
Method
                   q1172874
NCBI GI
BLAST score
                   365
E value
                   5.0e-35
Match length
                   132
                   59
% identity
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                   >qi 479589 pir S34823 dehydration-induced protein RD22 -
                   Arabidopsis thaliana >gi 391608 dbj BAA01546 (D10703) rd22
                   [Arabidopsis thaliana] >qi 447134 prf 1913421A rd22 gene
                   [Arabidopsis thaliana]
Seq. No.
                   206115
                   LIB3083-108-Q1-L1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g71498
BLAST score
                   366
```

% identity

NCBI Description

thaliana]



```
206116
Seq. No.
                  LIB3083-108-Q1-L1-F10
Seq. ID
                  BLASTX
Method
                  g464840
NCBI GI
                  497
BLAST score
                  2.0e-50
E value
                  119
Match length
                  86
% identity
                  TUBULIN ALPHA-1 CHAIN >gi_421781_pir S32666 tubulin
NCBI Description
                  alpha-1 chain - fern (Anemia phyllitidis)
                  >gi 296494 emb CAA48927_ (X69183) alpha tubulin [Anemia
                  phyllitidis]
                  206117
Seq. No.
                  LIB3083-108-Q1-L1-F11
Seq. ID
Method
                  BLASTX
                  g3548803
NCBI GI
BLAST score
                  504
E value
                  3.0e-51
Match length
                  115
                  89
% identity
                  (AC005313) putative DNA-binding protein [Arabidopsis
NCBI Description .
                   thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative
                   SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
                   206118
Seq. No.
                  LIB3083-108-Q1-L1-F4
Seq. ID
                   BLASTN
Method
                   g4151090
NCBI GI
                   33
BLAST score
                   6.0e-09
E value
Match length
                   53
                   91
% identity
                  Stylosanthes guianensis microsatellite SSR1-24
NCBI Description
                   206119
Seq. No.
                   LIB3083-108-Q1-L1-F5
Seq. ID
                   BLASTX
Method
                   g1871185
NCBI GI
BLAST score
                   574
                   2.0e-59
E value
                   127
Match length
                   82
% identity
                  (U90439) seven in absentia isolog [Arabidopsis thaliana]
NCBI Description
                   206120
Seq. No.
                   LIB3083-108-Q1-L1-F6
Seq. ID
                   BLASTX
Method
                   g4455206
NCBI GI
BLAST score
                   372
                   8.0e-36
E value
                   96
Match length
                   73
```

(AL035440) putative beta-1, 3-glucanase [Arabidopsis

Seq. No. 206121 LIB3083-108-Q1-L1-F9 Seq. ID BLASTX Method g2129495 NCBI GI 445 BLAST score 8.0e-46 E value 113 Match length 83 % identity fiber protein E6 (clone SIE6-2A) - sea-island cotton NCBI Description >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi\_1000090  $(U3\overline{0}508)$  E6 [Gossypium barbadense] 206122 Seq. No. LIB3083-108-Q1-L1-G11 Seq. ID Method BLASTN g1143223 NCBI GI BLAST score 219 1.0e-120 E value 346 Match length 29 % identity Gossypium barbadense FbLate-2 gene, complete cds NCBI Description Seq. No. 206123 LIB3083-108-Q1-L1-G6 Seq. ID Method BLASTX NCBI GI g1332579 BLAST score 548 E value 9.0e-58 121 Match length % identity (X98063) polyubiquitin [Pinus sylvestris] NCBI Description Seq. No. 206124 LIB3083-108-Q1-L1-G7 Seq. ID Method BLASTX g3287691 NCBI GI 145 BLAST score 3.0e-09 E value

92 Match length 38 % identity

(AC003979) Contains similarity to RING zinc finger protein NCBI Description

gb X95455 from Gallus gallus. [Arabidopsis thaliana]

206125 Seq. No.

LIB3083-108-Q1-L1-G8 Seq. ID

Method BLASTX q1729980 NCBI GI 286 BLAST score 8.0e-26 E value 61 Match length % identity

THAUMATIN-LIKE PROTEIN PRECURSOR >gi 2129751 pir\_S71175 NCBI Description

thaumatin-like protein - Arabidopsis thaliana >gi\_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana]

>gi 1094863 prf 2106421A thaumatin-like protein

[Arabidopsis thaliana]



```
206126
Seq. No.
                  LIB3083-108-Q1-L1-G9
Seq. ID
                  BLASTX
Method
                  g1531674
NCBI GI
                  581
BLAST score
                  3.0e-60
E value
                  131
Match length
                  84
% identity
                  (U68462) actin [Striga asiatica]
NCBI Description
                  206127
Seq. No.
                  LIB3083-108-Q1-L1-H11
Seq. ID
Method
                  BLASTN
                   q2921165
NCBI GI
BLAST score
                   38
                   5.0e-12
E value
Match length
                   102
% identity
                   85
                  Solanum tuberosum ATP synthase gamma chain mRNA, nuclear
NCBI Description
                   gene encoding mitochondrial protein, partial cds
                   206128
Seq. No.
Seq. ID
                   LIB3083-108-Q1-L1-H3
Method
                   BLASTX
                   g606942
NCBI GI
                   597
BLAST score
                   4.0e-62
E value
Match length
                   123
% identity
                   96
                  (U13760) unknown [Gossypium hirsutum]
NCBI Description
                   206129
Seq. No.
                   LIB3083-108-Q1-L1-H4
Seq. ID
                   BLASTX
Method
                   g3123100
NCBI GI
                   236
BLAST score
                   8.0e-20
E value
                   93
Match length
                   49
% identity
                   HYPOTHETICAL 15.9 KD PROTEIN C4A8.02C IN CHROMOSOME I
NCBI Description
                   >gi 4490640 emb CAB11472.1 (Z98762) SPAC4A8.02c, unknown,
                   len:142aa, similar eg. to YJBQ ECOLI, P32698, hypothetical
                   15.7 kd protein, (138aa), fast \overline{a} scores, opt:403, E():
                   2.4e-32, (41.0% identity in 134 aa overlap)
                   [Schizosaccharomyces pombe]
                   206130
 Seq. No.
                   LIB3083-108-Q1-L1-H5
 Seq. ID
                   BLASTX
Method
                   g2827143
NCBI GI
BLAST score
                   465
                   1.0e-46
```

E value Match length 107 80 % identity

(AF027174) cellulose synthase catalytic subunit NCBI Description

[Arabidopsis thaliana]



```
Seq. No.
                  LIB3083-108-Q1-L1-H7
Seq. ID
                  BLASTX
Method
                  g136636
NCBI GI
                  576
BLAST score
                  1.0e-59
E value
Match length
                  107
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                  >gi 1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                  Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                  Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                  Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                  >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                  thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
                  206132
Seq. No.
                  LIB3083-108-Q1-L1-H8
Seq. ID
                  BLASTX
Method
                   q729880
NCBI GI
                   581
BLAST score
E value
                   2.0e-60
Match length
                   117
                   86
% identity
                  CASEIN KINASE II BETA CHAIN (CK II) >gi 1076299 pir S47967
NCBI Description
                   casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis
                   thaliana >gi 468264 (L22563) casein kinase II beta subunit
                   CKB1 [Arabidopsis thaliana]
                   206133
Seq. No.
                   LIB3083-108-Q1-L1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4193388
BLAST score
                   418
                   2.0e-41
E value
                   90
Match length
                   89
% identity
                   (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                   brasiliensis]
                   206134
Seq. No.
                   LIB3083-109-Q1-L1-A10
Seq. ID
Method
                   BLASTX
                   g3935176
NCBI GI
BLAST score
                   285
E value
                   1.0e-25
                   77
Match length
 % identity
                   69
                  (AC004557) F17L21.19 [Arabidopsis thaliana]
```

NCBI Description

206135 Seq. No.

LIB3083-109-Q1-L1-A11 Seq. ID

BLASTX Method g3080420 NCBI GI 389 BLAST score

9.0e-38 E value Match length 115 % identity (AL022604) putative sugar transporter protein [Arabidopsis NCBI Description thaliana] 206136 Seq. No. LIB3083-109-Q1-L1-A3 Seq. ID Method BLASTX NCBI GI g4469023 283 BLAST score 2.0e-25 E value 118 Match length 52 % identity NCBI Description (AL035602) putative protein [Arabidopsis thaliana] 206137 Seq. No. Seq. ID LIB3083-109-Q1-L1-A4 BLASTX Method g2660677 NCBI GI BLAST score 307 E value 4.0e-41117 Match length 73 % identity (AC002342) unknown protein [Arabidopsis thaliana] NCBI Description 206138 Seq. No. LIB3083-109-Q1-L1-A5 Seq. ID BLASTX Method g2281115 NCBI GI BLAST score 291 E value 3.0e-26 Match length 70 79 % identity (AC002330) putative cullin-like 1 protein [Arabidopsis NCBI Description thaliana] 206139 Seq. No. Seq. ID LIB3083-109-Q1-L1-A6 Method BLASTX NCBI GI g267077 BLAST score 348 2.0e-46 E value Match length 120 % identity 81 TUBULIN BETA-5 CHAIN >qi 320186 pir JQ1589 tubulin beta-5 NCBI Description chain - Arabidopsis thaliana >gi 166902 (M84702) beta-5

tubulin [Arabidopsis thaliana]

206140 Seq. No.

LIB3083-109-Q1-L1-A8 Seq. ID

Method BLASTX NCBI GI q960289 BLAST score 538 3.0e-55 E value Match length 120 % identity 88



NCBI Description (L34343) anthranilate synthase alpha subunit [Ruta graveolens]

Seq. No. 206141

Seq. ID LIB3083-109-Q1-L1-B1

Method BLASTX
NCBI GI g3885343
BLAST score 234
E value 1.0e-19

Match length 80 % identity 49

NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No. 206142

Seq. ID LIB3083-109-Q1-L1-B10

Method BLASTX
NCBI GI g2244861
BLAST score 244
E value 8.0e-21
Match length 83
% identity 61

NCBI Description (Z97337) cucumisin [Arabidopsis thaliana]

Seq. No. 206143

Seq. ID LIB3083-109-Q1-L1-B12

Method BLASTX
NCBI GI g3868758
BLAST score 484
E value 5.0e-49
Match length 93
% identity 92

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 206144

Seq. ID LIB3083-109-Q1-L1-B2

Method BLASTN
NCBI GI g4126472
BLAST score 226
E value 1.0e-124
Match length 282
% identity 98

NCBI Description Gossypium hirsutum GhCAP mRNA for adenylyl cyclase

associated protein, complete cds

Seq. No. 206145

Seq. ID LIB3083-109-Q1-L1-B4

Method BLASTX
NCBI GI g1841464
BLAST score 617
E value 2.0e-64
Match length 121
% identity 53

NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 206146

Seq. ID LIB3083-109-Q1-L1-B5

Method BLASTX



```
g2252841
NCBI GI
                  227
BLAST score
                  8.0e-19
E value
                  108
Match length
                  50
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206147
                  LIB3083-109-Q1-L1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1477428
                  645
BLAST score
                  8.0e-68
E value
                  120
Match length
                  98
% identity
                 (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
                  206148
Seq. No.
                  LIB3083-109-Q1-L1-C10
Seq. ID
                  BLASTX
Method
                  g3885334
NCBI GI
BLAST score
                  541
                  1.0e-55
E value
                  120
Match length
                  85
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  206149
Seq. No.
                  LIB3083-109-Q1-L1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172001
                  281
BLAST score
                   4.0e-25
E value
                   85
Match length
                   68
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 541843 pir JQ2265
NCBI Description
                   phenylalanine ammonia-lyase (EC 4.3.1.5) - western balsam
                   poplar x cottonwood >gi 169454 (L11747) phenylalanine
                   ammonia lyase [Populus trichocarpa x Populus deltoides]
                   206150
Seq. No.
Seq. ID
                   LIB3083-109-Q1-L1-C2
                   BLASTX
Method
NCBI GI
                   q3114901
                   216
BLAST score
                   2.0e-17
E value
                   54
Match length
                   78
% identity
                   (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa]
NCBI Description
                   >gi 3114905 emb CAA06709 (AJ005806) pceberh [Populus
                   balsamifera subsp. trichocarpa]
```

206151 Seq. No.

Seq. ID LIB3083-109-Q1-L1-C3

Method BLASTX NCBI GI g1706956

NCBI Description

hirsutum]



```
BLAST score
                   2.0e-29
E value
                   64
Match length
                   98
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   206152
Seq. No.
                  LIB3083-109-Q1-L1-C4
Seq. ID
                  BLASTX
Method
                   g3668086
NCBI GI
BLAST score
                   262
                   3.0e-25
E value
                   117
Match length
                   52
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                   206153
Seq. No.
                   LIB3083-109-Q1-L1-C7
Seq. ID
                   BLASTX
Method
                   g3080412
NCBI GI
                   356
BLAST score
E value
                   6.0e - 34
                   119
Match length
                   58
% identity
                   (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   206154
Seq. No.
                   LIB3083-109-Q1-L1-C9
Seq. ID
                   BLASTX
Method
                   g1841464
NCBI GI
                   607
BLAST score
E value
                   2.0e-63
Match length
                   118
                   53
% identity
                  (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
NCBI Description
                   206155
Seq. No.
Seq. ID
                   LIB3083-109-Q1-L1-D1
                   BLASTX
Method
NCBI GI
                   q3309170
BLAST score
                   277
                   1.0e-24
E value
Match length
                   118
                   49
% identity
                   (AF071314) COP9 complex subunit 4 [Mus musculus]
NCBI Description
Seq. No.
                   206156
                   LIB3083-109-Q1-L1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2829204
BLAST score
                   423
E value
                   8.0e-42
Match length
                   102
% identity
                   85
```

(AF044204) lipid transfer protein precursor [Gossypium



```
206157
Seq. No.
                  LIB3083-109-Q1-L1-D3
Seq. ID
                  BLASTX
Method
                  g4204575
NCBI GI
                  386
BLAST score
                  2.0e-37
E value
                  109
Match length
                  68
% identity
                  (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
NCBI Description
                  206158
Seq. No.
                  LIB3083-109-Q1-L1-D4
Seq. ID
Method
                  BLASTX
                  q3080414
NCBI GI
                   195
BLAST score
                   2.0e-15
E value
Match length
                   42
% identity
                   88
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   206159
Seq. No.
Seq. ID
                   LIB3083-109-Q1-L1-D5
Method
                   BLASTX
NCBI GI
                   g2529665
BLAST score
                   426
                   4.0e-42
E value
Match length
                   107
                   79
% identity
                   (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                   thaliana]
                   206160
Seq. No.
Seq. ID
                   LIB3083-109-Q1-L1-D7
Method
                   BLASTN
NCBI GI
                   g2829205
                   315
BLAST score
                   1.0e-177
E value
                   323
Match length
% identity
                   90
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
                   206161
Seq. No.
Seq. ID
                   LIB3083-109-Q1-L1-D8
                   BLASTX
Method
                   q3763925
NCBI GI
                   515
BLAST score
                   1.0e-52
E value
                   110
Match length
                   87
% identity
                  (AC004450) putative Af10-protein [Arabidopsis thaliana]
NCBI Description
                   206162
Seq. No.
Seq. ID
                   LIB3083-109-Q1-L1-D9
```

28250

BLASTX

g425194 542

Method NCBI GI

BLAST score



90

[Arabidopsis thaliana]

% identity NCBI Description

```
E value
                   9.0e-56
Match length
                  118
% identity
                  88
                  (L26243) heat shock protein [Spinacia oleracea] >gi 2660772
NCBI Description
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
                  oleracea]
Seq. No.
                  206163
Seq. ID
                  LIB3083-109-Q1-L1-E1
Method
                  BLASTX
NCBI GI
                  g2558654
                  385
BLAST score
                  2.0e-37
E value
                  103
Match length
% identity
                  65
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.
                  206164
                  LIB3083-109-Q1-L1-E11
Seq. ID
Method
                  BLASTX
                  q3687240
NCBI GI
                  141
BLAST score
                  1.0e-08
E value
                  34
Match length
% identity
                  71
NCBI Description (AC005169) extensin-like protein [Arabidopsis thaliana]
Seq. No.
                  206165
Seq. ID
                  LIB3083-109-Q1-L1-E12
Method
                  BLASTX
NCBI GI
                  q1669573
BLAST score
                  618
E value
                  1.0e-64
                  122
Match length
                  93
% identity
NCBI Description (D88399) endosperm kinase [Oryza sativa]
Seq. No.
                  206166
                  LIB3083-109-Q1-L1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402722
BLAST score
                  240
E value
                  2.0e-20
Match length
                  94
% identity
                  47
NCBI Description (AC004261) CPDK-related protein [Arabidopsis thaliana]
Seq. No.
                  206167
Seq. ID
                  LIB3083-109-Q1-L1-E4
Method
                  BLASTX
NCBI GI
                  q2351374
BLAST score
                  591
E value
                  2.0e-61
Match length
                  120
```

28251

(U54560) putative 26S proteasome subunit athMOV34



206168 Seq. No. LIB3083-109-Q1-L1-E5 Seq. ID BLASTX Method g118926 NCBI GI BLAST score 183 1.0e-13 E value 123 Match length % identity DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR NCBI Description >gi\_320600\_pir\_\_E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi\_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi 227781 prf\_ 1710351E abscisic acid responsive protein E [Craterostigma plantagineum] 206169 Seq. No. LIB3083-109-Q1-L1-E7 Seq. ID BLASTX Method q586076 NCBI GI 584 BLAST score 1.0e-60 E value Match length 107 % identity 98 TUBULIN BETA-1 CHAIN >gi\_486734\_pir\_\_S35142 tubulin beta NCBI Description chain - white lupine >gi\_402636\_emb\_CAA49736\_ (X70184) Beta tubulin 1 [Lupinus albus] 206170 Seq. No. LIB3083-109-Q1-L1-E8 Seq. ID BLASTX Method g2129613 NCBI GI 158 BLAST score 1.0e-10 E value Match length 108 43 % identity homeotic protein BEL1 - Arabidopsis thaliana >gi\_1122533 NCBI Description (U39944) BELL1 [Arabidopsis thaliana] 206171 Seq. No. LIB3083-109-Q1-L1-E9 Seq. ID BLASTX Method g3183219 NCBI GI 113 BLAST score 2.0e-09 E value 71 Match length 48 % identity

NCBI Description HYPOTHETICAL PROTEIN KIAA0112 (HA0609)

>gi\_434779\_dbj\_BAA04948\_ (D25218) KIAA0112 [Homo sapiens]

Seq. No. 206172

Seq. ID LIB3083-109-Q1-L1-F1

Method BLASTN
NCBI GI g2267582
BLAST score 54
E value 1.0e-21
Match length 97



```
% identity
                  Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA,
NCBI Description
                  complete cds
                  206173
Seq. No.
Seq. ID
                  LIB3083-109-Q1-L1-F11
Method
                  BLASTX
NCBI GI
                   q4455234
BLAST score
                   320
                  1.0e-29
E value
                  119
Match length
                   53
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   206174
Seq. No.
                  LIB3083-109-Q1-L1-F2
Seq. ID
                   BLASTX
Method
                   g2529663
NCBI GI
BLAST score
                   174
                   7.0e-16
E value
Match length
                   101
% identity
                   46
                   (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                   [Arabidopsis Thaliana]
                   206175
Seq. No.
                   LIB3083-109-Q1-L1-F4
Seq. ID
                   BLASTX
Method
                   g3413716
NCBI GI
BLAST score
                   210
E value
                   8.0e-17
                   119
Match length
                   47
% identity
                   (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3643589 (AC005395) unknown protein [Arabidopsis
                   thalliana
                   206176
Seq. No.
Seq. ID
                   LIB3083-109-Q1-L1-F6
                   BLASTX
Method
                   q1706958
NCBI GI
BLAST score
                   653
                   9.0e-69
E value
Match length
                   124
                   99
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   206177
Seq. No.
                   LIB3083-109-Q1-L1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2746787
```

Method BLASTX
NCBI GI g2746787
BLAST score 237
E value 5.0e-20
Match length 81
% identity 57

NCBI Description (AF040642) contains similarity to RNA recognition motifs



### (RNP) [Caenorhabditis elegans]

```
206178
Seq. No.
                  LIB3083-109-Q1-L1-G1
Seq. ID
                  BLASTX
Method
                  g3650032
NCBI GI
                  237
BLAST score
                  5.0e-20
E value
                   49
Match length
                   73
% identity
                   (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
                   206179
Seq. No.
                   LIB3083-109-Q1-L1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2267567
                   406
BLAST score
                   8.0e-40
E value
                   89
Match length
                   87
% identity
                   (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                   x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                   protein 2 [Pelargonium x hortorum]
                   206180
Seq. No.
                   LIB3083-109-Q1-L1-G11
Seq. ID
Method
                   BLASTX
                   q3877951
NCBI GI
                   146
BLAST score
                   2.0e-09
E value
                   43
Match length
                   28
% identity
                   (Z81555) predicted using Genefinder [Caenorhabditis
NCBI Description
                   elegans]
                   206181
Seq. No.
                   LIB3083-109-Q1-L1-G3
Seq. ID
                   BLASTX
Method
                   g1174592
NCBI GI
                   612
BLAST score
                   6.0e-64
E value
                   114
Match length
                   99
 % identity
                   TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   206182
 Seq. No.
                   LIB3083-109-Q1-L1-G4
 Seq. ID
                   BLASTX
 Method
                    g3273202
 NCBI GI
                    161
 BLAST score
                    5.0e-11
 E value
                    47
 Match length
                    70
 % identity
```

NCBI Description (AB010918) responce reactor4 [Arabidopsis thaliana]



```
206183
Seq. No.
Seq. ID
                  LIB3083-109-Q1-L1-G6
Method
                  BLASTN
NCBI GI
                  g1143223
                  263
BLAST score
                  1.0e-146
E value
Match length
                  375
                  27
% identity
                  Gossypium barbadense FbLate-2 gene, complete cds
NCBI Description
                  206184
Seq. No.
```

LIB3083-109-Q1-L1-G7 Seq. ID BLASTX Method NCBI GI g1706958 667 BLAST score

2.0e-70 E value 119 Match length 100 % identity

(U58284) cellulose synthase [Gossypium hirsutum] NCBI Description

206185 Seq. No. LIB3083-109-Q1-L1-G9 Seq. ID BLASTX Method q1709358 NCBI GI 260 BLAST score 1.0e-22 E value 111 Match length

% identity NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE NCBI Description

PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir\_S48859

nucleoside triphosphatase - garden pea

>gi 2129890\_pir\_\_S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea

>gi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase

[Pisum sativum] >gi\_4519173\_dbj\_BAA75506.1\_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

206186

Seq. ID LIB3083-109-Q1-L1-H2

46

BLASTX Method g2497543 NCBI GI BLAST score 309 2.0e-28 E value Match length 72 78 % identity

Seq. No.

PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379 NCBI Description

pyruvate kinase - common tobacco >gi\_444023\_emb\_CAA82628\_

(Z29492) pyruvate kinase [Nicotiana tabacum]

206187 Seq. No.

LIB3083-109-Q1-L1-H3 Seq. ID

BLASTX Method q4185136 NCBI GI BLAST score 426 4.0e-42 E value Match length 123



```
% identity .
                  (AC005724) putative trehalose-6-phosphate synthase
NCBI Description
                  [Arabidopsis thaliana]
                  206188
Seq. No.
Seq. ID
                  LIB3083-109-Q1-L1-H5
Method
                  BLASTX
                  a1706958
NCBI GI
BLAST score
                  418
                  3.0e-63
E value
Match length
                  121
                  85
% identity
                 (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  206189
Seq. No.
                  LIB3083-109-Q1-L1-H6
Seq. ID
                  BLASTX
Method
                  g2129758
NCBI GI
                  206
BLAST score
                  2.0e-16
E value
                   44
Match length
                  77
% identity
                  ubiquitin conjugating enzyme E2 protein - Arabidopsis
NCBI Description
                  thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]
                   206190
Seq. No.
                  LIB3083-109-Q1-L1-H7
Seq. ID
                   BLASTX
Method
                   g4417283
NCBI GI
                   290
BLAST score
                   3.0e-26
E value
                   115
Match length
% identity
                   50
                  (AC007019) putative cytochrome p450 [Arabidopsis thaliana]
NCBI Description
                   206191
Seq. No.
                   LIB3083-109-Q1-L1-H8
Seq. ID
                   BLASTX
Method
                   g4539460
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   120
Match length
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   206192
Seq. No.
                   LIB3083-109-Q1-L1-H9
Seq. ID
```

BLASTX Method NCBI GI q543867 338 BLAST score 8.0e-32 E value 93 Match length 80 % identity

ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi\_1076684\_pir\_\_A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi\_303626\_dbj\_BAA03526\_ (D14699) F1-ATPase gammma subunit



### [Ipomoea batatas]

```
206193
Seq. No.
                  LIB3083-110-Q1-L1-A12
Seq. ID
                  BLASTX
Method
                  g2245032
NCBI GI
                  222
BLAST score
                  4.0e-18
E value
                  92
Match length
                  48
% identity
                  (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]
NCBI Description
                  206194
Seq. No.
Seq. ID
                  LIB3083-110-Q1-L1-A9
                  BLASTX
Method
                  g2500354
NCBI GI
                  594
BLAST score
                  8.0e-62
E value
                  121
Match length
                  94
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj_BAA19462_
NCBI Description
                  (AB001891) QM family protein [Solanum melongena]
                  206195
Seq. No.
                  LIB3083-110-Q1-L1-B10
Seq. ID
                  BLASTX
Method
                  g1706956
NCBI GI
                  604
BLAST score
                  6.0e-63
E value
                  129
Match length
                  91
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   206196
Seq. No.
                  LIB3083-110-Q1-L1-B11
Seq. ID
                   BLASTX
Method
                   q2493495
NCBI GI
                   144
BLAST score
                   5.0e-09
E value
                   46
Match length
% identity
                   SERINE CARBOXYPEPTIDASE-LIKE >gi 2129878_pir__S72370
NCBI Description
                   carboxypeptidase - garden pea (fragment)
                   >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum
                   satīvum] >gī_1587217_prf__2206338A Ser carboxypeptidase
                   [Pisum sativum]
                   206197
Seq. No.
                   LIB3083-110-Q1-L1-B12
Seq. ID
                   BLASTX
Method
                   q3641837
NCBI GI
BLAST score
                   355
                   8.0e-34
E value
                   86
Match length
% identity
                   (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
```

28257

[Arabidopsis thaliana]

24.c

Match length

% identity

50 66



```
٠<u>٠</u> .
                  206198
Seq. No.
Seq. ID
                  LIB3083-110-Q1-L1-B9
                  BLASTX
Method
                  g464621
NCBI GI
                  403
BLAST score
                  2.0e-39
E value
                  89
Match length
                  90
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                  206199
Seq. No.
                  LIB3083-110-Q1-L1-C10
Seq. ID
                  BLASTX
Method
                   g1351595
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   70
Match length
% identity
                   28
                  HYPOTHETICAL 88.2 KD PROTEIN C4G8.03C IN CHROMOSOME I
NCBI Description
                   >gi_2130430_pir__S62480 hypothetical protein SPAC4G8.03c -
                   fission yeast (Schizosaccharomyces pombe)
                   >gi_1022348_emb_CAA91204 (Z56276) unknown
                   [Schizosaccharomyces pombe]
                   206200
Seq. No.
                   LIB3083-110-Q1-L1-C12
Seq. ID
                   BLASTX
Method
                   g2982251
NCBI GI
BLAST score
                   240
                   1.0e-20
E value
                   65
Match length
                   74
% identity
                  (AF051208) putative RNA-binding protein [Picea mariana]
NCBI Description
                   206201
Seq. No.
                   LIB3083-110-Q1-L1-D10
Seq. ID
                   BLASTX
Method
                   g2160169
NCBI GI
                   262
BLAST score
                   7.0e-23
E value
                   95
Match length
                   58
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                   206202
Seq. No.
Seq. ID
                   LIB3083-110-Q1-L1-E10
                   BLASTX
Method
NCBI GI
                   q2739389
                   187
BLAST score
                   4.0e-14
E value
```

28258

NCBI Description (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]



```
206203
Seq. No.
Seq. ID
                  LIB3083-110-Q1-L1-E11
                  BLASTX
Method
NCBI GI
                  g3395440
                  304
BLAST score
                  9.0e-28
E value
                  129
Match length
                  41
% identity
                 (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  206204
Seq. No.
Seq. ID
                  LIB3083-110-Q1-L1-E12
                  BLASTX
Method
NCBI GI
                  g2129473
BLAST score
                  291
                  3.0e-26
E value
Match length
                  116
                  48
% identity
NCBI Description
                  arabinogalactan-like protein - loblolly pine >gi 607774
                  (U09556) arabinogalactan-like protein [Pinus taeda]
                  206205
Seq. No.
                  LIB3083-110-Q1-L1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1009234
BLAST score
                  546
E value
                  4.0e-56
Match length
                  128
% identity
                  83
NCBI Description (L38829) SUP2 gene product [Nicotiana tabacum]
Seq. No.
                  206206
                  LIB3083-110-Q1-L1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  475
E value
                  7.0e-48
Match length
                  121
% identity
                  81
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  206207
Seq. ID
                  LIB3083-110-Q1-L1-F11
Method
                  BLASTX
NCBI GI
                  q464840
BLAST score
                  261
E value
                  8.0e-23
                  55
Match length
                  91
% identity
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin
```

28259

alpha-1 chain - fern (Anemia phyllitidis)

phyllitidis]

>gi 296494 emb CAA48927 (X69183) alpha tubulin [Anemia



```
206208
Seq. No.
Seq. ID
                  LIB3083-110-Q1-L1-G11
                  BLASTX
Method
                  g4510383
NCBI GI
                  298
BLAST score
                  4.0e-27
E value
                  83
Match length
                  71
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                  206209
Seq. No.
                  LIB3083-110-Q1-L1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2980777
                   336
BLAST score
                   4.0e-33
E value
                   99
Match length
                   80
% identity
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   206210
Seq. No.
                   LIB3083-110-Q1-L1-H11
Seq. ID
                   BLASTX
Method
                   q2842481
NCBI GI
                   216
BLAST score
                   2.0e-17
E value
                   83
Match length
                   51
% identity
                  (AL021749) extensin-like protein [Arabidopsis thaliana]
NCBI Description
                   206211
Seq. No.
                   LIB3083-110-Q1-L1-H12
Seq. ID
                   BLASTX
Method
                   g3024360
NCBI GI
                   586
BLAST score
                   7.0e-61
E value
                   128
Match length
                   89
% identity
                   PHENYLALANINE AMMONIA-LYASE >gi 1276903 (U43338)
NCBI Description
                   phenylalanine ammonia-lyase [Citrus limon]
                   206212
Seq. No.
                   LIB3083-111-Q1-L1-A1
Seq. ID
                   BLASTX
Method
                   q1732587
NCBI GI
BLAST score
                   259
                   2.0e-22
E value
                   84
Match length
                   60
 % identity
                   (U73203) farnesyltransferase beta subunit [Nicotiana
NCBI Description
                   glutinosa]
```

206213 Seq. No.

Seq. ID LIB3083-111-Q1-L1-A2

BLASTX Method q3128175 NCBI GI



```
BLAST score
                   2.0e-13
E value
                   100
Match length
                   39
% identity
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206214
Seq. No.
                   LIB3083-111-Q1-L1-A6
Seq. ID
                   BLASTX
Method
                   g2827544
NCBI GI
                   259
BLAST score
                   1.0e-22
E value
                   54
Match length
                   94
% identity
                   (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                   thaliana]
                   206215
Seq. No.
                   LIB3083-111-Q1-L1-A8
Seq. ID
                   BLASTX
Method
                   g2827143
NCBI GI
BLAST score
                   223
                   2.0e-18
E value
                   50
Match length
                   82
% identity
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   206216
Seq. No.
                   LIB3083-111-Q1-L1-B1
Seq. ID
                   BLASTX
Method
                   g585973
NCBI GI
BLAST score
                   555
                   3.0e-57
E value
                   131
Match length
                   84
% identity
                   FRUCTOKINASE >gi 626018 pir S39997 fructokinase (EC
NCBI Description
                   2.7.1.4) - potato >gi_2\overline{9}701\overline{5} emb CAA78283 (Z12823)
                   fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A
                   fructokinase [Solanum tuberosum]
                   206217
Seq. No.
                   LIB3083-111-Q1-L1-B2
Seq. ID
                   BLASTX
Method
                   q4544399
NCBI GI
                   509
BLAST score
                    6.0e - 52
E value
                    115
Match length
% identity
                    (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                    thaliana]
```

Seq. No. 206218

Seq. ID LIB3083-111-Q1-L1-B4 Method BLASTX

Method BLASTX NCBI GI g1808656 BLAST score 409

```
E value
                   126
Match length
% identity
                   (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]
NCBI Description
                   206219
Seq. No.
                   LIB3083-111-Q1-L1-B5
Seq. ID
                   BLASTX
Method
                   g1706958
NCBI GI
                   507
BLAST score
                   1.0e-51
E value
Match length
                   111
% identity
                   86
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   206220
Seq. No.
                   LIB3083-111-Q1-L1-B7
Seq. ID
Method
                   BLASTX
                   g2924520
NCBI GI
                   524
BLAST score
                   1.0e-53
E value
                   114
Match length
                   89
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                   206221
Seq. No.
                   LIB3083-111-Q1-L1-C1
Seq. ID
Method
                   BLASTX
                   g4204313
NCBI GI
BLAST score
                   174
                   2.0e-12
E value
Match length
                   79
                   56
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   206222
Seq. No.
                   LIB3083-111-Q1-L1-C2
 Seq. ID
                   BLASTX
Method
                   g1706956
 NCBI GI
                   385
 BLAST score
                   1.0e-42
 E value
                   125
Match length
                   73
 % identity
                   (U58283) cellulose synthase [Gossypium hirsutum]
 NCBI Description
                   206223
 Seq. No.
                   LIB3083-111-Q1-L1-C4
 Seq. ID
                   BLASTX
 Method
                   g464849
 NCBI GI
                    596
 BLAST score
```

4.0e-62 E value 120 Match length 99 % identity

TUBULIN ALPHA CHAIN >gi\_486847\_pir\_\_S36232 tubulin alpha NCBI Description

chain - almond >gi\_20413\_emb\_CAA47635\_ (X67162)



### alpha-tubulin [Prunus dulcis]

```
206224
Seq. No.
                  LIB3083-111-Q1-L1-D2
Seq. ID
                  BLASTX
Method
                  g3747111
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  99
Match length
                   54
% identity
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   206225
Seq. No.
                  LIB3083-111-Q1-L1-D4
Seq. ID
                  BLASTX
Method
                   g3097321
NCBI GI
                   189
BLAST score
                   2.0e-14
E value
                   98
Match length
                   43
% identity
                   (AB013289) Bd 30K [Glycine max]
NCBI Description
                   206226
Seq. No.
                   LIB3083-111-Q1-L1-D8
Seq. ID
                   BLASTX
Method
                   q4467126
NCBI GI
BLAST score
                   313
                   8.0e-29
E value
                   132
Match length
                   52
% identity
                   (AL035538) guanine nucleotide-exchange protein-like
NCBI Description
                   [Arabidopsis thaliana]
                   206227
Seq. No.
                   LIB3083-111-Q1-L1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2501353
                   447
BLAST score
                   1.0e-44
E value
                   103
Match length
                   88
% identity
                   TRANSKETOLASE, CHLOROPLAST (TK) >gi 1084440 pir__S54300
NCBI Description
                   transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum
                   (fragment) >gi 664901_emb_CAA86607_ (Z46646) transketolase
                   [Craterostigma plantagineum]
                   206228
Seq. No.
Seq. ID
                   LIB3083-111-Q1-L1-E3
                   BLASTX
Method
NCBI GI
                   g4204265
                   537
BLAST score
                   4.0e-55
E value
                   123
Match length
                   77
% identity
                   (ACO05223) 45643 [Arabidopsis thaliana]
NCBI Description
```

28263

206229

Seq. No.

```
Seq. ID
                   LIB3083-111-Q1-L1-E5
Method
                   BLASTX
NCBI GI
                   q464846
BLAST score
                   594
E value
                   7.0e-62
Match length
                   117
% identity
                   92
NCBI Description
                  TUBULIN ALPHA-6 CHAIN >gi 322880 pir S28983 tubulin
                   alpha-6 chain - maize >gi 22158 emb CAA44863 (X63178)
                   alpha-tubulin #6 [Zea mays]
Seq. No.
                   206230
Seq. ID
                   LIB3083-111-Q1-L1-E6
Method
                   BLASTX
NCBI GI
                   q3080420
BLAST score
                   165
E value
                   8.0e-12
Match length
                   48
                   69
% identity
NCBI Description
                   (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]
Seq. No.
                  206231
Seq. ID
                  LIB3083-111-Q1-L1-E8
Method
                  BLASTX
NCBI GI
                   q3901294
BLAST score
                   141
E value
                   9.0e-09
Match length
                  114
% identity
                   34
NCBI Description (AF089711) rpp8 [Arabidopsis thaliana]
Seq. No.
                  206232
Seq. ID
                  LIB3083-111-Q1-L1-F2
Method
                  BLASTX
NCBI GI
                  g3434971
BLAST score
                  226
E value
                  8.0e-19
Match length
                   65
% identity
                   69
NCBI Description
                  (AB008105) ethylene responsive element binding factor 3
                   [Arabidopsis thaliana]
Seq. No.
                  206233
Seq. ID
                  LIB3083-111-Q1-L1-F3
                  BLASTX
                  g3150414
                  400
                  5.0e-39
Match length
                  97
```

Method NCBI GI BLAST score E value

% identity 77

NCBI Description (AC004165) AtRanBPlb protein [Arabidopsis thaliana]

Seq. No.

206234

Seq. ID

LIB3083-111-Q1-L1-F4

Method NCBI GI

BLASTX g3650032

% identity

NCBI Description

34



```
BLAST score
E value
                  7.0e-20
Match length
                  49
                  73
% identity
                   (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  206235
                  LIB3083-111-Q1-L1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1654140
BLAST score
                  216
                  2.0e-17
E value
Match length
                   69
                  58
% identity
                  (U37840) lipoxygenase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  206236
Seq. ID
                  LIB3083-111-Q1-L1-F6
Method
                  BLASTX
NCBI GI
                  q799177
BLAST score
                  169
                   5.0e-12
E value
                  71
Match length
% identity
                   48
                   (U22055) 100 kDa coactivator [Homo sapiens]
NCBI Description
                   206237
Seq. No.
                  LIB3083-111-Q1-L1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2827661
BLAST score
                   317
                   2.0e-29
E value
Match length
                   88
                   72
% identity
                   (AL021637) hyuC-like protein [Arabidopsis thaliana]
NCBI Description
                   206238
Seq. No.
                   LIB3083-111-Q1-L1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3608171
BLAST score
                   446
                   2.0e-44
E value
                   109
Match length
% identity
                   81
                   (D86306) proton-translocating inorganic pyrophosphatase
NCBI Description
                   [Cucurbita moschata]
                   206239
Seq. No.
                   LIB3083-111-Q1-L1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4335751
BLAST score
                   464
                   2.0e~46
E value
Match length
                   131
```

(AC006284) putative methyltransferase [Arabidopsis



. No. 206240

Seq. No. 206240 Seq. ID LIB3083-111-Q1-L1-G2

Method BLASTX
NCBI GI g2677830
BLAST score 490
E value 1.0e-49
Match length 112
% identity 86

NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No. 206241

Seq. ID LIB3083-111-Q1-L1-G3

Method BLASTN
NCBI GI g2829205
BLAST score 379
E value 0.0e+00
Match length 403
% identity 19

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 206242

Seq. ID LIB3083-111-Q1-L1-G5

Method BLASTX
NCBI GI g1702983
BLAST score 351
E value 3.0e-33
Match length 110
% identity 59

NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi\_99855\_pir\_\_S11850

hypothetical protein - garden strawberry

>gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria
x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 206243

Seq. ID LIB3083-111-Q1-L1-G8

Method BLASTX
NCBI GI g3668089
BLAST score 374
E value 6.0e-36
Match length 129
% identity 53

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 206244

Seq. ID LIB3083-111-Q1-L1-H3

Method BLASTX
NCBI GI g3688175
BLAST score 198
E value 2.0e-15
Match length 52
% identity 71

NCBI Description (AL031804) gamma-VPE (vacuolar processing enzyme)

[Arabidopsis thaliana]

Seq. No.

206250



```
206245
Seq. No.
Seq. ID
                  LIB3083-111-Q1-L1-H6
Method
                  BLASTX
                  g2129473
NCBI GI
                  292
BLAST score
                  2.0e-26
E value
                  131
Match length
                  47
% identity
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                  (U09556) arabinogalactan-like protein [Pinus taeda]
                  206246
Seq. No.
Seq. ID
                  LIB3083-111-Q1-L1-H7
                  BLASTX
Method
                  g571519
NCBI GI
                  215
BLAST score
                  1.0e-17
E value
                   63
Match length
                  12
% identity
                   (U16852) polyubiquitin [Gracilaria verrucosa]
NCBI Description
                  >gi_1095488_prf__2109223A poly-ubiquitin [Gracilaria
                   verrucosa]
                   206247
Seq. No.
                  LIB3083-111-Q1-L1-H8
Seq. ID
                  BLASTX
Method
                   g1174592
NCBI GI
                   688
BLAST score
                   8.0e-73
E value
                   131
Match length
                   100
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   206248
Seq. No.
Seq. ID
                   LIB3083-112-Q1-L1-A2
                   BLASTX
Method
                   g3063448
NCBI GI
BLAST score
                   460
                   4.0e-46
E value
Match length
                   125
                   70
% identity
                   (AC003981) F22013.10 [Arabidopsis thaliana]
NCBI Description
                   206249
Seq. No.
                   LIB3083-112-Q1-L1-A3
Seq. ID
                   BLASTX
Method
                   g2982458
NCBI GI
BLAST score
                   478
E value
                   3.0e-48
Match length
                   127
                   74
% identity
                   (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID



```
LIB3083-112-Q1-L1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334405
                  437
BLAST score
                  2.0e-43
E value
                  93
Match length
                  98
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
                  206251
Seq. No.
                  LIB3083-112-Q1-L1-A7
Seq. ID
                  BLASTX
Method
                  g441457
NCBI GI
                  625
BLAST score
                  2.0e-65
E value
                  120
Match length
                  97
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  206252
Seq. No.
Seq. ID
                  LIB3083-112-Q1-L1-B1
Method
                  BLASTX
                  g2288986
NCBI GI
BLAST score
                   459
                   6.0e-46
E value
                  128
Match length
                   68
% identity
NCBI Description (AC002335) glyoxalase II isolog [Arabidopsis thaliana]
                   206253
Seq. No.
                  LIB3083-112-Q1-L1-B2
Seq. ID
Method
                  BLASTX
                   g417154
NCBI GI
BLAST score
                   544
                   6.0e-56
E value
Match length
                   107
% identity
                   96
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi 20256 emb CAA77978 (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   206254
Seq. No.
Seq. ID
                   LIB3083-112-Q1-L1-B3
                   BLASTX
Method
NCBI GI
                   g4371290
BLAST score
                   254
E value
                   7.0e-22
Match length
                   58
                   74
% identity
                   (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206255
Seq. No.
                   LIB3083-112-Q1-L1-B4
```

Match length

NCBI Description

% identity

91 51



```
BLASTN
Method
                  q3309259
NCBI GI
BLAST score
                  33
                  6.0e-09
E value
Match length
                  77
% identity
                  Arabidopsis thaliana BAC F4H6, chromosome IV, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
                  206256
Seq. No.
                  LIB3083-112-Q1-L1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129826
BLAST score
                  597
E value
                   4.0e-62
                   130
Match length
% identity
                  dynamin-like protein phragmoplastin 5 - soybean >gi_1218004
NCBI Description
                   (U36430) SDL5A [Glycine max]
Seq. No.
                   206257
Seq. ID
                  LIB3083-112-Q1-L1-B8
                   BLASTX
Method
NCBI GI
                   g3142301
                   162
BLAST score
                   4.0e-11
E value
                   92
Match length
                   45
% identity
                   (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                   molecule 2, large isoform precursor gb M76710 from Xenopus
                   laevis, and beta transducin from S. cerevisiae gb Q05946.
                   ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101,
                   gb H3630
                   206258
Seq. No.
Seq. ID
                   LIB3083-112-Q1-L1-C1
                   BLASTX
Method
                   g464840
NCBI GI
BLAST score
                   277
                   1.0e-24
E value
Match length
                   53
                   100
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin
NCBI Description
                   alpha-1 chain - fern (Anemia phyllitidis)
                   >gi 296494 emb CAA48927_ (X69183) alpha tubulin [Anemia
                   phyllitidis]
                   206259
Seq. No.
Seq. ID
                   LIB3083-112-Q1-L1-C2
                   BLASTX
Method
NCBI GI
                   g3402282
BLAST score
                   242
                   2.0e-20
E value
```

28269

(AJ000997) proline-rich protein [Solanum tuberosum]

BLAST score

E value

177 7.0e-13

```
206260
Seq. No.
                  LIB3083-112-Q1-L1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2511693
                  450
BLAST score
                  7.0e-45
E value
                  117
Match length
                  71
% identity
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
                  206261
Seq. No.
                  LIB3083-112-Q1-L1-C7
Seq. ID
                  BLASTX
Method
                  g1706956
NCBI GI
                  681
BLAST score
                  5.0e-72
E value
                  129
Match length
                  99
% identity
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]
                  206262
Seq. No.
                  LIB3083-112-Q1-L1-D1
Seq. ID
                  BLASTX
Method
                   g3953470
NCBI GI
                   171
BLAST score
                   3.0e-12
E value
                   112
Match length
                   46
% identity
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
                   206263
Seq. No.
                   LIB3083-112-Q1-L1-D2
Seq. ID
                   BLASTX
Method
                   g2651310
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   76
Match length
                   36
% identity
                   (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
                   206264
Seq. No.
Seq. ID
                   LIB3083-112-Q1-L1-D3
                   BLASTX
Method
NCBI GI
                   q4455367
                   270
BLAST score
                   9.0e-24
E value
                   128
Match length
                   30
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   206265
Seq. No.
                   LIB3083-112-Q1-L1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2497743
```



Match length 57 % identity 61

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi 999315 bbs 166991 (S78173) LTP=lipid transfer protein

[Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]

[Gossypium hirsutum]

Seq. No. 206266

Seq. ID LIB3083-112-Q1-L1-E1

Method BLASTX
NCBI GI g4539390
BLAST score 584
E value 1.0e-60
Match length 125
% identity 88

NCBI Description (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)

[Arabidopsis thaliana]

Seq. No. 206267

Seq. ID LIB3083-112-Q1-L1-E3

Method BLASTX
NCBI GI g1172874
BLAST score 339
E value 7.0e-32
Match length 119
% identity 57

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi\_479589\_pir\_\_S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi\_391608\_dbj\_BAA01546\_ (D10703) rd22
[Arabidopsis thaliana] >gi\_447134\_prf\_\_1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 206268

Seq. ID LIB3083-112-Q1-L1-E7

Method BLASTX
NCBI GI g1518540
BLAST score 606
E value 3.0e-63
Match length 129
% identity 90

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 206269

Seq. ID LIB3083-112-Q1-L1-F1

Method BLASTX
NCBI GI g1326163
BLAST score 290
E value 3.0e-26
Match length 128
% identity 54

NCBI Description (U54704) stress related protein PvSRP [Phaseolus vulgaris]

Seq. No. 206270

Seq. ID LIB3083-112-Q1-L1-F2

Method BLASTX
NCBI GI g3878570
BLAST score 439



```
E value
                  131
Match length
% identity
                  (Z46381) similar to lipoic acid synthase; cDNA EST
NCBI Description
                  yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes
                  from this gene; cDNA EST yk472f5.3 comes from this gene;
                  cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3
                  206271
Seq. No.
                  LIB3083-112-Q1-L1-F3
Seq. ID
Method
                  BLASTX
                  q3273243
NCBI GI
                  425
BLAST score
                  6.0e-42
E value
                   132
Match length
                   36
% identity
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                   sativa]
                   206272
Seq. No.
                   LIB3083-112-Q1-L1-F7
Seq. ID
Method
                   BLASTX
                   g3668086
NCBI GI
                   314
BLAST score
                   6.0e-29
E value
                   89
Match length
% identity
                   66
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206273
Seq. No.
                   LIB3083-112-Q1-L1-G2
Seq. ID
                   BLASTX
Method
                   g1174600
NCBI GI
                   447
BLAST score
                   2.0e-44
E value
                   88
Match length
                   94
 % identity
                   TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717)
 NCBI Description
                   beta-tubulin [Oryza sativa]
                   206274
 Seq. No.
                   LIB3083-112-Q1-L1-G7
 Seq. ID
                   BLASTX
 Method
                   g3080420
 NCBI GI
                   457
 BLAST score
                   1.0e-45
 E value
                   127
 Match length
                   71
 % identity
```

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

206275 Seq. No.

Seq. ID LIB3083-112-Q1-L1-G8

BLASTX Method q1706958 NCBI GI

```
BLAST score
                  1.0e-74
E value
                  130
Match length
                  98
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  206276
Seq. No.
                  LIB3083-112-Q1-L1-H1
Seq. ID
                  BLASTX
Method
                   g4126473
NCBI GI
                   666
BLAST score
                   3.0e-70
E value
                   129
Match length
                   99
% identity
                   (AB014884) adenylyl cyclase associated protein [Gossypium
NCBI Description
                   hirsutum]
                   206277
Seq. No.
                   LIB3083-112-Q1-L1-H3
Seq. ID
Method
                   BLASTN
                   g4159706
NCBI GI
BLAST score
                   38
                   6.0e-12
E value
                   74
Match length
                   88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGL6, complete sequence [Arabidopsis thaliana]
                   206278
Seq. No.
                   LIB3083-113-Q1-L1-A1
Seq. ID
                   BLASTX
Method
                   g1399450
NCBI GI
                   570
BLAST score
                   4.0e-59
E value
                   111
Match length
                   96
% identity
                  (U47660) beta-tubulin 2 [Lupinus albus]
NCBI Description
                   206279
Seq. No.
                   LIB3083-113-Q1-L1-A11
Seq. ID
                   BLASTX
Method
                   g3643603
NCBI GI
BLAST score
                   406
                   9.0e-40
E value
                   97
Match length
                   77
 % identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                   206280
 Seq. No.
                   LIB3083-113-Q1-L1-A2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q484656
                    509
 BLAST score
                    6.0e-52
 E value
                    111
 Match length
                    85
 % identity
 NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
```

NCBI Description





cucumber >gi\_452165\_dbj\_BAA05408\_ (D26392)
monodehydroascorbate reductase [Cucumis sativus]

```
Seq. No.
                   206281
Seq. ID
                  LIB3083-113-Q1-L1-A3
Method
                  BLASTX
NCBI GI
                  g4567279
BLAST score
                  178
                   5.0e-13
E value
                   50
Match length
% identity
                   68
                   (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   206282
Seq. No.
Seq. ID
                  LIB3083-113-Q1-L1-A4
                  BLASTX
Method
                   g4415992
NCBI GI
BLAST score
                   481
E value
                   8.0e-49
Match length
                   93
                   99
% identity
                   (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
                   206283
Seq. No.
Seq. ID
                   LIB3083-113-Q1-L1-B11
Method
                   BLASTX
                   g4544403
NCBI GI
BLAST score
                   321
                   9.0e-30
E value
Match length
                   91
% identity
                   64
                   (AC007047) putative glucan endo-1,3-beta-D-glucosidase
NCBI Description
                   precursor [Arabidopsis thaliana]
                   206284
Seq. No.
                   LIB3083-113-Q1-L1-B12
Seq. ID
Method
                   BLASTX
                   g3283409
NCBI GI
BLAST score
                   153
E value
                   2.0e-10
                   60
Match length
% identity
                   50
                   (AF068754) heat shock factor binding protein 1 HSBP1 [Homo
NCBI Description
                   sapiens] >gi 4557647 ref NP 001528.1 pHSBP1 heat shock
                   factor binding protein
Seq. No.
                   206285
Seq. ID
                   LIB3083-113-Q1-L1-B6
Method
                   BLASTX
NCBI GI
                   g4006886
BLAST score
                   120
                   4.0e-14
E value
Match length
                   87
% identity
                   52
```

(Z99708) putative protein [Arabidopsis thaliana]



```
206286
Seq. No.
Seq. ID
                  LIB3083-113-Q1-L1-C1
Method
                  BLASTX
NCBI GI
                   g2827143
BLAST score
                   156
                   1.0e-10
E value
Match length
                   37
% identity
                   76
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   206287
Seq. ID
                   LIB3083-113-Q1-L1-C10
Method
                   BLASTX
NCBI GI
                   g2501490
BLAST score
                   363
E value
                   1.0e-34
Match length
                   126
% identity
                   52
NCBI Description
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID
                   3-O-GLUCOSYLTRANSFERASE) >qi 1620013 dbj BAA12737 (D85186)
                   UDP-glucose:flavonoid-3-glucosyltransferase [Gentiana
                   triflora]
Seq. No.
                   206288
Seq. ID
                   LIB3083-113-Q1-L1-C12
Method
                   BLASTX
NCBI GI
                   g1762130
BLAST score
                   567
E value
                   1.0e-58
Match length
                   124
% identity
                   93
                   (U46136) chaperonin-60 beta subunit [Solanum tuberosum]
NCBI Description
Seq. No.
                   206289
                   LIB3083-113-Q1-L1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3334112
BLAST score
                   302
E value
                   6.0e-28
                   79
Match length
                   72
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >qi 1938236 emb CAA70200
NCBI Description
                   (Y08996) acyl-CoA-binding protein [Ricinus communis]
                   206290
Seq. No.
Seq. ID
                   LIB3083-113-Q1-L1-C4
Method
                   BLASTX
NCBI GI
                   g1657382
BLAST score
                   318
E value
                   1.0e-29
Match length
                   60
% identity
                   95
NCBI Description
                   (Y09101) cholinephosphate cytidylyltransferase [Pisum
                   sativum]
```

28275

e 1 100

206291

Seq. No.

V2.

```
LIB3083-113-Q1-L1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82426
BLAST score
                  569
E value
                  6.0e-59
Match length
                  113
% identity
                  46
                  ubiquitin precursor - barley (fragment)
NCBI Description
                  >gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
                  206292
Seq. No.
                  LIB3083-113-Q1-L1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006886
BLAST score
                  220
                  6.0e-28
E value
Match length
                  108
% identity
                  65
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                  206293
Seq. No.
                  LIB3083-113-Q1-L1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g445613
                  331
BLAST score
                  6.0e-31
E value
                  95
Match length
                  71
% identity
NCBI Description
                  ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                  206294
Seq. ID
                  LIB3083-113-Q1-L1-C8
Method
                  BLASTX
NCBI GI
                  q4027897
BLAST score
                  296
                  2.0e-27
E value
Match length
                   66
% identity
                  77
NCBI Description
                  (AF049353) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.
                  206295
                  LIB3083-113-Q1-L1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2088649
BLAST score
                  268
                  7.0e-27
E value
Match length
                  106
% identity
                   61
NCBI Description
                   (AF002109) unknown protein [Arabidopsis thaliana]
```

Seq. No. 206296

Seq. ID LIB3083-113-Q1-L1-D12

Method BLASTX
NCBI GI g2894534
BLAST score 513
E value 3.0e-52



```
Match length
                  83
% identity
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                  206297
Seq. No.
                  LIB3083-113-Q1-L1-D2
Seq. ID
                  BLASTX
Method
                  g1362086
NCBI GI
                   158
BLAST score
                   7.0e-11
E value
                   40
Match length
% identity
                   75
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_2129919_pir_ S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
                   206298
Seq. No.
                   LIB3083-113-Q1-L1-D5
Seq. ID
Method
                   BLASTX
                   g3747111
NCBI GI
                   285
BLAST score
                   1.0e-25
E value
                   79
Match length
                   66
% identity
                   (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   206299
Seq. No.
                   LIB3083-113-Q1-L1-D6
Seq. ID
Method
                   BLASTX
                   g4510395
NCBI GI
                   469
BLAST score
                   2.0e-47
E value
                   100
Match length
                   86
 % identity
                   (AC006587) putative beta-galactosidase precursor
 NCBI Description
                   [Arabidopsis thaliana]
                   206300
 Seq. No.
                   LIB3083-113-Q1-L1-D7
 Seq. ID
                   BLASTX
 Method
                   g2967452
 NCBI GI
                   170
 BLAST score
                   4.0e-12
 E value
                   98
 Match length
                   38
 % identity
                   (AB010882) hSNF2H [Homo sapiens]
 NCBI Description
                   >gi_4507075_ref_NP_003592.1_pSMARCA5_ SWI/SNF related,
```

matrix associated, actin dependent regulator of chromatin,

subfamily a, member

206301 Seq. No.

Seq. ID LIB3083-113-Q1-L1-D9

BLASTX Method

Match length

% identity

91

44



```
g4406775
 NCBI GI
BLAST score
                    194
 E value
                    7.0e-15
                    125
 Match length
 % identity
 NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
                    206302
 Seq. No.
 Seq. ID
                    LIB3083-113-Q1-L1-E11
 Method
                    BLASTX
                    q4567226
 NCBI GI
 BLAST score
                    166
                    1.0e-11
 E value
 Match length
                    46
                    65
 % identity
 NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
                    206303
 Seq. No.
 Seq. ID
                    LIB3083-113-Q1-L1-E3
 Method
                    BLASTX
 NCBI GI
                    g4098129
                    374
 BLAST score
                    1.0e-36
 E value
                    72
 Match length
                    99
 % identity
 NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                    206304
 Seq. No.
                    LIB3083-113-Q1-L1-E4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3328231
 BLAST score
                    201
                    9.0e-16
 E value
                    87
 Match length
 % identity
                    51
                    (AF051784) 14S cohesin SMC1 subunit; SMC protein [Xenopus
 NCBI Description
                    laevis]
                    206305
 Seq. No.
 Seq. ID
                    LIB3083-113-Q1-L1-E6
 Method
                    BLASTX
 NCBI GI
                    q2829204
 BLAST score
                    295
                    3.0e-27
 E value
 Match length
                    57
 % identity
                    98
                    (AF044204) lipid transfer protein precursor [Gossypium
 NCBI Description
                    hirsutum]
                    206306
 Seq. No.
 Seq. ID
                    LIB3083-113-Q1-L1-E7
 Method
                    BLASTX
                    g4314378
 NCBI GI
 BLAST score
                    189
                    2.0e-14
 E value
```



(AC006232) putative lipase [Arabidopsis thaliana] NCBI Description

206307 Seq. No.

Seq. ID LIB3083-113-Q1-L1-E9

BLASTX Method q133320 NCBI GI 333 BLAST score 3.0e-31 E value 119 Match length 56 % identity

DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (A135) NCBI Description (RNA POLYMERASE I SUBUNIT 2) >gi\_101446\_pir\_\_A39607

DNA-directed RNA polymerase (EC  $\overline{2}.7.7.6$ ) I  $\overline{13}$ 5K chain yeast (Saccharomyces cerevisiae) >gi\_172464 (M62804) RNA polymerase I (second largest subunit) [Saccharomyces cerevisiae] >gi\_887587\_emb\_CAA90154\_ (Z49919) Rpa2p [Saccharomyces cerevisiae] >gi 939744 (U31900) Rpa135p [Saccharomyces cerevisiae] >gi\_1314085\_emb\_CAA95050\_

(Z71255) Rpa2p [Saccharomyces cerevisiae]

206308 Seq. No.

LIB3083-113-Q1-L1-F1 Seq. ID

BLASTX Method NCBI GI q1777312 BLAST score 297 3.0e-27 E value 94 Match length 64 % identity

(D30622) novel serine/threonine protein kinase [Arabidopsis NCBI Description

thaliana]

206309 Seq. No.

Seq. ID LIB3083-113-Q1-L1-F5

BLASTX Method q3776005 NCBI GI BLAST score 376 2.0e-36 E value 106 Match length 74 % identity

(AJ010466) RNA helicase [Arabidopsis thaliana] NCBI Description

206310 Seq. No.

LIB3083-113-Q1-L1-F8 Seq. ID

BLASTX Method q974782 NCBI GI BLAST score 488 1.0e-49 E value Match length 94 96 % identity

(Z49150) cobalamine-independent methionine synthase NCBI Description

[Solenostemon scutellarioides]

206311 Seq. No.

LIB3083-113-Q1-L1-G1 Seq. ID

BLASTX Method g2462762 NCBI GI 339 BLAST score



```
E value
                   7.0e-32
Match length
                  122
                  58
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  206312
Seq. No.
Seq. ID
                  LIB3083-113-Q1-L1-G10
Method
                  BLASTX
                  q4455158
NCBI GI
BLAST score
                  621
                  6.0e-65
E value
Match length
                  126
                  90
% identity
                  (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206313
                  LIB3083-113-Q1-L1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4322254
BLAST score
                  63
E value
                  7.0e-27
Match length
                  261
% identity
                  86
                  Corythophora alta rp120-5'-rps12 intergenic region,
NCBI Description
                  chloroplast sequence
Seq. No.
                  206314
Seq. ID
                  LIB3083-113-Q1-L1-G3
Method
                  BLASTX
NCBI GI
                  g2281102
BLAST score
                  190
                  2.0e-14
E value
Match length
                  123
% identity
                   46
                   (AC002333) SF16 isolog [Arabidopsis thaliana]
NCBI Description
                  206315
Seq. No.
                  LIB3083-113-Q1-L1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g343239
BLAST score
                  102
                  3.0e-50
E value
Match length
                  228
% identity
                   90
                  Mustard (S.alba) chloroplast 16S rRNA, 5' end, and Val-tRNA
NCBI Description
                  206316
Seq. No.
                  LIB3083-113-Q1-L1-G8
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2245127
BLAST score 166
E value 7.0e-12
Match length 60
% identity 60

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

NCBI Description



```
206317
Seq. No.
Seq. ID
                  LIB3083-113-Q1-L1-H1
Method
                  BLASTX
                  g1706958
NCBI GI
                  192
BLAST score
                  6.0e-15
E value
Match length
                  39
                  92
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  206318
Seq. No.
                  LIB3083-113-Q1-L1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1173218
BLAST score
                  635
                  1.0e-66
E value
                  125
Match length
% identity
                  98
                  40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  206319
Seq. No.
                  LIB3083-113-Q1-L1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1173218
                   533
BLAST score
                   1.0e-54
E value
                   114
Match length
% identity
                   91
                   40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                   cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                   206320
                   LIB3083-113-Q1-L1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82223
BLAST score
                   152
                   3.0e-10
E value
Match length
                   73
                   66
% identity
                   hypothetical protein 70B - common tobacco chloroplast
NCBI Description
                   >gi 11878 emb CAA77391 (Z00044) hypothetical protein
                   [Nicotiana tabacum] >qi 1223681 emb CAA77402 (Z00044)
                   hypothetical protein [Nicotiana tabacum]
                   >gi 225250 prf 1211235CJ ORF 70B [Nicotiana tabacum]
                   206321
Seq. No.
                   LIB3083-114-Q1-L1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160169
BLAST score
                   181
                   8.0e-14
E value
                   73
Match length
                   55
% identity
```

(AC000132) No definition line found [Arabidopsis thaliana]

Seq. ID

Method



```
206322
Seq. No.
                  LIB3083-114-Q1-L1-A10
Seq. ID
                  BLASTX
Method
                  g3024020
NCBI GI
                  593
BLAST score
                  1.0e-61
E value
                  116
Match length
                   96
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi_2225881_dbj_BAA20877 (AB004824) eukaryotic initiation
                   factor 5A3 [Solanum tuberosum]
                   206323
Seq. No.
                   LIB3083-114-Q1-L1-A11
Seq. ID
                   BLASTX
Method
                   g4455199
NCBI GI
                   420
BLAST score
                   2.0e-41
E value
                   110
Match length
                   79
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   206324
Seq. No.
                   LIB3083-114-Q1-L1-A12
Seq. ID
                   BLASTX
Method
                   q4558553
NCBI GI
BLAST score
                   380
                   1.0e-36
E value
                   125
Match length
                   62
% identity
                   (AC007138) putative potassium channel [Arabidopsis
NCBI Description
                   thaliana]
                   206325
Seq. No.
                   LIB3083-114-Q1-L1-A3
Seq. ID
                   BLASTX
Method
                   g1817584
NCBI GI
                   202
BLAST score
                   8.0e-16
E value
                   66
Match length
                   59
 % identity
NCBI Description (Y08991) adaptor protein [Homo sapiens]
                   206326
 Seq. No.
                   LIB3083-114-Q1-L1-A4
 Seq. ID
                   BLASTX
 Method
                   q1817584
 NCBI GI
                   159
 BLAST score
                   6.0e-11
 E value
                   44
 Match length
                   59
 % identity
 NCBI Description (Y08991) adaptor protein [Homo sapiens]
                   206327
 Seq. No.
```

28282

LIB3083-114-Q1-L1-A5

BLASTX



```
g1945611
NCBI GI
BLAST score
                  233
E value
                  2.0e-19
                  130
Match length
% identity
                  (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                  >qi 4506221 ref NP 002807.1 pPSMD12 proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
                  206328
Seq. No.
Seq. ID
                  LIB3083-114-Q1-L1-A8
Method
                  BLASTX
                  g125887
NCBI GI
BLAST score
                  225
                  2.0e-18
E value
                  116
Match length
% identity
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                  >qi 82092 pir S04765 LAT52 protein precursor - tomato
                  >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
                  esculentum]
                  206329
Seq. No.
                  LIB3083-114-Q1-L1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2961384
BLAST score
                  439
                  1.0e-43
E value
                  126
Match length
                   61
% identity
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
                   206330
Seq. No.
                   LIB3083-114-Q1-L1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006848
BLAST score
                   243
                   6.0e-38
E value
Match length
                   130
% identity
                   59
                   (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                   bisulcatus]
                   206331
Seq. No.
Seq. ID
                   LIB3083-114-Q1-L1-B6
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   525
                   9.0e-54
E value
Match length
                   131
```

% identity 80

(U97200) cobalamin-independent methionine synthase NCBI Description

[Arabidopsis thaliana]

206332 Seq. No.

LIB3083-114-Q1-L1-B7 Seq. ID

```
Method BLASTX
NCBI GI g3549666
BLAST score 317
E value 2.0e-29
Match length 76
% identity 80
```

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

 Seq. No.
 206333

 Seq. ID
 LIB3083-114-Q1-L1-B8

 Method
 BLASTX

 NCBI GI
 g1705678

 BLAST score
 578

 E value
 5.0e-60

E value 5.0e Match length 116% identity 50

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi\_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 206334

Seq. ID LIB3083-114-Q1-L1-B9

Method BLASTX
NCBI GI g4454026
BLAST score 311
E value 1.0e-28
Match length 106
% identity 58

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 206335

Seq. ID LIB3083-114-Q1-L1-C1

Method BLASTX
NCBI GI g3513727
BLAST score 555
E value 3.0e-57
Match length 137
% identity 55

NCBI Description (AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi\_4539358\_emb\_CAB40052.1\_ (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 206336

Seq. ID LIB3083-114-Q1-L1-C10

Method BLASTX
NCBI GI g3687223
BLAST score 146
E value 3.0e-09
Match length 78
% identity 49

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 206337

Seq. ID LIB3083-114-Q1-L1-C11

Method BLASTX



```
q3096939
NCBI GI
BLAST score
                  439
E value
                  1.0e-43
                  112
Match length
% identity
NCBI Description
                  (AL023094) putative protein [Arabidopsis thaliana]
                  206338
Seq. No.
Seq. ID
                  LIB3083-114-Q1-L1-C12
Method
                  BLASTX
NCBI GI
                  q434759
                  309
BLAST score
                  2.0e-28
E value
                  123
Match length
% identity
                  (D21163) similar to human elongation factor 2 mRNA (HSEF2).
NCBI Description
                  [Homo sapiens]
                  206339
Seq. No.
Seq. ID
                  LIB3083-114-Q1-L1-C2
Method
                  BLASTX
                  q267069
NCBI GI
                  727
BLAST score
                  2.0e-77
E value
Match length
                  135
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  206340
Seq. No.
Seq. ID
                  LIB3083-114-Q1-L1-C3
                  BLASTX
Method
NCBI GI
                  g119150
BLAST score
                  732
                  6.0e-78
E value
Match length
                  139
                  100
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_82081_pir__S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi 19273 emb CAA32618 (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >gi_295810_emb_CAA37212 (X53043) elongation factor 1-alpha
                   [Lycopersicon esculentum]
                  206341
Seq. No.
                  LIB3083-114-Q1-L1-C4
Seq. ID
Method
                  BLASTX
                  g285741
NCBI GI
```

BLAST score 214 3.0e-17 E value Match length 129 41 % identity

(D14550) EDGP precursor [Daucus carota] NCBI Description

206342 Seq. No.

Seq. ID

Method NCBI GI



```
LIB3083-114-Q1-L1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q586076
                  569
BLAST score
E value
                  7.0e-59
Match length
                  111
% identity
                  95
                  TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi 402636 emb CAA49736_ (X70184) Beta
                  tubulin 1 [Lupinus albus]
                  206343
Seq. No.
                  LIB3083-114-Q1-L1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075391
BLAST score
                  349
                  5.0e-33
E value
                  131
Match length
                  51
% identity
NCBI Description (ACOO4484) unknown protein [Arabidopsis thaliana]
                  206344
Seq. No.
                  LIB3083-114-Q1-L1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2098709
BLAST score
                  441
                  7.0e-44
E value
                  135
Match length
                   67
% identity
                  (U82975) pectinesterase [Citrus sinensis]
NCBI Description
Seq. No.
                  206345
                  LIB3083-114-Q1-L1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548488
BLAST score
                   397
                   1.0e-38
E value
Match length
                   106
% identity
NCBI Description
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi 166325
                   (L12019) polygalacturonase [Actinidia deliciosa]
Seq. No.
                  206346
Seq. ID
                  LIB3083-114-Q1-L1-D1
                  BLASTX
Method
NCBI GI
                   q3327868
BLAST score
                   169
E value
                   6.0e-12
Match length
                   112
% identity
                   38
                  (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
NCBI Description
                   thaliana]
                   206347
Seq. No.
```

28286

LIB3083-114-Q1-L1-D10

BLASTX

q3122914



```
BLAST score
                  2.0e-31
E value
Match length
                  128
                  53
% identity
                  VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
NCBI Description
                  >gi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis
                  thaliana]
                  206348
Seq. No.
Seq. ID
                  LIB3083-114-Q1-L1-D11
                  BLASTX
Method
                  g2811278
NCBI GI
                   461
BLAST score
E value
                   2.0e-46
                   96
Match length
                   84
% identity
                   (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   206349
Seq. No.
Seq. ID
                  LIB3083-114-Q1-L1-D2
Method
                   BLASTX
                   g2129495
NCBI GI
                   659
BLAST score
                   2.0e-69
E value
                   135
Match length
                   91
% identity
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                   (U30508) E6 [Gossypium barbadense]
Seq. No.
                   206350
Seq. ID
                   LIB3083-114-Q1-L1-D3
                   BLASTX
Method
                   q3868853
NCBI GI
                   285
BLAST score
E value
                   2.0e-25
                   81
Match length
                   65
% identity
                   (AB013853) GPI-anchored protein [Vigna radiata]
NCBI Description
Seq. No.
                   206351
                   LIB3083-114-Q1-L1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q135452
BLAST score
                   683
                   3.0e-72
E value
Match length
                   134
                   91
% identity
                   TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin
NCBI Description
                   [Glycine max]
```

206352 Seq. No.

LIB3083-114-Q1-L1-D5 Seq. ID

Method BLASTN q2656030 NCBI GI 42 BLAST score 2.0e-14 E value



```
Match length
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUL8
                  206353
Seq. No.
                  LIB3083-114-Q1-L1-D7
Seq. ID
                  BLASTX
Method
                  g3694872
NCBI GI
BLAST score
                  404
                  2.0e-39
E value
Match length
                   86
% identity
                   86
                  (AF092547) profilin [Ricinus communis]
NCBI Description
                   206354
Seq. No.
                   LIB3083-114-Q1-L1-D8
Seq. ID
Method
                   BLASTX
                   g4098129
NCBI GI
BLAST score
                   266
                   3.0e-23
E value
Match length
                   74
% identity
                   66
                  (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   206355
Seq. No.
Seq. ID
                   LIB3083-114-Q1-L1-D9
Method
                   BLASTX
NCBI GI
                   g606942
BLAST score
                   421
                   2.0e-41
E value
                   128
Match length
% identity
                   70
                   (U13760) unknown [Gossypium hirsutum]
NCBI Description
                   206356
Seq. No.
                   LIB3083-114-Q1-L1-E1
Seq. ID
                   BLASTX
Method
                   g3169719
NCBI GI
                   501
BLAST score
                   7.0e-51
E value
                   108
Match length
                   87
% identity
                   (AF007109) similar to yeast dcpl [Arabidopsis thaliana]
NCBI Description
                   206357
Seq. No.
Seq. ID
                   LIB3083-114-Q1-L1-E10
                   BLASTX
Method
```

q2583125 NCBI GI 556 BLAST score 2.0e-57 E value Match length 115 % identity

(AC002387) putative transketolase precursor [Arabidopsis NCBI Description

thaliana]

206358 Seq. No.

Seq. ID

Method



```
LIB3083-114-Q1-L1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3046906
BLAST score
                  48
E value
                  6.0e-18
Match length
                  76
                  91
% identity
                  Onchocerca volvulus beta-tubulin (tub) gene, complete cds
NCBI Description
                  206359
Seq. No.
                  LIB3083-114-Q1-L1-E12
Seq. ID
                  BLASTN
Method
                  q995906
NCBI GI
BLAST score
                  69
                  2.0e-30
E value
                  113
Match length
% identity
NCBI Description
                  Gossypium hirsutum nonspecific lipid transfer protein
                  precursor mRNA, complete cds
                  206360
Seq. No.
                  LIB3083-114-Q1-L1-E2
Seq. ID
Method
                  BLASTX
                  q1174592
NCBI GI
BLAST score
                  594
                   9.0e-62
E value
                  132
Match length
                   87
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
Seq. No.
                   206361
Seq. ID
                  LIB3083-114-Q1-L1-E3
Method
                  BLASTX
NCBI GI
                   g1619602
BLAST score
                   332
                   4.0e-31
E value
                   100
Match length
% identity
                   67
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
Seq. No.
                   206362
                  LIB3083-114-Q1-L1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q82426
                   602
BLAST score
                   1.0e-62
E value
                   121
Match length
                   47
% identity
                  ubiquitin precursor - barley (fragment)
NCBI Description
                   >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor
                   (171 aa) [Hordeum vulgare]
                   206363
Seq. No.
```

28289

LIB3083-114-Q1-L1-E7

BLASTX



```
q2914706
NCBI GI
BLAST score
                   169
E value
                   2.0e-12
Match length
                   62
% identity
                   58
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206364
                   LIB3083-114-Q1-L1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g267069
                   557
BLAST score
                   2.0e-57
E value
Match length
                   103
                   99
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   206365
Seq. ID
                   LIB3083-114-Q1-L1-F1
                   BLASTX
Method
NCBI GI
                   q2924792
BLAST score
                   584
                   1.0e-60
E value
                   133
Match length
                   84
% identity
                   (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206366
                   LIB3083-114-Q1-L1-F10
Seq. ID
                   BLASTX
Method
                   q4567304
NCBI GI
BLAST score
                   268
E value
                   1.0e-23 -
                   107
Match length
                   48
% identity
                   (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206367
Seq. ID
                   LIB3083-114-Q1-L1-F3
Method
                   BLASTX
NCBI GI
                   q3775985
BLAST score
                   650
E value
                   2.0e-68
Match length
                   132
% identity
                   93
                   (AJ010456) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206368
                   LIB3083-114-Q1-L1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2494112
BLAST score
                   605
```

28290

5.0e-63

134

E value Match length



% identity (AC002376) Match to Arabidopsis ATHKCP (gb\_L40948). ESTs NCBI Description gb\_ATTS0764, gb\_R90646, gb\_AA389809, gb\_ATTS2615 come from this gene. [Arabidopsis thaliana] >gi\_3126868 (AF061570) potassium channel beta subunit homolog [Arabidopsis thaliana] 206369 Seq. No. LIB3083-114-Q1-L1-F8 Seq. ID Method BLASTX NCBI GI g4335745 BLAST score 272 5.0e-24

E value Match length 130 46 % identity

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 206370 LIB3083-114-Q1-L1-F9 Seq. ID Method BLASTX NCBI GI g2494112 BLAST score 542 1.0e-55 E value

Match length 124 % identity

(AC002376) Match to Arabidopsis ATHKCP (gb L40948). ESTs NCBI Description

gb ATTS0764, gb\_R90646, gb\_AA389809, gb\_ATTS2615 come from this gene. [Arabidopsis thaliana]  $>gi_3126868$  (AF061570)

potassium channel beta subunit homolog [Arabidopsis

thalianal

Seq. No. 206371

Seq. ID LIB3083-114-Q1-L1-G1

Method BLASTX g4105633 NCBI GI 224 BLAST score 2.0e-18 E value Match length 135 % identity

(AF048982) putative ethylene receptor [Arabidopsis NCBI Description

thaliana]

Seq. No. 206372

LIB3083-114-Q1-L1-G12 Seq. ID

Method BLASTX g3096944 NCBI GI BLAST score 333 E value 4.0e-31 114 Match length % identity 57

(AL023094) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 206373

Seq. ID LIB3083-114-Q1-L1-G4

Method BLASTX



q4388829 NCBI GI BLAST score 438 4.0e-44E value 137 Match length % identity 65 (AC006528) putative pol polyprotein with a Zn-finger CCHC NCBI Description type domain (prosite:QDOC50158) and a DDE integrase signature motif [Arabidopsis thaliana] 206374 Seq. No. LIB3083-114-Q1-L1-G5 Seq. ID Method BLASTX NCBI GI g135404 BLAST score 181 9.0e-14 E value 60 Match length 62 % identity TUBULIN ALPHA-1/ALPHA-2 CHAIN >gi\_81291\_pir\_\_S04694 tubulin NCBI Description alpha chain - Volvox carteri f. nagariensis >gi\_22001\_emb\_CAA31326\_ (X12846) alpha-1 tubulin [Volvox carteri] >gi\_404089 (L24546) alpha-2 tubulin [Volvox carteri] 206375 Seq. No. LIB3083-114-Q1-L1-G6 Seq. ID BLASTX Method g4235430 NCBI GI 313 BLAST score 6.0e-29 E value Match length 95 % identity 68 (AF098458) latex-abundant protein [Hevea brasiliensis] NCBI Description 206376 Seq. No. LIB3083-114-Q1-L1-G7 Seq. ID Method BLASTX g3548810 NCBI GI 221 BLAST score 5.0e-18 E value Match length 133 % identity 44 (AC005313) putative chloroplast nucleoid DNA binding NCBI Description protein [Arabidopsis thaliana] Seq. No. 206377 Seq. ID LIB3083-114-Q1-L1-G9 Method BLASTX g485512 NCBI GI 417 BLAST score 5.0e-41 E value

Match length 111 68 % identity

salt-associated protein csaA - sweet orange NCBI Description

206378 Seq. No.

LIB3083-114-Q1-L1-H1 Seq. ID

BLASTX Method

% identity

NCBI Description

71

thaliana]



```
NCBI GI
BLAST score
                  550
                  1.0e-56
E value
Match length
                  137
% identity
                  80
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2)
NCBI Description
                  (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP
                  2) >gi 82172_pir__PQ0262 luminal binding protein BLP-2 -
                  common tobacco (fragment) >gi_100338_pir__S21878 heat shock
                  protein BiP homolog blp2 - common tobacco (fragment)
                  >gi_19807_emb_CAA42661_ (X60059) luminal binding protein
                   (BiP) [Nicotiana tabacum]
Seq. No.
                  206379
Seq. ID
                  LIB3083-114-Q1-L1-H10
                  BLASTX
Method
                  q136057
NCBI GI
BLAST score
                   424
                   8.0e-42
E value
Match length
                   110
                   74
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_99499_pir _A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi_556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
                   206380
Seq. No.
                   LIB3083-114-Q1-L1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1134957
BLAST score
                   148
                   8.0e-10
E value
                   78
Match length
                   38
% identity
                   (U41162) unidentified ORF [Burkholderia cepacia]
NCBI Description
                   206381
Seq. No.
                   LIB3083-114-Q1-L1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1743277
BLAST score
                   393
                   2.0e-38
E value
Match length
                   78
                   95
% identity
                   (Y09741) beta-tubulin 1 [Hordeum vulgare]
NCBI Description
Seq. No.
                   206382
                   LIB3083-114-Q1-L1-H3
Seq. ID
Method
                   BLASTX
                   g3892054
NCBI GI
BLAST score
                   446
                   2.0e-44
E value
Match length
                   112
```

(AC002330) putative glycosyltransferase [Arabidopsis



```
206383
Seq. No.
Seq. ID
                  LIB3083-114-Q1-L1-H5
Method
                  BLASTX
                  g2335100
NCBI GI
BLAST score
                   643
E value
                  2.0e-67
                  133
Match length
                   88
% identity
                  (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206384
Seq. No.
                  LIB3083-114-Q1-L1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4006941
                   278
BLAST score
                   9.0e-25
E value
                   129
Match length
                   45
% identity
                  (AJ131391) voltage-dependent anion-selective channel
NCBI Description
                   protein [Arabidopsis thaliana]
                   206385
Seq. No.
                   LIB3083-114-Q1-L1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1931641
                   400
BLAST score
                   5.0e-39
E value
                   127
Match length
                   63
% identity
                  (U95973) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206386
Seq. No.
                   LIB3083-116-Q1-L1-A10
Seq. ID
                   BLASTX
Method
                   g3334115
NCBI GI
BLAST score
                   615
                   3.0e-64
E value
                   127
Match length
                   97
% identity
                   ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
                   206387
Seq. No.
                   LIB3083-116-Q1-L1-A2
Seq. ID
Method
                   BLASTX
                   g2346970
NCBI GI
BLAST score
                   159
                   6.0e-11
E value
Match length
                   53
% identity
                   43
                   (AB006597) ZPT2-10 [Petunia x hybrida]
NCBI Description
```

LIB3083-116-Q1-L1-A4 Seq. ID Method BLASTX

206388

Seq. No.

% identity

83

```
g4006873
NCBI GI
BLAST score
                  298
                  3.0e-27
E value
                  102
Match length
% identity
                  54
NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]
                  206389
Seq. No.
                  LIB3083-116-Q1-L1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4210948
BLAST score
                  160
                  5.0e-11
E value
                  34
Match length
                  88
% identity
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                  206390
Seq. No.
Seq. ID
                  LIB3083-116-Q1-L1-A8
Method
                  BLASTX
NCBI GI
                  g1706958
BLAST score
                  339
                  5.0e-32
E value
Match length
                  62
% identity
                  100
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
Seq. No.
                  206391
Seq. ID
                  LIB3083-116-Q1-L1-A9
Method
                  BLASTX
NCBI GI
                  g4098246
BLAST score
                   547
                  3.0e-56
E value
Match length
                  132
% identity
                  83
                  (U76410) homeobox 2 protein [Lycopersicon esculentum]
NCBI Description
                  206392
Seq. No.
                  LIB3083-116-Q1-L1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2495365
                  522
BLAST score
                  1.0e-53
E value
                  106
Match length
                   96
% identity
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf __1908431B
NCBI Description
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
                  206393
Seq. No.
Seq. ID
                  LIB3083-116-Q1-L1-B3
Method
                  BLASTX
NCBI GI
                  g2493052
BLAST score
                  327
                  1.0e-30
E value
Match length
                   69
```

28295

NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL





>gi\_1655486\_dbj\_BAA13602\_ (D88377) epsilon subunit of mitochondrial FI-ATPase [Arabidopsis thaliana]

Seq. No. 206394 LIB3083-116-Q1-L1-B7 Seq. ID Method BLASTX NCBI GI g3702333 BLAST score 325 2.0e-30 E value Match length 101 % identity 63 NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana] Seq. No. 206395 Seq. ID LIB3083-116-Q1-L1-C4 Method BLASTX NCBI GI q114336 BLAST score 420 2.0e-41 E value Match length 106 % identity 81 PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) NCBI Description 206396 Seq. No. Seq. ID LIB3083-116-Q1-L1-C7 Method BLASTN NCBI GI g1143223 BLAST score 172 5.0e-92 E value Match length 307 % identity 96 NCBI Description Gossypium barbadense FbLate-2 gene, complete cds Seq. No. 206397 Seq. ID LIB3083-116-Q1-L1-C8 Method BLASTN NCBI GI g2811277 BLAST score 163 1.0e-86 E value Match length 179 % identity 98 NCBI Description Gossypium hirsutum expansin (GhEX1) mRNA, complete cds Seq. No. 206398 LIB3083-116-Q1-L1-D12 Seq. ID Method BLASTX NCBI GI g3378493 BLAST score 185 6.0e-14 E value Match length 46 % identity 74 NCBI Description (AJ007579) cysteine proteinase [Ribes nigrum]

28296

206399

BLASTX

g1945611

LIB3083-116-Q1-L1-D3

Seq. No.

Seq. ID Method

NCBI GI

```
BLAST score
E value
                   4.0e-12
                  75
Match length
% identity
                   44
                   (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                  >gi 4506221 ref NP 002807.1 pPSMD12 proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
                   206400
Seq. No.
                  LIB3083-116-Q1-L1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2191131
BLAST score
                   510
E value
                   4.0e-52
Match length
                   106
                   84
% identity
                   (AF007269) A IG002N01.8 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206401
                   LIB3083-116-Q1-L1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2731377
BLAST score
                   188
E value
                   2.0e-14
Match length
                   97
                   40
% identity
                   (U28739) similar to alcohol dehydrogenase/ribitol
NCBI Description
                   dehydrogenase [Caenorhabditis elegans]
Seq. No.
                   206402
                   LIB3083-116-Q1-L1-D8
Seq. ID
```

Method BLASTX
NCBI GI g625985
BLAST score 183
E value 1.0e-13
Match length 41
% identity 88

NCBI Description expressed sequence tag R10D - rape (fragment)

>gi\_688009\_bbs\_156143 calmodulin homolog {EST} [Brassica

napus, Naehan, root, Peptide Partial, 53 aa]

Seq. No. 206403

Seq. ID LIB3083-116-Q1-L1-E10

Method BLASTX
NCBI GI g1304227
BLAST score 296
E value 8.0e-27
Match length 69
% identity 74

NCBI Description (D63781) Epoxide hydrolase [Glycine max]

>gi 2764804 emb CAA55293\_ (X78547) epoxide hydrolase

[Glycine max]

Seq. No. 206404

Seq. ID LIB3083-116-Q1-L1-E11

Method BLASTX NCBI GI g629791



BLAST score 2.0e-71 E value Match length 129 98 % identity tubulin beta chain - rice >gi 460991 emb CAA55022 (X78143) NCBI Description beta tubulin [Oryza sativa] 206405 Seq. No. LIB3083-116-Q1-L1-E2 Seq. ID BLASTX Method g2914700 NCBI GI 428 BLAST score 2.0e-42 E value Match length 83 % identity (AC003974) tRNA-processing protein SEN3-like [Arabidopsis NCBI Description thaliana] 206406 Seq. No. Seq. ID LIB3083-116-Q1-L1-E9 Method BLASTX g1730109 NCBI GI 485 BLAST score 5.0e-49 E value 114 Match length 82 % identity LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN NCBI Description HYDROXYLASE) >qi 499022 emb CAA53580 (X75966) leucoanthocyanidin dioxygenase [Vitis vinifera] Seq. No. 206407 LIB3083-116-Q1-L1-F2 Seq. ID BLASTX Method q3776027 NCBI GI BLAST score 347 6.0e-33 E value Match length 76 88 % identity (AJ010475) RNA helicase [Arabidopsis thaliana] NCBI Description Seq. No. 206408 Seq. ID LIB3083-116-Q1-L1-F5 Method BLASTX NCBI GI q3785983 BLAST score 168 E value 5.0e-12 Match length 53 58 % identity (AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 206409

Seq. ID LIB3083-116-Q1-L1-F8

Method BLASTN
NCBI GI g166919
BLAST score 77
E value 3.0e-35
Match length 89

% identity Arabidopsis thaliana alpha-6 tubulin (TUA6) gene, complete NCBI Description 206410 Seq. No. LIB3083-116-Q1-L1-F9 Seq. ID Method BLASTX NCBI GI q3511285 BLAST score 495 2.0e-50 E value Match length 100 86 % identity NCBI Description (AF081534) cellulose synthase [Populus alba x Populus tremula] 206411 Seq. No. Seq. ID LIB3083-116-Q1-L1-G11 Method BLASTX NCBI GI g2811025 BLAST score 283 2.0e-25 E value 93 Match length % identity 63 ASPARTIC PROTEINASE PRECURSOR >qi 1944181 dbj BAA19607 NCBI Description (AB002695) aspartic endopeptidase [Cucurbita pepo] 206412 Seq. No. Seq. ID LIB3083-116-Q1-L1-G2 BLASTX Method q4191774 217 9.0e-18 49 86

NCBI GI BLAST score E value Match length % identity

NCBI Description (AC005917) putative beta-1,3-endoglucanase [Arabidopsis

thaliana]

206413 Seq. No.

LIB3083-116-Q1-L1-G4 Seq. ID

Method BLASTX NCBI GI g4115377 BLAST score 210 7.0e-17 E value Match length 45 % identity 87

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

206414 Seq. No.

LIB3083-116-Q1-L1-G7 Seq. ID

Method BLASTX NCBI GI g464855 BLAST score 224 E value 1.0e-18 Match length 49 84 % identity

TUBULIN GAMMA CHAIN >gi 541798 pir S39553 tubulin gamma NCBI Description chain - fern (Anemia phyllitidis) >gi\_429151\_emb\_CAA48932\_





## (X69188) gamma tubulin [Anemia phyllitidis]

```
Seq. No.
                  206415
Seq. ID
                  LIB3083-116-Q1-L1-G8
                  BLASTX
Method
NCBI GI
                  q345829
BLAST score
                  325
E value
                  2.0e-30
Match length
                  97
                  63
% identity
NCBI Description
                  ubiquitin carrier protein E2 - human
                  206416
Seq. No.
Seq. ID
                  LIB3083-116-Q1-L1-H11
                  BLASTX
Method
                  q2935416
NCBI GI
BLAST score
                  470
E value
                  3.0e-48
                  126
Match length
% identity
                  77
NCBI Description
                  (AF047896) isoflavone reductase homolog [Betula pendula]
                  206417
Seq. No.
Seq. ID
                  LIB3083-116-Q1-L1-H8
Method
                  BLASTX
NCBI GI
                  q135452
BLAST score
                   447
                   1.0e-44
E value
Match length
                   94
% identity
                   86
NCBI Description
                  TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin
                   [Glycine max]
Seq. No.
                   206418
Seq. ID
                  LIB3083-119-Q1-L1-A11
Method
                  BLASTX
NCBI GI
                   g2706450
BLAST score
                   220
                   3.0e-18
E value
Match length
                   59
% identity
                   75
NCBI Description
                   (AJ225172) magnesium dependent soluble inorganic
                  pyrophosphatase [Solanum tuberosum]
                   206419
Seq. No.
Seq. ID
                  LIB3083-119-Q1-L1-A2
Method
                  BLASTX
NCBI GI
                   g125887
BLAST score
                   156
                   1.0e-10
E value
Match length
                  85
                   45
% identity
NCBI Description
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                  >gi 82092 pir S04765 LAT52 protein precursor - tomato
                   >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
```

28300

esculentum]

Seq. ID

Method



```
Seq. No.
                   206420
Seq. ID
                   LIB3083-119-Q1-L1-A4
Method
                   BLASTX
NCBI GI
                   g4263787
BLAST score
                   173
                   1.0e-12
E value
Match length
                   73
% identity
                   56
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206421
Seq. ID
                  LIB3083-119-Q1-L1-A8
Method
                  BLASTX
NCBI GI
                   g2995405
BLAST score
                   441
E value
                   4.0e-44
Match length
                   97
% identity
                   81
NCBI Description
                  (Y12432) polyprotein [Ananas comosus]
Seq. No.
                   206422
Seq. ID
                   LIB3083-119-Q1-L1-A9
Method
                   BLASTX
NCBI GI
                   g2129622
BLAST score
                   289
E value
                   3.0e-26
Match length
                   62
                   85
% identity
NCBI Description
                   immunophilin FKBP15-1 - Arabidopsis thaliana >qi 1272406
                   (U52046) immunophilin [Arabidopsis thaliana]
Seq. No.
                   206423
                   LIB3083-119-Q1-L1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                  g2961372
BLAST score
                   368
                   1.0e-35
E value
                   77
Match length
                   88
% identity
NCBI Description
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
                   thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                   protein L2 [Arabidopsis thaliana]
Seq. No.
                   206424
Seq. ID
                   LIB3083-119-Q1-L1-B11
Method
                   BLASTN
NCBI GI
                   g3355463
                   48
BLAST score
E value
                   4.0e-18
Match length
                   76
% identity
                   91
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   206425
Seq. No.
```

28301

LIB3083-119-Q1-L1-B2

BLASTX

```
q3176098
NCBI GI
BLAST score
                  347
E value
                  5.0e-33
Match length
                  94
% identity
NCBI Description
                  (Y15036) annexin [Medicago truncatula]
                  206426
Seq. No.
Seq. ID
                  LIB3083-119-Q1-L1-B6
                  BLASTX
Method
NCBI GI
                  q2213590
BLAST score
                  276
                  1.0e-24
E value
Match length
                  99
                  55
% identity
                  (AC000348) T7N9.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206427
Seq. ID
                  LIB3083-119-Q1-L1-B8
Method
                  BLASTX
NCBI GI
                  g3201554
                   426
BLAST score
                  3.0e-42
E value
                   96
Match length
% identity
                  82
                  (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
                  206428
Seq. No.
                  LIB3083-119-Q1-L1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                  q99751
BLAST score
                   231
                   2.0e-19
E value
Match length
                   47
                   91
% identity
                  phosphoprotein phosphatase (EC 3.1.3.16) 1A catalytic chain
NCBI Description
                   - Arabidopsis thaliana >qi 16433 emb CAA78153 (Z12163)
                  protein phosphatase 1A [Arabidopsis thaliana]
Seq. No.
                   206429
Seq. ID
                   LIB3083-119-Q1-L1-C11
Method
                   BLASTX
NCBI GI
                   q3935145
BLAST score
                   188
E value
                   2.0e-14
Match length
                   64
% identity
                   56
                   (AC005106) T25N20.9 [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 206430

Seq. ID LIB3083-119-Q1-L1-C3

Method BLASTN
NCBI GI g483546
BLAST score 37
E value 2.0e-11
Match length 53
% identity 92



NCBI Description R.communis gene for pyrophosphate-dependent phosphofructokinase alpha subunit

Seq. No. 206431

Seq. ID LIB3083-119-Q1-L1-C7

Method BLASTX
NCBI GI g2661840
BLAST score 283
E value 1.0e-25
Match length 72
% identity 75

NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 206432

Seq. ID LIB3083-119-Q1-L1-C8

Method BLASTN
NCBI GI g1143223
BLAST score 172
E value 5.0e-92
Match length 267

% identity 26
NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 206433

Seq. ID LIB3083-119-Q1-L1-C9

Method BLASTX
NCBI GI g2935416
BLAST score 339
E value 4.0e-32
Match length 81
% identity 81

NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No. 206434

Seq. ID LIB3083-119-Q1-L1-D5

Method BLASTX
NCBI GI g3334115
BLAST score 438
E value 1.0e-43
Match length 98
% identity 81

% identity 81
NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium

-7.

hirsutum]

Seq. No. 206435

Seq. ID LIB3083-119-Q1-L1-D9

Method BLASTN
NCBI GI 9451543
BLAST score 222
E value 1.0e-122
Match length 226
% identity 100

NCBI Description Gossypium barbadense Sea Island proline-rich cell wall protein gene complete cds. >gi\_1598725\_gb\_I18370\_I18370

Sequence 25 from patent US



```
206436
Seq. No.
Seq. ID
                  LIB3083-119-Q1-L1-E1
                  BLASTX
Method
NCBI GI
                  g4539292
BLAST score
                  221
                  3.0e-18
E value
                  42
Match length
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  206437
Seq. No.
Seq. ID
                  LIB3083-119-Q1-L1-E10
Method
                  BLASTX
                  g4103635
NCBI GI
                  256
BLAST score
E value
                  2.0e-22
                  87
Match length
% identity
                  55
                  (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
                  206438
Seq. No.
                  LIB3083-119-Q1-L1-E11
Seq. ID
                  BLASTX
Method
                  g602758
NCBI GI
BLAST score
                   424
                   4.0e-42
E value
                   95
Match length
                  83
% identity
NCBI Description
                  (L38581) clp-like energy-dependent protease [Lycopersicon
                  esculentum]
                   206439
Seq. No.
Seq. ID
                  LIB3083-119-Q1-L1-E12
Method
                   BLASTX
NCBI GI
                   q629806
BLAST score
                   505
                   1.0e-51
E value
Match length
                   97
% identity
                  tubulin beta chain - rice >gi 493725 emb CAA55912 (X79367)
NCBI Description
                  beta tubulin [Oryza sativa]
Seq. No.
                   206440
Seq. ID
                  LIB3083-119-Q1-L1-E3
Method
                   BLASTX
NCBI GI
                   g134101
BLAST score
                   424
                   4.0e-42
E value
Match length
                   97
                   91
% identity
```

RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi 72958 pir HHCSBA ribulose-bisphosphate carboxylase

subunit-binding protein alpha chain - castor bean

(fragment)

NCBI Description

```
Seq. No.
                  206441
                  LIB3083-119-Q1-L1-E6
Seq. ID
Method
                  BLASTX
                  q2500197
NCBI GI
                  513
BLAST score
                  2.0e-52
E value
                  97
Match length
                  100
% identity
                  RAC-LIKE GTP BINDING PROTEIN RAC13 >gi 1361976 pir S57325
NCBI Description
                  GTP-binding protein Rac 13 - upland cotton
                  >gi_1087111_bbs_170156 (S79308) 21.8 kda GTP-binding
                  protein=Rac13 [Gossypium hirsutum=cotton plants, cv. Acala
                  SJ-2, boll fibers, Peptide, 196 aa] [Gossypium hirsutum]
Seq. No.
                  206442
Seq. ID
                  LIB3083-119-Q1-L1-E8
Method
                  BLASTX
NCBI GI
                  g1495251
BLAST score
                  325
                  2.0e-30
E value
Match length
                  69
                  90
% identity
NCBI Description
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  206443
                  LIB3083-119-Q1-L1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739000
BLAST score
                  395
                  1.0e-38
E value
                  96
Match length
% identity
                  71
                  (AF022459) CYP71D10p [Glycine max]
NCBI Description
                  206444
Seq. No.
                  LIB3083-119-Q1-L1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  268
                  1.0e-149
E value
                  276
Match length
                  27
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  206445
Seq. No.
                  LIB3083-119-Q1-L1-F3
Seq. ID
Method
                  BLASTX
                  g2655888
NCBI GI
                  365
BLAST score
                   4.0e-35
E value
                  98
Match length
                   11
% identity
                  (AL009171) 62D9.a [Drosophila melanogaster]
NCBI Description
```

28305

206446

Seq. No.

```
LIB3083-119-Q1-L1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1402888
BLAST score
                  390
E value
                  4.0e-38
Match length
                  98
                  74
% identity
NCBI Description
                  (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                  206447
Seq. ID
                  LIB3083-119-Q1-L1-F5
Method
                  BLASTN
NCBI GI
                  g1143223
BLAST score
                  285
                  1.0e-159
E value
                  301
Match length
                  27
% identity
NCBI Description
                  Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.
                  206448
Sea. ID
                  LIB3083-119-Q1-L1-F7
Method
                  BLASTX
NCBI GI
                  q4090884
BLAST score
                  449
E value
                  5.0e-45
                  97
Match length
                  89
% identity
                   (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                  synaptobrevin 7B [Arabidopsis thaliana]
Seq. No.
                  206449
Seq. ID
                  LIB3083-119-Q1-L1-F8
Method
                  BLASTX
NCBI GI
                  g3273243
BLAST score
                   436
                   2.0e-43
E value
                  98
Match length
                   38
% identity
                  (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >gi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                   sativa]
Seq. No.
                  206450
                  LIB3083-119-Q1-L1-F9
Seq. ID
Method
                  BLASTX
```

NCBI GI g3790443
BLAST score 464
E value 9.0e-47
Match length 94
% identity 95

NCBI Description (AF043928) alpha-tubulin-1 [Chlorarachnion CCMP621]

Seq. No. 206451

Seq. ID LIB3083-119-Q1-L1-G1

Method BLASTN
NCBI GI g289371
BLAST score 38

NCBI GI

E value

BLAST score

Match length

q2119934

2.0e-37

384

79



```
E value
                   4.0e-12
Match length
                  58
                  91
% identity
                  Brassica napus serine/threonine protein kinase (BSK1) mRNA,
NCBI Description
                  complete cds
                  206452
Seq. No.
Seq. ID
                  LIB3083-119-Q1-L1-G12
Method
                  BLASTX
NCBI GI
                  g2497542
BLAST score
                  457
                  6.0e-46
E value
                  97
Match length
                  92
% identity
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
NCBI Description
                  >gi 629696 pir S44287 pyruvate kinase, plastid - common
                  tobacco >qi 482938 emb CAA82223 (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
Seq. No.
                  206453
                  LIB3083-119-Q1-L1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204300
BLAST score
                  204
E value
                  3.0e-16
Match length
                  74
% identity
                  61
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206454
                  LIB3083-119-Q1-L1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1632822
BLAST score
                  343
                  1.0e-32
E value
                  89
Match length
                  80
% identity
                  (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
NCBI Description
                   (U77297) transmembrane protein [Oryza sativa]
                  206455
Seq. No.
                  LIB3083-119-Q1-L1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706958
BLAST score
                  295
                  6.0e-27
E value
Match length
                  56
                  98
% identity
NCBI Description
                  (U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  206456
Seq. ID
                  LIB3083-119-Q1-L1-H12
Method
                  BLASTX
```



% identity 92

NCBI Description translation initiation factor eIF-4A.7 - common tobacco

Seq. No. 206457

Seq. ID LIB3083-119-Q1-L1-H2

Method BLASTX
NCBI GI g1172995
BLAST score 187
E value 3.0e-14
Match length 80
% identity 53

NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi\_1083790\_pir\_\_S52084 ribosomal

protein L22 - rat >gi\_710295\_emb\_CAA55204\_ (X78444)

ribosomal protein L22 [Rattus norvegicus]

>gi 1093952 prf 2105193A ribosomal protein L22 [Rattus

norvegicus]

Seq. No. 206458

Seq. ID LIB3083-119-Q1-L1-H3

Method BLASTX
NCBI GI g547683
BLAST score 401
E value 2.0e-39
Match length 76
% identity 96

NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum]
>gi 445601 prf 1909348A heat shock protein hsp80

4.

[Lycopersicon esculentum]

Seq. No. 206459

Seq. ID LIB3083-119-Q1-L1-H5

Method BLASTX
NCBI GI g4239845
BLAST score 183
E value 8.0e-14
Match length 90
% identity 47

NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 206460

Seq. ID LIB3083-119-Q1-L1-H6

Method BLASTX
NCBI GI 93790569
BLAST score 183
E value 7.0e-14
Match length 49
% identity 59

NCBI Description (AF078822) RING-H2 finger protein RHA2a [Arabidopsis

thaliana]

Seq. No. 206461

Seq. ID LIB3083-120-Q1-L1-A10

Method BLASTX
NCBI GI g3023195
BLAST score 408
E value 3.0e-40



Match length 8.5 % identity

14-3-3-LIKE PROTEIN B (SGF14B) >gi 1575727 (U70534) SGF14B NCBI Description

[Glycine max]

Seq. No.

206462

Seq. ID Method

LIB3083-120-Q1-L1-A11 BLASTX

NCBI GI

g2564066 392

BLAST score E value

3.0e-38

Match length % identity

99 74

NCBI Description

(D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Seq. No.

206463

Seq. ID

LIB3083-120-Q1-L1-A2

Method NCBI GI BLASTX g1702983

BLAST score

144

E value

1.0e-09

Match length % identity

68 46

NCBI Description

AUXIN-REPRESSED 12.5 KD PROTEIN >gi\_99855\_pir\_\_S11850

hypothetical protein - garden strawberry

>gi 22573 emb CAA36676 (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi 927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No.

206464

Seq. ID

LIB3083-120-Q1-L1-A4

Method NCBI GI BLASTN

g860887

BLAST score

47

E value

2.0e-17

Match length

59

95

% identity NCBI Description

B.vulgaris chloroplast petG gene, ycf7 gene, psbE gene,

psbF gene & ORF32 (fertile pollen)

Seq. No.

206465

Seq. ID

LIB3083-120-Q1-L1-A5

Method

BLASTX

NCBI GI

q3334138

BLAST score

178

E value

2.0e-13

Match length

70

% identity NCBI Description

54 CALNEXIN HOMOLOG PRECURSOR >gi\_669003 (U20502) calnexin

[Glycine max]

Seq. No.

206466

Seq. ID

LIB3083-120-Q1-L1-A9

Method NCBI GI BLASTX

BLAST score

g4510363

212

E value

2.0e-17



Match length % identity

NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 206467

LIB3083-120-Q1-L1-B1 Seq. ID

Method BLASTX NCBI GI g2306917 BLAST score 227 5.0e-19 E value 75 Match length % identity 59

NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis

thaliana]

206468 Seq. No.

Seq. ID LIB3083-120-Q1-L1-B10

Method BLASTX NCBI GI q464849 BLAST score 434 3.0e-43 E value Match length 105 % identity 83

NCBI Description TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha

chain - almond >gi 20413 emb CAA47635 (X67162)

alpha-tubulin [Prunus dulcis]

206469 Seq. No.

Seq. ID LIB3083-120-Q1-L1-B11

Method BLASTX g2342719 NCBI GI BLAST score 247 1.0e-21 E value Match length 71

% identity 65

NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No. 206470

Seq. ID LIB3083-120-Q1-L1-B12

Method BLASTX NCBI GI q4104242 BLAST score 249 E value 1.0e-21 Match length 93 % identity 58

(AF034266) palmitoyl-acyl carrier protein thioesterase NCBI Description

[Gossypium hirsutum]

206471 Seq. No.

Seq. ID LIB3083-120-Q1-L1-C10

Method BLASTX NCBI GI g2894598 BLAST score 255 2.0e-22 E value Match length 85 62 % identity



NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No. 206472

 Seq. ID
 LIB3083-120-Q1-L1-C11

 Method
 BLASTX

 NCBI GI
 g2270994

 BLAST score
 312

 E value
 9.0e-29

Match length 112 % identity 54 NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No. 206473

Seq. ID LIB3083-120-Q1-L1-C3

Method BLASTX
NCBI GI g1256259
BLAST score 489
E value 1.0e-49
Match length 121
% identity 79

NCBI Description (U50900) voltage-dependent anion channel protein [Spinacia

oleracea]

Seq. No. 206474

Seq. ID LIB3083-120-Q1-L1-C4

Method BLASTX
NCBI GI g3695059
BLAST score 431
E value 8.0e-43
Match length 107
% identity 85

NCBI Description (AF064787) rac GTPase activating protein 1 [Lotus

japonicus]

Seq. No. 206475

Seq. ID LIB3083-120-Q1-L1-C5

Method BLASTN
NCBI GI g2244737
BLAST score 205
E value 1.0e-112
Match length 237
% identity 97

NCBI Description Cotton mRNA for endo-1,3-beta-glucanase, clone CF922,

partial cds

Seq. No. 206476

Seq. ID LIB3083-120-Q1-L1-C7

Method BLASTX
NCBI GI g2642238
BLAST score 338
E value 7.0e-32
Match length 80
% identity 85

NCBI Description (AF031241) endoplasmic reticulum HSC70-cognate binding

protein precursor [Glycine max]

Seq. No. 206477



```
LIB3083-120-Q1-L1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455208
BLAST score
                   427
E value
                   2.0e-42
Match length
                  104
                  75
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  206478
Seq. No.
Seq. ID
                  LIB3083-120-Q1-L1-D5
Method
                  BLASTX
NCBI GI
                  g2827655
BLAST score
                  142
                   5.0e-09
E value
Match length
                   50
                   27
% identity
NCBI Description
                  (AL021637) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   206479
Seq. ID
                  LIB3083-120-Q1-L1-D7
Method
                  BLASTX
NCBI GI
                   g1619297
BLAST score
                   588
                   4.0e-61
E value
Match length
                   110
                   98
% identity
                  (Y08490) alpha-tubulin 2 [Hordeum vulgare]
NCBI Description
                   206480
Seq. No.
Seq. ID
                  LIB3083-120-Q1-L1-D8
Method
                  BLASTN
NCBI GI
                   q3510343
                   59
BLAST score
                   2.0e-24
E value
Match length
                   247
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   206481
Seq. ID
                   LIB3083-120-Q1-L1-E11
Method
                   BLASTX
NCBI GI
                   q4115377
BLAST score
                   452
E value
                   4.0e-45
Match length
                   127
                   68
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206482
                   LIB3083-120-Q1-L1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464849
                   570
BLAST score
```

28312

4.0e-59

114

E value Match length



% identity 99

NCBI Description TUBULIN ALPHA CHAIN >gi\_486847\_pir\_\_S36232 tubulin alpha

chain - almond >gi 20413 emb CAA47635 (X67162)

alpha-tubulin [Prunus dulcis]

Seq. No. 206483

Seq. ID LIB3083-120-Q1-L1-E7

Method BLASTX
NCBI GI g2702281
BLAST score 438
E value 1.0e-43
Match length 108
% identity 43

% identity 43 NCBI Description (AC003033) putative protein disulfide isomerase precursor

[Arabidopsis thaliana]

Seq. No. 206484

Seq. ID LIB3083-120-Q1-L1-E8

Method BLASTN
NCBI GI g606941
BLAST score 313
E value 1.0e-176
Match length 317
% identity 100

% identity 100 NCBI Description Gossypium hirsutum C312 clone Fb-B6 unidentified fiber

mRNA, complete cds

Seq. No. 206485

Seq. ID LIB3083-120-Q1-L1-E9

Method BLASTX
NCBI GI g136739
BLAST score 603
E value 7.0e-63
Match length 125
% identity 89

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi 67061\_pir\_\_XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 206486

Seq. ID LIB3083-120-Q1-L1-F1

Method BLASTX
NCBI GI g3953463
BLAST score 97
E value 5.0e-10
Match length 50
% identity 48

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No. 206487

Seq. ID LIB3083-120-Q1-L1-F10

Method BLASTX
NCBI GI g4539335
BLAST score 231
E value 2.0e-19

```
Match length
                   46
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  206488
Seq. No.
Seq. ID
                  LIB3083-120-Q1-L1-F11
                  BLASTX
Method
                  q2920706
NCBI GI
BLAST score
                  282
                  3.0e-25
E value
                  121
Match length
                  45
% identity
                  (Y13568) beta-xylosidase [Emericella nidulans]
NCBI Description
                  206489
Seq. No.
                  LIB3083-120-Q1-L1-F12
Seq. ID
                  BLASTX
Method
                  g3184283
NCBI GI
BLAST score
                  196
E value
                  1.0e-15
Match length
                   62
                   66
% identity
                   (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   206490
Seq. ID
                  LIB3083-120-Q1-L1-F3
Method
                  BLASTX
NCBI GI
                   g167369
BLAST score
                   378
E value
                   2.0e-36
Match length
                   88
                   83
% identity
                   (M77700) ribulosebisphosphate carboxylase [Gossypium
NCBI Description
                  hirsutum]
                   206491
Seq. No.
                   LIB3083-120-Q1-L1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2501850
BLAST score
                   438
                   8.0e-44
E value
Match length
                   89
```

94 % identity

(AF012823) GDP dissociation inhibitor [Nicotiana tabacum] NCBI Description

Seq. No. 206492

LIB3083-120-Q1-L1-F6 Seq. ID

Method BLASTX NCBI GI g3935168 BLAST score 556 E value 2.0e-57 Match length 130 % identity 78

(AC004557) F17L21.11 [Arabidopsis thaliana] NCBI Description

Seq. No. 206493

Method

NCBI GI

BLASTX

q2529680



```
LIB3083-120-Q1-L1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4324967
BLAST score
                  639
                   4.0e-67
E value
Match length
                  128
                  98
% identity
NCBI Description
                  (AF114796) ADP-ribosylation factor [Glycine max]
Seq. No.
                  206494
                  LIB3083-120-Q1-L1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g484656
BLAST score
                   400
                  2.0e-39
E value
Match length
                  83
                   90
% identity
NCBI Description
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
                  cucumber >qi 452165 dbj BAA05408 (D26392)
                  monodehydroascorbate reductase [Cucumis sativus]
Seq. No.
                  206495
Seq. ID
                  LIB3083-120-Q1-L1-G1
Method
                  BLASTX
NCBI GI
                  g4455351
BLAST score
                   262
E value
                   7.0e-23
Match length
                   69
                   68
% identity
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
                   206496
Seq. No.
                  LIB3083-120-Q1-L1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2459429
BLAST score
                   256
                   1.0e-22
E value
                   69
Match length
% identity
                   67
NCBI Description
                   (AC002332) unknown protein [Arabidopsis thaliana]
                   206497
Seq. No.
                  LIB3083-120-Q1-L1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1076746
BLAST score
                   208
                   5.0e-17
E value
Match length
                   42
                   100
% identity
NCBI Description
                  heat shock protein 70 - rice (fragment)
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   206498
Seq. No.
Seq. ID
                  LIB3083-120-Q1-L1-G3
```



BLAST score 352 E value 1.0e-33 Match length 80 % identity 44

NCBI Description (AC002535) putative protein disulfide-isomerase precursor

[Arabidopsis thaliana]

Seq. No. 206499

Seq. ID LIB3083-120-Q1-L1-G4

Method BLASTN
NCBI GI g3985934
BLAST score 86
E value 1.0e-40
Match length 194

% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJE7, complete sequence [Arabidopsis thaliana]

Seq. No. 206500

Seq. ID LIB3083-120-Q1-L1-G8

Method BLASTX
NCBI GI g3386619
BLAST score 223
E value 1.0e-18
Match length 86
% identity 50

NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 206501

Seq. ID LIB3083-120-Q1-L1-G9

Method BLASTN
NCBI GI g1143223
BLAST score 127
E value 3.0e-65
Match length 261
% identity 90

NCBI Description Gossypium barbadense FbLate-2 gene, complete cds

Seq. No. 206502

Seq. ID LIB3083-120-Q1-L1-H11

Method BLASTX
NCBI GI g2827143
BLAST score 551
E value 8.0e-57
Match length 119
% identity 83

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 206503

Seq. ID LIB3083-120-Q1-L1-H12

Method BLASTX
NCBI GI g2851455
BLAST score 278
E value 3.0e-25
Match length 74
% identity 73





```
NCBI Description DYNAMIN-LIKE PROTEIN >gi_2267213 (L36939) dynamin-like GTP binding protein [Arabidopsis thaliana]

Seq. No. 206504
Seq. ID LIB3083-120-Q1-L1-H2
Method BLASTX
NCBI GI g2244732
BLAST score 462
```

BLAST score 462 E value 1.0e-46 Match length 81 % identity 100

NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

 Seq. No.
 206505

 Seq. ID
 LIB3120-001-Q1-K1-A10

 Method
 BLASTX

 NCBI GI
 g1769905

BLAST score 472 E value 2.0e-47 Match length 114 % identity 78

NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)

[Arabidopsis thaliana]

Seq. No. 206506

Seq. ID LIB3120-001-Q1-K1-A12

Method BLASTX
NCBI GI g1469930
BLAST score 310
E value 1.0e-28
Match length 112
% identity 70

NCBI Description (U48777) fiber-specific acyl carrier protein [Gossypium

hirsutum]

Seq. No. 206507

Seq. ID LIB3120-001-Q1-K1-A2

Method BLASTX
NCBI GI g548774
BLAST score 297
E value 3.0e-27
Match length 82
% identity 71

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal

protein L7a - rice >gi 303855 dbj BAA02156\_ (D12631)

ribosomal protein L7A [Oryza sativa]

Seq. No. 206508

Seq. ID LIB3120-001-Q1-K1-A4

Method BLASTX
NCBI GI g2499879
BLAST score 607
E value 3.0e-63
Match length 147
% identity 78

NCBI Description CYSTEINE PROTEINASE 3 PRECURSOR >gi\_2129935\_pir\_\_S66348 senescence-associated cysteine proteinase precursor (clone

 $1.3r_{p}$ 





SENU3) - tomato >gi\_1235545\_emb\_CAA88629\_ (248736) pre-pro-cysteine proteinase [Lycopersicon esculentum]

206509 Seq. No. Seq. ID LIB3120-001-Q1-K1-A5 Method BLASTX q289920 NCBI GI 395 BLAST score 1.0e-38 E value 89 Match length % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum]

Seq. No. 206510 Seq. ID LIB3120-001-Q1-K1-A7

Method BLASTX
NCBI GI g2864617
BLAST score 335
E value 2.0e-31
Match length 139
% identity 52

NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like

protein [Arabidopsis thaliana]

Seq. No. 206511

Seq. ID LIB3120-001-Q1-K1-A8

Method BLASTX
NCBI GI g4432841
BLAST score 144
E value 5.0e-09
Match length 45
% identity 67

NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No. 206512

Seq. ID LIB3120-001-Q1-K1-B1

Method BLASTX
NCBI GI g4544447
BLAST score 144
E value 6.0e-09
Match length 69
% identity 51

NCBI Description (AC006592) putative GTP cyclohydrolase [Arabidopsis

thaliana]

Seq. No. 206513

Seq. ID LIB3120-001-Q1-K1-B10

Method BLASTX
NCBI GI g1352821
BLAST score 590
E value 2.0e-61
Match length 123
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain



98

% identity

NCBI Description

precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091);
ribulose bisphosphate carboxylase [Gossypium hirsutum]

206514 Seq. No. LIB3120-001-Q1-K1-B12 Seq. ID Method BLASTX NCBI GI g4512613 399 BLAST score 6.0e-39 E value 120 Match length 68 % identity NCBI Description (AC004793) F28K20.12 [Arabidopsis thaliana] 206515 Seq. No. LIB3120-001-Q1-K1-B3 Seq. ID Method BLASTX NCBI GI g2499535 220 BLAST score E value 2.0e-26 Match length 125 59 % identity 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi 595681 NCBI Description (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea] 206516 Seq. No. LIB3120-001-Q1-K1-B4 Seq. ID Method BLASTX NCBI GI g3913651 BLAST score 373 8.0e-36 E value 91 Match length 75 % identity FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR NCBI Description (FNR) >gi 2225993\_emb\_CAA74359 (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum] 206517 Seq. No. LIB3120-001-Q1-K1-B6 Seq. ID Method BLASTX NCBI GI g3158476 BLAST score 631 5.0e-66 E value 140 Match length 86 % identity (AF067185) aquaporin 2 [Samanea saman] NCBI Description 206518 Seq. No. LIB3120-001-Q1-K1-B7 Seq. ID Method BLASTX NCBI GI g1703115 BLAST score 637 E value 9.0e-67 Match length 121

28319

ACTIN 3 >gi 2129526 pir S68112 actin 3 - Arabidopsis

thaliana >gi 1145695 (U39480) actin [Arabidopsis thaliana]



>gi\_3236244 (AC004684) actin 3 protein [Arabidopsis
thaliana]

Seq. No. 206519

Seq. ID LIB3120-001-Q1-K1-C1

Method BLASTX
NCBI GI g1708313
BLAST score 557
E value 2.0e-57
Match length 117
% identity 96

NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637

(S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis

thaliana]

Seq. No. 206520

Seq. ID LIB3120-001-Q1-K1-C10

Method BLASTX
NCBI GI g1173345
BLAST score 203
E value 5.0e-16
Match length 108
% identity 44

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi\_1076403\_pir\_\_S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi\_786466\_bbs\_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa]

[Arabidopsis thaliana]

Seq. No. 206521

Seq. ID LIB3120-001-Q1-K1-C11

Method BLASTX
NCBI GI g4406530
BLAST score 157
E value 8.0e-11
Match length 54
% identity 63

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 206522

Seq. ID LIB3120-001-Q1-K1-C12

Method BLASTX
NCBI GI g1658197
BLAST score 621
E value 2.0e-65
Match length 134
% identity 88

NCBI Description (U74630) calreticulin [Ricinus communis] >gi 1763297

(U74631) calreticulin [Ricinus communis]

Seq. No. 206523

Seq. ID LIB3120-001-Q1-K1-C3

Method BLASTX NCBI GI g3738316



BLAST score 271 E value 7.0e-24 Match length 82 % identity 63

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 206524

Seq. ID LIB3120-001-Q1-K1-C4

Method BLASTX
NCBI GI g1352821
BLAST score 564
E value 3.0e-58
Match length 107
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206525

Seq. ID LIB3120-001-Q1-K1-C5

Method BLASTX
NCBI GI g421826
BLAST score 482
E value 1.0e-48
Match length 137
% identity 66

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi\_298036\_emb CAA50712 (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 206526

Seq. ID LIB3120-001-Q1-K1-C6

Method BLASTX
NCBI GI g4455208
BLAST score 600
E value 2.0e-62
Match length 134
% identity 86

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 206527

Seq. ID LIB3120-001-Q1-K1-C8

Method BLASTX
NCBI GI g1352821
BLAST score 270
E value 4.0e-24
Match length 73
% identity 68

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206528



```
LIB3120-001-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  414
E value
                  8.0e-41
                  91
Match length
                  90
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
```

206529

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carbo $\overline{x}$ ylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

LIB3120-001-Q1-K1-D1 Seq. ID Method BLASTX NCBI GI q3288821 BLAST score 518 8.0e-53 E value Match length 121 81 % identity

Seq. No.

(AF063901) alanine:glyoxylate aminotransferase; NCBI Description

transaminase [Arabidopsis thaliana]

Seq. No. 206530

LIB3120-001-Q1-K1-D10 Seq. ID

Method BLASTX q2651307 NCBI GI BLAST score 199 2.0e-20 E value Match length 86 65 % identity

NCBI Description (AC002336) putative uroporphyinogen decarboxylase

[Arabidopsis thaliana]

206531 Seq. No.

LIB3120-001-Q1-K1-D12 Seq. ID

Method BLASTX NCBI GI g3080440 BLAST score 203 E value 8.0e-16 Match length 81 % identity 53

NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

206532 Seq. No.

LIB3120-001-Q1-K1-D2 Seq. ID

Method BLASTN g3821780 NCBI GI BLAST score 36 E value 1.0e-10 Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 206533

LIB3120-001-Q1-K1-D4 Seq. ID



Method BLASTX
NCBI GI g125887
BLAST score 248
E value 4.0e-21
Match length 142
% identity 41

NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

>gi\_82092\_pir\_\_S04765 LAT52 protein precursor - tomato
>gi\_295812\_emb\_CAA33854\_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 206534

Seq. ID LIB3120-001-Q1-K1-D5

Method BLASTX
NCBI GI g400890
BLAST score 281
E value 3.0e-25
Match length 90
% identity 61

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi\_282837\_pir\_\_S26953 photosystem II 22K protein precursor
- spinach >gi\_21307\_emb\_CAA48557\_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi\_260917\_bbs\_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 206535

Seq. ID LIB3120-001-Q1-K1-D6

Method BLASTX
NCBI GI g2129944
BLAST score 215
E value 2.0e-17
Match length 113
% identity 44

NCBI Description RNA-binding protein RZ-1 - wood tobacco

>gi\_1395193\_dbj\_BAA12064\_ (D83696) RNA-binding protein RZ-1
[Nicotiana sylvestris] >gi\_1435062\_dbj\_BAA06012\_ (D28861)

RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No. 206536

Seq. ID LIB3120-001-Q1-K1-E1

Method BLASTX
NCBI GI g1345698
BLAST score 467
E value 7.0e-47
Match length 103
% identity 88

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

a/b-binding protein - upland cotton

>gi 452314 emb CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 206537

Seq. ID LIB3120-001-Q1-K1-E11

Method BLASTX NCBI GI g2961378



BLAST score 2.0e-29 E value Match length 122 % identity

(AL022141) putative protein [Arabidopsis thaliana] NCBI Description

206538 Seq. No.

Seq. ID LIB3120-001-Q1-K1-E2

Method BLASTX a3860264 NCBI GI 255 BLAST score 6.0e-22 E value 91 Match length 60 % identity

(AC005824) unknown protein [Arabidopsis thaliana] NCBI Description

206539 Seq. No.

Seq. ID LIB3120-001-Q1-K1-E4

Method BLASTX NCBI GI g289920 BLAST score 411 6.0e-50 E value 102 Match length % identity 95

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

206540 Seq. No.

LIB3120-001-Q1-K1-E6 Seq. ID

Method BLASTX NCBI GI q1354515 276 BLAST score 2.0e-24 E value 136 Match length % identity

(U55837) carbonic anhydrase [Populus tremula x Populus NCBI Description

tremuloides]

Seq. No. 206541

Seq. ID LIB3120-001-Q1-K1-E7

Method BLASTX NCBI GI g1352821 BLAST score 196 3.0e-15 E value Match length 64 67 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

206542 Seq. No.

LIB3120-001-Q1-K1-E9 Seq. ID

BLASTX Method NCBI GI g2739375 215 BLAST score



```
2.0e-17
E value
Match length
                   81
% identity
                   56
NCBI Description
                   (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                   206543
Seq. ID
                  LIB3120-001-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   505
                   2.0e-51
E value
                   107
Match length
% identity
                   90
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                   206544
Seq. No.
Seq. ID
                   LIB3120-001-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   q3822036
BLAST score
                   201
E value
                   1.0e-15
Match length
                   123
                   35
% identity
NCBI Description
                  (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
                   206545
Seq. No.
                   LIB3120-001-Q1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g304040
BLAST score
                   110
                   7.0e-55
E value
                   150
Match length
                   93
% identity
NCBI Description
                  Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene
                   206546
Seq. No.
Seq. ID
                   LIB3120-001-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   q1619956
BLAST score
                   343
E value
                   3.0e-32
Match length
                   77
                   88
% identity
NCBI Description
                   (U72151) voltage-gated chloride channel [Arabidopsis
                   thaliana]
Seq. No.
                   206547
Seq. ID
                   LIB3120-001-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g100196
BLAST score
                   579
                   5.0e-60
E value
Match length
                   128
```

chlorophyll a/b-binding protein (cab-11) - tomato

82

% identity

NCBI Description



```
Seq. No.
                  206548
                  LIB3120-001-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006881
BLAST score
                  280
E value
                  7.0e-25
Match length
                  119
                  57
% identity
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                  206549
Seq. No.
                  LIB3120-001-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g425194
BLAST score
                  609
                  2.0e-63
E value
Match length
                  130
                  89
% identity
NCBI Description
                  (L26243) heat shock protein [Spinacia oleracea] >qi 2660772
                  (AF034618) cytosolic heat shock 70 protein [Spinacia
                  oleracea]
                  206550
Seq. No.
Seq. ID
                  LIB3120-001-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1935914
BLAST score
                  228
                  9.0e-19
E value
Match length
                  77
% identity
                  53
NCBI Description
                  (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]
Seq. No.
                  206551
                  LIB3120-001-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115765
BLAST score
                  566
                  2.0e-58
E value
Match length
                  131
% identity
                  49
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
                  (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding
                  protein type II (cab-7) - tomato >gi 19180 emb CAA32197
                   (X14036) chlorophyll a/b-binding protein [Lycopersicon
                  esculentum] >gi 170431 (M20241) chlorophyll a/b-binding
                  protein [Lycopersicon esculentum] >gi 226546 prf 1601518A
                  chlorophyll a/b binding protein II [Lycopersicon
                  esculentum]
Seq. No.
                  206552
```

Seq. ID

LIB3120-001-Q1-K1-G11

Method BLASTX g2618731 NCBI GI BLAST score 444 E value 4.0e-4498 Match length 84 % identity



NCBI Description (U49077) IAA21 [Arabidopsis thaliana]

Seq. No. 206553

Seq. ID LIB3120-001-Q1-K1-G12

Method BLASTX
NCBI GI g1168655
BLAST score 335
E value 2.0e-31
Match length 102
% identity 55

NCBI Description PROBABLE BETA-GLUCOSIDASE (GENTIOBIASE) (CELLOBIASE)

(BETA-D-GLUCOSIDE GLUCOHYDROLASE) (AMYGDALASE)
>gi\_710632\_dbj\_BAA06429\_ (D30762) beta-glucosidase
[Bacillus subtilis] >gi\_1805413\_dbj\_BAA08975\_ (D50453)
homologue of beta-glucosidase of B. circulans [Bacillus subtilis] >gi\_2632627\_emb\_CAB12135\_ (Z99105) similar to

beta-glucosidase [Bacillus subtilis]

Seq. No. 206554

Seq. ID LIB3120-001-Q1-K1-G4

Method BLASTX
NCBI GI g2407800
BLAST score 329
E value 9.0e-31
Match length 73
% identity 89

NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 206555

Seq. ID LIB3120-001-Q1-K1-G5

Method BLASTX
NCBI GI g3641838
BLAST score 505
E value 3.0e-51
Match length 140
% identity 71

NCBI Description (AL023094) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 206556

Seq. ID LIB3120-001-Q1-K1-G6

Method BLASTX
NCBI GI g3914940
BLAST score 551
E value 2.0e-65
Match length 141
% identity 89

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi\_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

[Spinacia oleracea]

Seq. No. 206557

Seq. ID LIB3120-001-Q1-K1-G7

Method BLASTX NCBI GI g2583108 BLAST score 423



```
E value
Match length
                  110
% identity
                  72
                  (ACO02387) putative surface protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206558
                  LIB3120-001-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2341033
BLAST score
                  287
                  1.0e-25
E value
Match length
                  85
% identity
                  71
NCBI Description
                   (AC000104) Similar to Babesia aldo-keto reductase
                   (gb_M93122). [Arabidopsis thaliana]
                  206559
Seq. No.
Seq. ID
                  LIB3120-001-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  q2894534
BLAST score
                  546
E value
                  5.0e-56
                  132
Match length
                  83
% identity
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
                  206560
Seq. No.
                  LIB3120-001-Q1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2440044
BLAST score
                   455
                  3.0e-58
E value
                  132
Match length
                  86
% identity
                  (AJ001293) major intrinsic protein PIPB [Craterostigma
NCBI Description
                  plantagineum]
Seq. No.
                  206561
                  LIB3120-001-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1181599
BLAST score
                   486
E value
                   4.0e-49
Match length
                  127
% identity
NCBI Description
                   (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                  206562
                  LIB3120-001-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2911082
```

Method BLASTX
NCBI GI g2911082
BLAST score 141
E value 1.0e-08
Match length 96
% identity 35

NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]



```
206563
Seq. No.
                  LIB3120-001-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                  g1431629
NCBI GI
BLAST score
                  234
                  1.0e-34
E value
Match length
                  133
                  56
% identity
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                  206564
Seq. No.
                  LIB3120-002-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3924597
BLAST score
                  200
                   2.0e-15
E value
                   108
Match length
% identity
                   39
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                   206565
Seq. No.
                  LIB3120-002-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                   q3122053
NCBI GI
BLAST score
                   324
                   9.0e-36
E value
                   91
Match length
                   87
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_1235582_emb_CAA65391_ (X96555) elongation factor
                   1-alpha [Pisum sativum]
Seq. No.
                   206566
Seq. ID
                   LIB3120-002-Q1-K1-A6
                   BLASTX
Method
NCBI GI
                   g1709825
BLAST score
                   334
E value
                   3.0e-31
Match length
                   125
% identity
                   64
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
                   206567
Seq. No.
                   LIB3120-002-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g542103
                   700
BLAST score
                   4.0e-74
E value
                   140
Match length
% identity
                   93
                   P protein - Flaveria pringlei >gi 438003 emb CAA81076_
NCBI Description
                   (Z25857) P protein [Flaveria pringlei]
```

Seq. No. 206568

Seq. ID LIB3120-002-Q1-K1-B10

Method BLASTX



NCBI GI g1352821
BLAST score 417
E value 2.0e-41
Match length 89
% identity 90
NCBI Description RIBULOSE

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206569

Seq. ID LIB3120-002-Q1-K1-B11

Method BLASTX
NCBI GI g2497753
BLAST score 308
E value 4.0e-28
Match length 88
% identity 58

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)

>gi 1321915 emb CAA65477 (X96716) lipid transfer protein

[Prunus dulcis]

Seq. No. 206570

Seq. ID LIB3120-002-Q1-K1-B5

Method BLASTX
NCBI GI g3983125
BLAST score 300
E value 3.0e-27
Match length 130
% identity 53

NCBI Description (AF097648) phosphate/triose-phosphate translocator

precursor [Arabidopsis thaliana]

Seq. No. 206571

Seq. ID LIB3120-002-Q1-K1-B6

Method BLASTX
NCBI GI g3142292
BLAST score 335
E value 2.0e-31
Match length 92
% identity 77

NCBI Description (AC002411) Contains similarity to tetratricopeptide repeat

protein gb\_U46571 from home sapiens. EST gb\_Z47802 and gb Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No. 206572

Seq. ID LIB3120-002-Q1-K1-B9

Method BLASTX
NCBI GI g3914442
BLAST score 454
E value 2.0e-45
Match length 128
% identity 70

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>qi 1916350 (U92504) PSI-H subunit [Brassica rapa]



206573 Seq. No. Seq. ID LIB3120-002-Q1-K1-C10 Method BLASTX NCBI GI q2052383 BLAST score 405 1.0e-39 E value Match length 80 91 % identity (U66345) calreticulin [Arabidopsis thaliana] NCBI Description 206574 Seq. No. Seq. ID LIB3120-002-Q1-K1-C11 Method BLASTX NCBI GI g1352821 BLAST score 541 2.0e-55 E value Match length 103 % identity 98 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 206575 Seq. ID LIB3120-002-Q1-K1-C12 Method BLASTX NCBI GI g289920 BLAST score 744 3.0e-79 E value Match length 140 % identity 99 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum] 206576 Seq. No. LIB3120-002-Q1-K1-C2 Seq. ID Method BLASTX NCBI GI g289920 BLAST score 584 4.0e-69 E value Match length 128 89 % identity NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 206577

Seq. ID LIB3120-002-Q1-K1-C4

Method BLASTX
NCBI GI g461999
BLAST score 687
E value 1.0e-72
Match length 140
% identity 96

NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)



```
Seq. No.
                   206578
                  LIB3120-002-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3237304
BLAST score
                  378
                  5.0e-37
E value
Match length
                  132
% identity
                  58
NCBI Description
                   (U91561) pyridoxine 5'-phosphate oxidase [Rattus
                  norvegicus]
Seq. No.
                  206579
Seq. ID
                  LIB3120-002-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1169494
BLAST score
                  262
E value
                  8.0e-23
Match length
                  86
% identity
                   62
NCBI Description
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                  >gi 2119915 pir S60659 EF-Tu protein precursor - soybean
                  >gi_949873_emb_CAA61444 (X89058) EF-Tu protein [Glycine
                  max]
Seq. No.
                  206580
Seq. ID
                  LIB3120-002-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q3850621
BLAST score
                  138
E value
                  1.0e-08
Match length
                  67
% identity
                   45
NCBI Description
                   (Y15382) putative RNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  206581
                  LIB3120-002-Q1-K1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  74
E value
                  2.0e-33
                  278
Match length
% identity
                  82
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  206582
Seq. ID
                  LIB3120-002-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2435517
```

BLAST score 389 E value 9.0e-38 Match length 125 % identity 58

NCBI Description (AF024504) contains similarity to peptidase family A1

[Arabidopsis thaliana]

206583 Seq. No.



Seq. ID LIB3120-002-Q1-K1-D10 Method BLASTX

NCBI GI g133028 BLAST score 354 E value 1.0e-33 Match length 129 % identity 57

NCBI Description 50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9)

>gi\_71257\_pir\_\_R5MUL9 ribosomal protein L9 precursor,
chloroplast - Arabidopsis thaliana >gi\_16499\_emb\_CAA77480\_
(Z11129) plastid ribosomal protein CL9 [Arabidopsis

thaliana] >gi\_16501\_emb\_CAA77594\_ (Z11509) Chloroplast ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No. 206584

Seq. ID LIB3120-002-Q1-K1-D11

Method BLASTX
NCBI GI g2129559
BLAST score 538
E value 4.0e-55
Match length 126
% identity 84

NCBI Description cellulase homolog OR16pep - Arabidopsis thaliana

>gi\_1022807 (U37702) cellulase [Arabidopsis thaliana]
>gi\_3493633 (AF074092) cellulase [Arabidopsis thaliana]
>gi\_3598956 (AF074375) cellulase [Arabidopsis thaliana]
>gi\_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN

[Arabidopsis thaliana]

Seq. No. 206585

Seq. ID LIB3120-002-Q1-K1-D12

Method BLASTX
NCBI GI g114654
BLAST score 238
E value 3.0e-22
Match length 81
% identity 71

NCBI Description ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)

>gi 67898 pir LWNTA H+-transporting ATP synthase (EC

3.6.1.34) lipid-binding protein - common tobacco

chloroplast >gi\_11812\_emb\_CAA77343\_ (Z00044) ATPase III subunit [Nicotiana tabacum] >gi\_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi\_224347\_prf\_\_1102209A

ATPase III, H translocating [Nicotiana sp.]

>gi 225272 prf 1211235G ATPase III [Nicotiana tabacum]

Seq. No. 206586

Seq. ID LIB3120-002-Q1-K1-D2

Method BLASTX
NCBI GI g289920
BLAST score 728
E value 2.0e-77
Match length 136
% identity 99

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]



Seq. No. 206587

Seq. ID LIB3120-002-Q1-K1-D3

Method BLASTX
NCBI GI 9421826
BLAST score 324
E value 3.0e-30
Match length 102
% identity 62

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>qi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 206588

Seq. ID LIB3120-002-Q1-K1-D4

Method BLASTX
NCBI GI g417154
BLAST score 678
E value 1.0e-71
Match length 144
% identity 92

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir\_\_S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi\_20256\_emb\_CAA77978\_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 206589

Seq. ID LIB3120-002-Q1-K1-D5

Method BLASTX
NCBI GI g417154
BLAST score 164
E value 3.0e-11
Match length 36
% identity 86

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi\_20256\_emb\_CAA77978\_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 206590

Seq. ID LIB3120-002-Q1-K1-D8

Method BLASTX
NCBI GI g1170567
BLAST score 683
E value 4.0e-72
Match length 142
% identity 92

NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi\_1085960\_pir\_\_S52648 INO1 protein - Citrus paradisi
>gi\_602565\_emb\_CAA83565\_ (Z32632) INO1 [Citrus x paradisi]

Seq. No. 206591

Seq. ID LIB3120-002-Q1-K1-E2

Method BLASTX
NCBI GI 94335750
BLAST score 166
E value 1.0e-11
Match length 46



% identity (AC006284) putative beta-1,3-endoglucanase [Arabidopsis NCBI Description thaliana] 206592 Seq. No. LIB3120-002-Q1-K1-E4 Seq. ID Method BLASTX g1345698 NCBI GI 498 BLAST score 2.0e-50 E value 100 Match length 91 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR NCBI Description (CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll a/b-binding protein - upland cotton >qi 452314 emb CAA38025 (X54090) chlorophyll ab binding protein [Gossypium hirsutum] 206593 Seq. No. LIB3120-002-Q1-K1-E5 Seq. ID Method BLASTX g4512651 NCBI GI 416 BLAST score E value 8.0e-41Match length 134 % identity 58 (AC007048) putative tyrosine transaminase [Arabidopsis NCBI Description thaliana] Seq. No. 206594 LIB3120-002-Q1-K1-E6 Seq. ID BLASTX Method NCBI GI g1354515 BLAST score 323 2.0e-30 E value 136 Match length 57 % identity (U55837) carbonic anhydrase [Populus tremula x Populus NCBI Description tremuloides] 206595 Seq. No. LIB3120-002-Q1-K1-E7 Seq. ID BLASTX Method g2335104 NCBI GI BLAST score 712 2.0e-75 E value 146 Match length 47 % identity (AC002339) putative villin [Arabidopsis thaliana] NCBI Description 206596 Seq. No. LIB3120-002-Q1-K1-E8 Seq. ID Method BLASTX

NCBI GI g3152597 BLAST score 217 E value 2.0e-17 Match length 140



```
% identity
                  (AC002986) Contains similarity to S. cerevisiae
NCBI Description
                  hypothetical protein YOR197w, gb Z75105. [Arabidopsis
                  thaliana]
                  206597
Seq. No.
                  LIB3120-002-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  746
                  2.0e-79
E value
                  141
Match length
                  96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  206598
Seq. ID
                  LIB3120-002-Q1-K1-F12
Method
                  BLASTX
                  g20729
NCBI GI
BLAST score
                  442
E value
                  7.0e-44
Match length
                  121
                  75
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
                  206599
Seq. No.
Seq. ID
                  LIB3120-002-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q3980416
                  436
BLAST score
                  3.0e-43
E value
Match length
                  137
% identity
                  (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  206600
                  LIB3120-002-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  q231688
NCBI GI
BLAST score
                  662
                  1.0e-69
E value
Match length
                  125
                  100
% identity
```

CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC NCBI Description 1.11.1.6) - upland cotton >gi\_18488\_emb\_CAA39998\_ (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No. 206601

Seq. ID LIB3120-002-Q1-K1-F4

Method BLASTX q1168739 NCBI GI BLAST score 591



E value 2.0e-61 Match length 133 % identity 83

NCBI Description CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi\_438449

(L18901) carbonic anhydrase [Arabidopsis thaliana]

Seq. No. 206602

Seq. ID LIB3120-002-Q1-K1-F6

Method BLASTX
NCBI GI g1351408
BLAST score 701
E value 3.0e-74
Match length 146
% identity 84

NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)

>gi\_1076563\_pir\_\_S51117 cystein proteinase - sweet orange
>gi\_633185\_emb\_CAA87720\_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi\_1588548\_prf\_\_2208463A

vascular processing protease [Citrus sinensis]

Seq. No. 206603

Seq. ID LIB3120-002-Q1-K1-F8

Method BLASTX
NCBI GI g115833
BLAST score 540
E value 2.0e-55
Match length 110
% identity 90

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR

(CAB-10A) (LHCP) >gi\_100195\_pir\_\_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi 170394 (M32605)

a-binding protein [Lycopersicon esculentum]

Seq. No. 206604

Seq. ID LIB3120-002-Q1-K1-F9

Method BLASTX
NCBI GI g1175381
BLAST score 257
E value 3.0e-22
Match length 122
% identity 39

NCBI Description HYPOTHETICAL 44.9 KD PROTEIN C18B11.02C IN CHROMOSOME I

>gi\_2130286 pir S58301 hypothetical protein SPAC18B11.02c

- fission yeast (Schizosaccharomyces pombe)

>gi 929888 emb CAA90587 (Z50728) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 206605

Seq. ID LIB3120-002-Q1-K1-G1

Method BLASTX
NCBI GI g133867
BLAST score 527
E value 7.0e-54
Match length 121
% identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal

protein S11 - maize >gi 22470 emb CAA39438 (X55967)



## ribosomal protein S11 [Zea mays]

```
Seq. No.
                   206606
Seq. ID
                   LIB3120-002-Q1-K1-G10
                   BLASTX
Method
NCBI GI
                   q3107905
BLAST score
                   236
E value
                   8.0e-25
Match length
                   99
                   13
 % identity
                   (D85101) leaf protein [Ipomoea nil]
NCBI Description
Seq. No.
                   206607
Seq. ID
                   LIB3120-002-Q1-K1-G12
                   BLASTX
Method
                   q1352821
NCBI GI
BLAST score
                   540
E value
                   2.0e-55
                   104
Match length
 % identity
                   97
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   206608
 Seq. No.
                   LIB3120-002-Q1-K1-G2
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q430947
 BLAST score
                   288
                   7.0e-26
 E value
                   59
 Match length
                    95
 % identity
                    (U01103) PSI type III chlorophyll a/b-binding protein
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                   206609
                   LIB3120-002-Q1-K1-G3
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g228403
 BLAST score
                    450
 E value
                    6.0e - 45
 Match length
                   104
                   83
 % identity
 NCBI Description
                   glycolate oxidase [Lens culinaris]
 Seq. No.
                   206610
                   LIB3120-002-Q1-K1-G4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1076414
 BLAST score
                   574
                   2.0e-59
. E value
 Match length
                   146
 % identity
                   74
                   subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
 NCBI Description
                   thaliana (fragment) >gi 757534 emb CAA59963 (X85974)
```

Seq. ID Method

NCBI GI



## subtilisin-like protease [Arabidopsis thaliana]

```
Seq. No.
                  206611
Seq. ID
                  LIB3120-002-Q1-K1-G5
                  BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  590
                  3.0e-61
E value
Match length
                  110
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  206612
Seq. No.
Seq. ID
                  LIB3120-002-Q1-K1-G6
                  BLASTX
Method
NCBI GI
                  q479406
                  552
BLAST score
                  8.0e-57
E value
                  120
Match length
% identity
                  62
NCBI Description
                  chlorophyll a/b-binding protein - garden pea
                  >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
                  206613
Seq. No.
Seq. ID
                  LIB3120-002-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  q120669
BLAST score
                  534
                  1.0e-54
E value
Match length
                  124
% identity
                  82
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  206614
Seq. ID
                  LIB3120-002-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  719
                   2.0e-76
E value
Match length
                   134
                   99
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   206615
Seq. No.
```

28339

LIB3120-002-Q1-K1-H1

BLASTX

q3874247



```
BLAST score
                  2.0e-12
E value
Match length
                  86
% identity
                  41
                  (Z70205) predicted using Genefinder [Caenorhabditis
NCBI Description
                  elegans]
                  206616
Seq. No.
Seq. ID
                  LIB3120-002-Q1-K1-H11
Method
                  BLASTX
                  g68200
NCBI GI
BLAST score
                  368
E value
                  3.0e-35
                  96
Match length
                  80
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi 22633 emb_CAA47293_ (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.
                  206617
                  LIB3120-002-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g3874247
NCBI GI
                  168
BLAST score
                  9.0e-12
E value
                  86
Match length
% identity
                   40
                   (270205) predicted using Genefinder [Caenorhabditis
NCBI Description
                  elegans]
Seq. No.
                   206618
                  LIB3120-002-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  q289920
NCBI GI
                   515
BLAST score
                   1.0e-52
E value
Match length
                   110
                   87
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   206619
Seq. No.
Seq. ID
                   LIB3120-002-Q1-K1-H4
                   BLASTX
Method
                   q1351270
NCBI GI
BLAST score
                   406
E value
                   9.0e-40
Match length
                   117
                   68
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
                   5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
```

isomerase [Oryza sativa]

206620 Seq. No.

LIB3120-002-Q1-K1-H5 Seq. ID

BLASTX Method

28340



NCBI GI g1352821 BLAST score 431 E value 9.0e-43 Match length 84 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206621

Seq. ID LIB3120-002-Q1-K1-H6

Method BLASTX
NCBI GI g1352821
BLAST score 716
E value 4.0e-76
Match length 131
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206622

\*

Seq. ID LIB3120-002-Q1-K1-H7

Method BLASTX
NCBI GI g4567279
BLAST score 378
E value 2.0e-36
Match length 127
% identity 61

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 206623

Seq. ID LIB3120-003-Q1-K1-A1

Method BLASTX
NCBI GI g542100
BLAST score 588
E value 5.0e-61
Match length 135
% identity 84

NCBI Description H-protein - Flaveria pringlei >gi\_2147453\_pir\_\_S60195

H-protein precursor (clone HFC1) - Flaveria cronquistii >gi\_437993\_emb\_CAA81073\_ (Z25854) H-protein [Flaveria cronquistii] >gi\_437999\_emb\_CAA81074\_ (Z25855) H-protein [Flaveria pringlei] >gi\_3688299\_emb\_CAB16912\_ (Z99763)

H-protein [Flaveria pringlei]

Seq. No. 206624

Seq. ID LIB3120-003-Q1-K1-A10

Method BLASTX
NCBI GI g2632254
BLAST score 386
E value 7.0e-40



Match length 60 % identity

(Y12465) serine/threonine kinase [Sorghum bicolor] NCBI Description

Seq. No.

206625

Seq. ID LIB3120-003-Q1-K1-A12 BLASTX Method

a515377 NCBI GI BLAST score 255 2.0e-22 E value 55 Match length % identity 95

(X79715) histone H4 [Lolium temulentum] NCBI Description

Seq. No. 206626

LIB3120-003-Q1-K1-A2 Seq. ID

Method BLASTX NCBI GI q131167 BLAST score 443 E value 5.0e-44 Match length 137 67 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR NCBI Description

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi 100292 pir S18348 photosystem I chain II precursor wood tobacco >gi 19748\_emb\_CAA42623\_ (X60008) PSI-D2

[Nicotiana sylvestris]

206627 Seq. No.

Seq. ID LIB3120-003-Q1-K1-A3

Method BLASTX NCBI GI q2305107 BLAST score 275 2.0e-24 E value 127 Match length % identity 54

NCBI Description (AF009954) phytoene synthase [Arabidopsis thaliana]

Seq. No. 206628

Seq. ID LIB3120-003-Q1-K1-A4

Method BLASTX NCBI GI q115833 BLAST score 508 E value 1.0e-51 Match length 126 % identity 79

CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR NCBI Description

(CAB-10A) (LHCP) >gi\_100195\_pir\_\_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi\_170394 (M32605)

a-binding protein [Lycopersicon esculentum]

Seq. No. 206629

Seq. ID LIB3120-003-Q1-K1-A5

Method BLASTX g120659 NCBI GI BLAST score 585 1.0e-60 E value



Match length 132 % identity 88

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST

>gi\_81721\_pir\_\_B24796 glyceraldehyde-3-phosphate

dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13),

chloroplast - white mustard (fragment)

>gi\_829288\_emb\_CAA27845\_ (X04302) chloroplast GAPDH (233aa)

[Sinapis alba]

Seq. No. 206630

Seq. ID LIB3120-003-Q1-K1-A6

Method BLASTX
NCBI GI g231688
BLAST score 718
E value 3.0e-76
Match length 135
% identity 100

NCBI Description CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC

1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No. 206631

Seq. ID LIB3120-003-Q1-K1-A7

Method BLASTX
NCBI GI g2494793
BLAST score 536
E value 5.0e-55
Match length 130
% identity 78

NCBI Description [Segment 2 of 2] FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE

(FD-GOGAT) >gi\_2146724\_pir\_\_S67496 ferredoxin-dependent glutamate synthase (EC 1.4.7.1) - spinach (fragment)

>gi 414979 (U03006) ferredoxin-dependent glutamate synthase

[Spinacia oleracea]

Seq. No. 206632

Seq. ID LIB3120-003-Q1-K1-A8

Method BLASTX
NCBI GI g1352821
BLAST score 524
E value 1.0e-53
Match length 116
% identity 86

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206633

Seq. ID LIB3120-003-Q1-K1-B1

Method BLASTX
NCBI GI g3738316
BLAST score 334
E value 3.0e-31
Match length 92
% identity 67



```
NCBI Description
                   (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
                  206634
                  LIB3120-003-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3582021
BLAST score
                   366
E value
                   6.0e-35
Match length
                  145
                   50
% identity
NCBI Description
                  (Y09423) cytochrome P450 [Nepeta racemosa]
Seq. No.
                   206635
                  LIB3120-003-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g131770
BLAST score
                   467
E value
                   8.0e-47
Match length
                   123
% identity
                   70
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                   (VEGETATIVE SPECIFIC PROTEIN V12) >qi 70880 pir R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                   discoideum) >gi_7353 emb CAA29844 (X06636) rp1024 protein
                   [Dictyostelium discoideum]
                  206636
Seq. No.
Seq. ID
                  LIB3120-003-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2894378
BLAST score
                   300
E value
                  3.0e-27
Match length
                  132
% identity
                   49
NCBI Description
                  (Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.
                  206637
                  LIB3120-003-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g81601
BLAST score
                  316
E value
                  3.0e-29
Match length
                  118
                  59
% identity
NCBI Description
                  chaperonin 60 beta - Arabidopsis thaliana
Seq. No.
                  206638
                  LIB3120-003-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249385
```

Method BLASTX
NCBI GI g4249385
BLAST score 392
E value 5.0e-38
Match length 118
% identity 65

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No. 206639

28344

Seq. ID

Method



```
Seq. ID
                  LIB3120-003-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4027895
BLAST score
                  163
E value
                  3.0e-11
Match length
                  42
% identity
                  74
NCBI Description (AF049352) alpha-expansin precursor [Nicotiana tabacum]
                  206640
Seq. No.
                  LIB3120-003-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  142
E value
                  5.0e-09
Match length
                  68
% identity
                  49
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  206641
                  LIB3120-003-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006932
BLAST score
                  161
E value
                  5.0e-11
Match length
                  74
                  49
% identity
NCBI Description
                  (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit
                  [Bos taurus]
Seq. No.
                  206642
Seq. ID
                  LIB3120-003-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g535780
BLAST score
                  661
E value
                  1.0e-69
Match length
                  143
                  88
% identity
NCBI Description (D26609) transmembrane protein [Arabidopsis thaliana]
Seq. No.
                  206643
Seq. ID
                  LIB3120-003-Q1-K1-C5
Method
                  BLASTX
                  g1352821
NCBI GI
BLAST score
                  346
E value
                  7.0e-45
                  124
Match length
                  82
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  206644
```

28345

LIB3120-003-Q1-K1-C9

BLASTX

BLAST score

E value

304 1.0e-27



```
g4027895
NCBI GI
BLAST score
                   163
                   3.0e-11
E value
Match length
                   42
% identity
                   74
                   (AF049352) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                   206645
Seq. No.
Seq. ID
                   LIB3120-003-Q1-K1-D3
                   BLASTX
Method
NCBI GI
                   g1001478
BLAST score
                   186
                   7.0e-14
E value
Match length
                   120
% identity
                   (D63999) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   206646
                   LIB3120-003-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1370603
BLAST score
                   544
                   8.0e-56
E value
                   160
Match length
% identity
                   69
                   (X98245) annexin p35 [Zea mays]
NCBI Description
                   206647
Seq. No.
                   LIB3120-003-Q1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4001803
BLAST score
                   196
E value
                   5.0e-15
Match length
                   132
                   33
 % identity
                   (AF041474) BAF53a [Homo sapiens] >gi 4218064 dbj BAA74577_
NCBI Description
                   (AB015907) actin-related protein [Homo sapiens]
                   206648
Seq. No.
Seq. ID
                   LIB3120-003-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   g1709651
BLAST score
                   406
                   1.0e-39
E value
Match length
                   137
 % identity
                   61
                   PLASTOCYANIN A PRECURSOR >gi 2117431 pir __S58209
NCBI Description
                   plastocyanin a precursor - black poplar
                   >gi 929813 emb_CAA90564_ (Z50185) plastocyanin a [Populus
                   nigra]
                   206649
 Seq. No.
                   LIB3120-003-Q1-K1-E4
 Seq. ID
Method
                   BLASTX
                   g1709651
NCBI GI
```

28346



Match length 105 % identity 57

NCBI Description PLASTOCYANIN A PRECURSOR >gi\_2117431\_pir\_\_S58209

plastocyanin a precursor - black poplar

>gi\_929813\_emb\_CAA90564\_ (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 206650

Seq. ID LIB3120-003-Q1-K1-F1

Method BLASTX
NCBI GI 94314357
BLAST score 144
E value 6.0e-09
Match length 128
% identity 20

NCBI Description (AC006340) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 206651

Seq. ID LIB3120-003-Q1-K1-F11

Method BLASTX
NCBI GI g2653290
BLAST score 170
E value 2.0e-21
Match length 93
% identity 65

NCBI Description (AJ003124) enoyl-ACP reductase [Petunia x hybrida]

Seq. No. 206652

Seq. ID LIB3120-003-Q1-K1-F12

Method BLASTX
NCBI GI g2653285
BLAST score 149
E value 2.0e-19
Match length 104
% identity 56

NCBI Description (AJ003025) enoyl-ACP reductase [Oryza sativa]

Seq. No. 206653

Seq. ID LIB3120-003-Q1-K1-F6

Method BLASTX
NCBI GI g2464899
BLAST score 382
E value 7.0e-37
Match length 142
% identity 60

NCBI Description (Z99708) geranylgeranyl pyrophosphate synthase [Arabidopsis

thaliana]

Seq. No. 206654

Seq. ID LIB3120-003-Q1-K1-G1

Method BLASTX
NCBI GI g2464872
BLAST score 257
E value 3.0e-22
Match length 93
% identity 54





```
NCBI Description
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  206655
Seq. ID
                  LIB3120-003-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q2920839
BLAST score
                  358
E value
                  5.0e-34
Match length
                  134
                  54
% identity
                  (U95136) Os-FIERG2 gene product [Oryza sativa]
NCBI Description
                  206656
Seq. No.
Seq. ID
                  LIB3120-003-Q1-K1-G2
                  BLASTX
Method
NCBI GI
                  q131399
BLAST score
                  510
E value
                  7.0e-52
                  120
Match length
% identity
                  81
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
NCBI Description
                  TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411
                  photosystem II 10K protein precursor - potato
                  >qi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                  tuberosum]
                   206657
Seq. No.
                  LIB3120-003-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1657948
BLAST score
                   599
                   3.0e-62
E value
Match length
                   135
                   86
% identity
NCBI Description
                  (U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.
                   206658
                  LIB3120-003-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406530
BLAST score
                   392
E value
                   5.0e-38
Match length
                   111
% identity
                   74
                   (AF126870) rubisco activase [Vigna radiata]
NCBI Description
Seq. No.
                   206659
                   LIB3120-003-Q1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023752
```

Method BLASTX
NCBI GI g3023752
BLAST score 352
E value 2.0e-33
Match length 118
% identity 62

NCBI Description FERREDOXIN I PRECURSOR >gi\_1418982\_emb\_CAA99756\_ (Z75520)

ferredoxin-I [Lycopersicon esculentum]



```
Seq. No.
                  206660
                  LIB3120-003-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g2507458
NCBI GI
                  296
BLAST score
                  8.0e-27
E value
                  119
Match length
% identity
                  47
                  THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi_81491_pir__S20496
NCBI Description
                  thioredoxin m precursor - spinach >gi_21348_emb_CAA35826
                   (X51462) thioredoxin M precursor (AA -67 to 114) [Spinacia
                  oleracea]
                  206661
Seq. No.
                  LIB3120-003-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115471
BLAST score
                  449
E value
                  1.0e-44
Match length
                  110
                  76
% identity
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                  DEHYDRATASE) >gi 100078 pir S10200 carbonate dehydratase
                   (EC 4.2.1.1) precursor - garden pea >gi 20673_emb_CAA36792
                   (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
                   206662
Seq. No.
                  LIB3120-003-Q1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4559327
BLAST score
                   270
                   1.0e-23
E value
Match length
                   134
                   40
% identity
                   (AC007087) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   206663
Seq. No.
                  LIB3120-004-Q1-K1-A3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3386611
BLAST score
                   252
                   1.0e-21
E value
Match length
                   135
                   39
% identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206664
Seq. No.
                  LIB3120-004-Q1-K1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2895866
BLAST score
                   192
```

2.0e-22 E value Match length 138 48 % identity

(AF045770) methylmalonate semi-aldehyde dehydrogenase NCBI Description

[Oryza sativa]

% identity

NCBI Description

68



```
Seq. No.
                  206665
Seq. ID
                  LIB3120-004-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2500576
BLAST score
                  194
                  9.0e-15
E value
                  82
Match length
% identity
                  16
                  HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H' (HNRNP H')
NCBI Description
                   (FTP-3) >qi 1684915 (U78027) FTP3 [Homo sapiens]
                  206666
Seq. No.
Seq. ID
                  LIB3120-004-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g505482
BLAST score
                  659
E value
                  3.0e-69
Match length
                  158
% identity
NCBI Description
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
                  photosystem II [Nicotiana tabacum]
Seq. No.
                  206667
Seq. ID
                  LIB3120-004-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g115794
BLAST score
                  429
E value
                  1.0e-59
Match length
                  136
% identity
                  83
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
                   (CAB-13) >gi 72748 pir CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi 19277 emb CAA42818 (X60275) LHCII type III
                   [Lycopersicon esculentum]
                  206668
Seq. No.
                  LIB3120-004-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617219
BLAST score
                  354
E value
                  1.0e-33
                  90
Match length
                   72
% identity
                   (X99301) CPD photolyase [Arabidopsis thaliana] >gi 2984707
NCBI Description
                   (AF053365) type II CPD photolyase PHR1 [Arabidopsis
                   thaliana]
                  206669
Seq. No.
Seq. ID
                  LIB3120-004-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2695931
BLAST score
                  379
E value
                  2.0e-36
Match length
                  109
```

28350

(AJ222779) hypothetical protein [Hordeum vulgare]



```
Seq. No.
                  206670
                  LIB3120-004-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                  q133940
NCBI GI
BLAST score
                  354
E value
                  7.0e-34
Match length
                  93
% identity
                  82
NCBI Description
                  40S RIBOSOMAL PROTEIN S3A (S1A) >qi 70851 pir R3XL3A
                  ribosomal protein S3a - African clawed frog
                  >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a
                  [Xenopus laevis]
                  206671
Seq. No.
                  LIB3120-004-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914442
BLAST score
                  438
E value
                  2.0e-43
Match length
                  99
                  84
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  206672
Seq. ID
                  LIB3120-004-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q464986
BLAST score
                  521
E value
                  4.0e-53
Match length
                  115
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857 pir__S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
```

enzyme E2 [Arabidopsis thaliana] >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 206673 Seq. ID LIB3120-004-Q1-K1-C5

Method BLASTX NCBI GI g1352821 BLAST score 296 E value 3.0e-49 Match length 139 67 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain



precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206674 LIB3120-004-Q1-K1-C8 Seq. ID Method BLASTX NCBI GI g1354515 BLAST score 243 1.0e-22 E value 146 Match length 49 % identity (U55837) carbonic anhydrase [Populus tremula x Populus NCBI Description tremuloides] Seq. No. 206675 Seq. ID LIB3120-004-Q1-K1-D1 Method BLASTX NCBI GI g2760834 BLAST score 456 8.0e-46 E value Match length 151 66 % identity NCBI Description (AC003105) putative nitrate transporter [Arabidopsis thaliana] Seq. No. 206676 LIB3120-004-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 335 E value 2.0e-57 Match length 127 % identity 76 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206677

Seq. ID LIB3120-004-Q1-K1-D3

Method BLASTX
NCBI GI g1666173
BLAST score 284
E value 2.0e-29
Match length 114
% identity 64

NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]

Seq. No. 206678

Seq. ID LIB3120-004-Q1-K1-D5

Method BLASTX
NCBI GI g407946
BLAST score 254
E value 2.0e-22
Match length 109
% identity 51

28352





```
NCBI Description (U02498) epoxide hydrolase [Solanum tuberosum]
```

Seq. No. 206679

Seq. ID LIB3120-004-Q1-K1-D6

Method BLASTX
NCBI GI g131397
BLAST score 137
E value 1.0e-18
Match length 139
% identity 47

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_81480\_pir\_\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 206680

Seq. ID LIB3120-004-Q1-K1-E1

Method BLASTX
NCBI GI g1279654
BLAST score 311
E value 6.0e-29
Match length 78
% identity 76

NCBI Description (X97351) peroxidase [Populus balsamifera subsp.

trichocarpa]

Seq. No. 206681

Seq. ID LIB3120-004-Q1-K1-E2

Method BLASTN
NCBI GI 94371278
BLAST score 34
E value 2.0e-09
Match length 50
% identity 92

NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 206682

Seq. ID LIB3120-004-Q1-K1-E3

Method BLASTX
NCBI GI g121953
BLAST score 194
E value 7.0e-15
Match length 47
% identity 83

NCBI Description HISTONE H1 >gi 81905 pir S00033 histone H1.b - garden pea

>gi 20762 emb CAA29123 (X05636) H1 histone (AA 1-263)

[Pisum sativum]

Seq. No. 206683

Seq. ID LIB3120-004-Q1-K1-E8

Method BLASTX NCBI GI g2760834

28353



```
BLAST score
                  4.0e-32
E value
                  131
Match length
                  57
% identity
                  (AC003105) putative nitrate transporter [Arabidopsis
NCBI Description
                  thaliana]
                  206684
Seq. No.
                  LIB3120-004-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                  g584893
NCBI GI
                  126
BLAST score
                  1.0e-10
E value
                  89
Match length
                  51
% identity
                  SERINE CARBOXYPEPTIDASE III PRECURSOR
NCBI Description
                  >gi 283002 pir S22530 carboxypeptidase III (EC 3.4.16.-) -
                  rice >gi_218153_dbj_BAA01757_ (D10985) serine
                  carboxypeptidase III [Oryza sativa]
                  206685
Seq. No.
                  LIB3120-004-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g3885334
NCBI GI
                  678
BLAST score
                  1.0e-71
E value
                  147
Match length
% identity
                  82
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  206686
Seq. ID
                  LIB3120-004-Q1-K1-F5
Method
                  BLASTX
                  g3800853
NCBI GI
BLAST score
                  159
                  8.0e-12
E value
                  78
Match length
                   49
% identity
                   (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                  activase precursor [Zea mays]
Seq. No.
                  206687
                  LIB3120-004-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  a3929333
NCBI GI
BLAST score
                   315
```

6.0e-29 E value 148 Match length 46 % identity

CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD) NCBI Description (PHENYLUREA DEALKYLASE) >gi 2370230 emb\_CAA71054 (Y09920)

7-ethoxycoumarin O-deethylase [Helianthus tuberosus]

Seq. No. 206688

Seq. ID LIB3120-004-Q1-K1-G4

Method BLASTX



```
g3913018
NCBI GI
BLAST score
                  617
E value
                  2.0e-64
                  131
Match length
% identity
                  89
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  206689
Seq. No.
                  LIB3120-004-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  489
                  2.0e-75
E value
Match length
                  155
                  92
% identity
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >qi 2119270 pir S60233 alpha-tubulin
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
                  206690
Seq. No.
                  LIB3120-004-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076534
BLAST score
                  326
E value
                  3.0e-30
Match length
                  110
% identity
NCBI Description
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden
                  pea >gi 497120 (U06461) monodehydroascorbate reductase
                  [Pisum sativum]
Seq. No.
                  206691
Seq. ID
                  LIB3120-004-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g132659
BLAST score
                  267
E value
                  2.0e-23
Match length
                  111
% identity
                  52
NCBI Description
                  50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)
                  >gi 81483 pir A32033 ribosomal protein L13 precursor,
                  chloroplast - spinach >gi 170133 (J04461) ribosomal protein
                  L13 [Spinacia oleracea]
Seq. No.
                  206692
Seq. ID
                  LIB3120-005-Q1-K1-A10
Method
                  BLASTX
```

NCBI GI g3885511 BLAST score 265 4.0e-23 E value Match length 105 % identity 59

(AF084200) similar to PSI-K subunit of photosystem I from NCBI Description

barley [Medicago sativa]

Seq. No.

Seq. ID

206698

LIB3120-005-Q1-K1-B12



```
Seq. No.
                  206693
Seq. ID
                  LIB3120-005-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  q950299
BLAST score
                  513
                  2.0e-52
E value
Match length
                  109
% identity
                  86
                  (L46792) xyloglucan endotransglycosylase precursor
NCBI Description
                  [Actinidia deliciosa]
                  206694
Seq. No.
Seq. ID
                  LIB3120-005-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3834323
BLAST score
                  194
E value
                  7.0e-15
Match length
                  121
% identity
                  36
                  (AC005679) F9K20.25 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206695
                  LIB3120-005-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  669
                  1.0e-70
E value
Match length
                  125
% identity
                  98
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  206696
Seq. ID
                  LIB3120-005-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2970654
BLAST score
                  338
                  1.0e-31
E value
Match length
                  112
% identity
                  68
                   (AF052058) ferritin subunit cowpea2 precursor [Vigna
NCBI Description
                  unguiculata]
Seq. No.
                  206697
                  LIB3120-005-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g68200
BLAST score
                  335
E value
                  2.0e-31
Match length
                  92
% identity
                  77
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
```



Method BLASTX
NCBI GI g3913437
BLAST score 490
E value 2.0e-49
Match length 137
% identity 70
NCBI Description PUTATIVE

CBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
HELICASE >gi\_1402875\_emb\_CAA66825\_ (X98130) RNA helicase
[Arabidopsis thaliana] >gi\_1495271\_emb\_CAA66613\_ (X97970)

RNA helicase [Arabidopsis thaliana]

Seq. No. 206699

Seq. ID LIB3120-005-Q1-K1-B3

Method BLASTX
NCBI GI g2961390
BLAST score 516
E value 1.0e-52
Match length 114
% identity 75

NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 206700

Seq. ID LIB3120-005-Q1-K1-B9

Method BLASTX
NCBI GI g421826
BLAST score 400
E value 2.0e-45
Match length 130
% identity 75

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 206701

Seq. ID LIB3120-005-Q1-K1-C10

Method BLASTX
NCBI GI g320618
BLAST score 289
E value 3.0e-26
Match length 65
% identity 86

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi\_218172\_dbj\_BAA00536\_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 206702

Seq. ID LIB3120-005-Q1-K1-C11

Method BLASTX
NCBI GI g505482
BLAST score 437
E value 1.0e-43
Match length 111
% identity 82

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of



## photosystem II [Nicotiana tabacum]

```
Seq. No.
                  206703
Seq. ID
                  LIB3120-005-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g3914136
BLAST score
                  268
                  2.0e-23
E value
Match length
                  116
                  46
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                  >qi 2632171 emb CAA05771 (AJ002958) lipid transfer protein
                   [Cicer arietinum]
                  206704
Seq. No.
Seq. ID
                  LIB3120-005-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  353
E value
                  1.0e - 33
                  102
Match length
                  71
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
Seq. No.
                  206705
                  LIB3120-005-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2618686
BLAST score
                   390
E value
                   9.0e-38
Match length
                   140
                   54
% identity
                  (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206706
                  LIB3120-005-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  g3860249
NCBI GI
BLAST score
                  180
E value
                   4.0e-13
Match length
                   67
% identity
                   54
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  206707
Seq. No.
                  LIB3120-005-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                   g1354515
NCBI GI
BLAST score
                   224
E value
                   2.0e-18
Match length
                  113
                   50
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   206708
Seq. No.
                  LIB3120-005-Q1-K1-D7
Seq. ID
```

28358



```
Method
                  BLASTX
NCBI GI
                  q1168408
BLAST score
                  395
                  8.0e-54
E value
Match length
                  124
% identity
                  82
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                  >qi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi 927507 emb CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  206709
Seq. No.
                  LIB3120-005-Q1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18058
                  346
BLAST score
                  0.0e+00
E value
Match length
                  450
% identity
                  94
NCBI Description Citrus limon cistron for 26S ribosomal RNA
Seq. No.
                  206710
                  LIB3120-005-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3646373
BLAST score
                  424
                   4.0e-48
E value
                  105
Match length
% identity
                  (AJ011078) RGP1 protein [Oryza sativa]
NCBI Description
Seq. No.
                  206711
Seq. ID
                  LIB3120-005-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3127031
BLAST score
                  211
                   2.0e-20
E value
                   99
Match length
                   59
% identity
NCBI Description
                   (AF014802) (S)-N-methylcoclaurine 3'-hydroxylase
                   [Eschscholzia californica]
Seq. No.
                  206712
                  LIB3120-005-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1899188
BLAST score
                  257
                  3.0e-22
E value
Match length
                   68
                  24
% identity
NCBI Description
                  (U90212) DNA binding protein ACBF [Nicotiana tabacum]
```

Seq. No. 206713

Seq. ID LIB3120-005-Q1-K1-E12

Method BLASTX NCBI GI g289920 BLAST score 435



E value 2.0e-43 Match length 88 % identity 94

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 206714

Seq. ID LIB3120-005-Q1-K1-E2

Method BLASTX
NCBI GI g1352821
BLAST score 399
E value 5.0e-39
Match length 79
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir\_ RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206715

Seq. ID LIB3120-005-Q1-K1-E3

Method BLASTX
NCBI GI g1448941
BLAST score 421
E value 5.0e-46
Match length 120
% identity 81

NCBI Description (L48181) ypt-related protein [Brassica campestris]

Seq. No. 206716

Seq. ID LIB3120-005-Q1-K1-E6

Method BLASTX
NCBI GI g266893
BLAST score 708
E value 4.0e-75
Match length 141
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi\_322416\_pir\_\_S28172 ribulose-bisphosphate carboxylase activase - cucumber

>gi\_18284\_emb\_CAA47906\_ (X67674) rubisco activase [Cucumis

sativus]

Seg. No. 206717

Seq. ID LIB3120-005-Q1-K1-F10

Method BLASTX
NCBI GI 9479406
BLAST score 616
E value 3.0e-64
Match length 132
% identity 66

NCBI Description chlorophyll a/b-binding protein - garden pea

 $>gi_20671_emb_CAA49149_ (X69215)$  chlorophyll a/b-binding

protein [Pisum sativum]

Seq. No. 206718



```
LIB3120-005-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131397
BLAST score
                  216
                  2.0e-17
E value
Match length
                  118
                  47
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >qi 81480 pir S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi 755802 emb CAA29056 (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                  [Spinacia oleracea]
                  206719
Seq. No.
Seq. ID
                  LIB3120-005-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3914605
BLAST score
                  405
                  1.0e-39
E value
Match length
                  135
% identity
                  61
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >qi 541930 pir S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >qi 415852 emb CAA79857 (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Malus domestica]
Seq. No.
                  206720
Seq. ID
                  LIB3120-005-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q671737
BLAST score
                  652
                  9.0e-70
E value
Match length
                  147
% identity
                  85
NCBI Description
                  (X74731) Chloropyll a/b binding protein [Amaranthus
                  hypochondriacus]
                  206721
Seq. No.
                  LIB3120-005-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q445116
                  127
BLAST score
                  2.0e-16
E value
Match length
                  84
                  61
% identity
                  light-harvesting complex IIa protein; [Hordeum vulgare]
NCBI Description
```

Seq. No. 206722

Seq. ID LIB3120-005-Q1-K1-H10

Method BLASTN NCBI GI g4220640

BLAST score 34



E value 69 Match length 53 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MPE11, complete sequence [Arabidopsis thaliana] 206723 Seq. No. Seq. ID LIB3120-005-Q1-K1-H9 BLASTX Method NCBI GI a2244813 BLAST score 144 4.0e-09 E value 48 Match length 60 % identity (Z97336) acylaminoacyl-peptidase homolog [Arabidopsis NCBI Description thaliana] 206724 Seq. No. Seq. ID LIB3120-006-Q1-K1-A10 Method BLASTX g115471 NCBI GI 543 BLAST score 8.0e-56 E value 121 Match length 83 % identity CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE NCBI Description DEHYDRATASE) >gi 100078 pir S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi 20673 emb CAA36792 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum] 206725 Seq. No. LIB3120-006-Q1-K1-A2 Seq. ID BLASTX Method q289920 NCBI GI 479 BLAST score 2.0e-48 E value 107 Match length 87 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 206726 Seq. No. LIB3120-006-Q1-K1-A4 Seq. ID BLASTX Method q3335378 NCBI GI 124 BLAST score 3.0e-09 E value 71 Match length 52 % identity (AC003028) Myb-related transcription activator [Arabidopsis NCBI Description thaliana] 206727

Seq. No.

Seq. ID LIB3120-006-Q1-K1-A5

Method BLASTX g3281846 NCBI GI BLAST score 185



63

% identity

NCBI Description

```
8.0e-14
E value
Match length
                   124
% identity
                   40
                   (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206728
                   LIB3120-006-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2980793
BLAST score
                   208
                   6.0e-17
E value
Match length
                   74
                   59
% identity
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   206729
Seq. No.
Seq. ID
                   LIB3120-006-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g3334112
BLAST score
                   299
                   4.0e-27
E value
                   82
Match length
% identity
                   70
                   ACYL-COA-BINDING PROTEIN (ACBP) >gi 1938236_emb_CAA70200_
NCBI Description
                   (Y08996) acyl-CoA-binding protein [Ricinus communis]
                   206730
Seq. No.
                   LIB3120-006-Q1-K1-B6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q167366
BLAST score
                   101
                   4.0e-50
E value
Match length
                   133
% identity
                   94
NCBI Description
                   Gossypium hirsutum peroxidase mRNA, complete cds
                   206731
Seq. No.
                   LIB3120-006-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q430947
BLAST score
                   169
E value
                   5.0e-12
Match length
                   60
% identity
                   63
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   206732
Seq. No.
                   LIB3120-006-Q1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g20729
                   325
BLAST score
                   2.0e-30
E value
                   109
Match length
```

(X15190) precursor (AA -68 to 337) [Pisum sativum]

NCBI Description



```
206733
Seq. No.
                  LIB3120-006-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                  g1181599
NCBI GI
                   393
BLAST score
                   3.0e-38
E value
                  105
Match length
% identity
                   74
                   (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                   206734
Seq. No.
                  LIB3120-006-Q1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170568
BLAST score
                   501
                   5.0e-51
E value
Match length
                   108
% identity
                   91
                   MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                   >gi_2147316_pir__S60302 D-myo-inositol-3-phosphate synthase
                   (EC 5.5.1.4) - Spirodela polyrrhiza
                   >gi 558648 emb CAA77751 (Z11693)
                   D-myo-inositol-3-phosphate synthase [Spirodela polyrrhiza]
Seq. No.
                   206735
                   LIB3120-006-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115833
BLAST score
                   483
E value
                   8.0e-49
Match length
                   120
                   78
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                   a/b-binding protein CablOA - tomato >gi_170394 (M32605)
                   a-binding protein [Lycopersicon esculentum]
                   206736
Seq. No.
                   LIB3120-006-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2695931
BLAST score
                   227
                   8.0e-19
E value
                   50
Match length
                   82
% identity
                   (AJ222779) hypothetical protein [Hordeum vulgare]
NCBI Description
                   206737
Seq. No.
                   LIB3120-006-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3334405
                   552
BLAST score
E value
                   7.0e-57
Match length
                   118
                   96
% identity
```

VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)

>gi 2267583 (AF009338) vacuolar H+-ATPase subunit E

Match length

98



## [Gossypium hirsutum]

```
206738
Seq. No.
                  LIB3120-006-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244749
                  625
BLAST score
                  2.0e-65
E value
Match length
                  141
% identity
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                  206739
Seq. No.
Seq. ID
                  LIB3120-006-Q1-K1-D12
                  BLASTX
Method
                  g82188
NCBI GI
                  430
BLAST score
                  2.0e-42
E value
                  123
Match length
                  73
% identity
                  photosystem II oxygen-evolving complex protein 2 precursor
NCBI Description
                   - common tobacco (fragment) >gi 19896 emb_CAA41713
                   (X58910) photosystem II 23 kDa polypeptide [Nicotiana
                   tabacum]
                   206740
Seq. No.
                  LIB3120-006-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                   g2266947
NCBI GI
                   329
BLAST score
E value
                   7.0e-31
Match length
                   94
% identity
                   (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium
NCBI Description
                   hirsutum]
                   206741
Seq. No.
Seq. ID
                   LIB3120-006-Q1-K1-E1
                   BLASTX
Method
                   q1352821
NCBI GI
BLAST score
                   403
                   2.0e-39
E value
Match length
                   81
                   94
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   206742
Seq. No.
                   LIB3120-006-Q1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g20729
BLAST score
                   366
                   5.0e-35
E value
```



```
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                  206743
Seq. No.
                  LIB3120-006-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g4455345
NCBI GI
BLAST score
                  452
                  3.0e-45
E value
                  99
Match length
                  92
% identity
NCBI Description (AL035522) putative protein [Arabidopsis thaliana]
                  206744
Seq. No.
                  LIB3120-006-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  q3172538
NCBI GI
BLAST score
                  213
                   5.0e-17
E value
Match length
                   54
% identity
                  (AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]
NCBI Description
                   206745
Seq. No.
                   LIB3120-006-Q1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3559814
                   487
BLAST score
                   6.0e-50
E value
                   122
Match length
% identity
                  (Y15781) transketolase 1 [Capsicum annuum]
NCBI Description
                   206746
Seq. No.
                   LIB3120-006-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   g20729
NCBI GI
BLAST score
                   483
                   9.0e-49
E value
Match length
                   129
% identity
                   77
                   (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   206747
Seq. No.
                   LIB3120-006-Q1-K1-F5
Seq. ID
Method
                   BLASTX
                   g3420050
NCBI GI
                   261
BLAST score
                   1.0e-22
E value
                   102
Match length
% identity
                   55
                   (AC004680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   206748
Seq. No.
                   LIB3120-006-Q1-K1-F6
Seq. ID
```

28366

BLASTX

g289920

Method

NCBI GI



595 BLAST score E value 6.0e-62 Match length 112 98 % identity

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

Seq. No. 206749

LIB3120-006-Q1-K1-F8 Seq. ID

Method BLASTX NCBI GI g1352821 BLAST score 178 2.0e-13 E value Match length 56 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

206750 Seq. No.

LIB3120-006-Q1-K1-G1 Seq. ID

BLASTX Method NCBI GI q1773330 379 BLAST score 1.0e-36 E value 100 Match length % identity

(U80071) glycolate oxidase [Mesembryanthemum crystallinum] NCBI Description

Seq. No. 206751

LIB3120-006-Q1-K1-G2 Seq. ID

Method BLASTX NCBI GI q3914442 BLAST score 404 1.0e-39 E value Match length 102 78 % identity

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR

(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

206752 Seq. No.

LIB3120-006-Q1-K1-G5 Seq. ID

Method BLASTX g115794 NCBI GI 441 BLAST score 4.0e-44 E value 94 Match length 91 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR NCBI Description

(CAB-13) >gi\_72748\_pir\_\_CDTO33 chlorophyll a/b-binding

protein type III precursor (cab-13) - tomato >gi\_19277\_emb\_CAA42818\_ (X60275) LHCII type III

[Lycopersicon esculentum]

NCBI Description

1.35



```
206753
Seq. No.
                  LIB3120-006-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g2501578
NCBI GI
                  221
BLAST score
                  2.0e-33
E value
                  117
Match length
                  76
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi_1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  206754
Seq. No.
                  LIB3120-006-Q1-K1-H12
Seq. ID
                  {\tt BLASTX}
Method
                   g3510256
NCBI GI
                   171
BLAST score
                   2.0e-12
E value
                   82
Match length
% identity
                   46
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                   206755
Seq. No.
                   LIB3120-006-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   q20733
NCBI GI
BLAST score
                   466
                   8.0e-47
E value
                   126
Match length
                   73
% identity
                   (X15188) precursor C-terminal fragment (AA -80 to 367)
NCBI Description
                   [Pisum sativum]
                   206756
Seq. No.
                   LIB3120-006-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   q625546
NCBI GI
                   409
BLAST score
                   5.0e-40
E value
                   124
Match length
                   66
% identity
                   photosystem II oxygen-evolving complex protein 2 precursor
NCBI Description
                   - common tobacco >gi 417604 emb CAA45699 (X64347) 23 kDa
                   polypeptide of water-oxidizing complex of photosystem II
                   [Nicotiana tabacum]
                   206757
Seq. No.
Seq. ID
                   LIB3120-006-Q1-K1-H8
                   BLASTX
Method
                   q1370194
NCBI GI
BLAST score
                   182
                   1.0e-13
E value
                   51
Match length
                   75
 % identity
```

(Z73946) RAB8C [Lotus japonicus]

NCBI Description



```
206758
Seq. No.
                  LIB3120-007-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  g2764574
NCBI GI
BLAST score
                  314
                  3.0e-29
E value
                  93
Match length
                  67
% identity
                  (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
NCBI Description
                  206759
Seq. No.
Seq. ID
                  LIB3120-007-Q1-K1-A12
                  BLASTX
Method
                  g4455226
NCBI GI
                  196
BLAST score
                  4.0e-15
E value
                  108
Match length
                  44
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  206760
Seq. No.
                  LIB3120-007-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g120657
NCBI GI
                  138
BLAST score
                  7.0e-14
E value
                  58
Match length
                   72
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_66024_pir__DEZMG3
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                   maize >gi 168479 (M18976) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays] >gi 763035 emb CAA33455 (X15408)
                   glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                   206761
                   LIB3120-007-Q1-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129538
BLAST score
                   207
                   2.0e-16
E value
Match length
                   45
                   87
% identity
                  AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
NCBI Description
                   AT103 [Arabidopsis thaliana]
                   206762
Seq. No.
                   LIB3120-007-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   g3929651
NCBI GI
BLAST score
                   427
                   3.0e-42
E value
Match length
                   95
% identity
                   87
```

28369

[Arabidopsis thaliana]

(AJ131206) microbody NAD-dependent malate dehydrogenase



```
206763
Seq. No.
                  LIB3120-007-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  g2853219
NCBI GI
                  535
BLAST score
                  9.0e-55
E value
                  126
Match length
% identity
                  (AJ000923) glutathione transferase [Carica papaya]
NCBI Description
                  206764
Seq. No.
                  LIB3120-007-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g114643
NCBI GI
                  152
BLAST score
                  3.0e-11
E value
                   52
Match length
                   80
% identity
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_67879_pir__PWSPG H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, chloroplast - spinach
                   >gi 21238_emb_CAA35158_ (X17257) gamma-subunit of
                   chloroplast ATP synthase [Spinacia oleracea]
                   >gi_531111_emb_CAA53734_ (X\overline{7}6131) gamma subunit of the
                   chloroplast ATP synthase [Spinacia oleracea]
                   206765
Seq. No.
                   LIB3120-007-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g1053093
NCBI GI
                   665
BLAST score
                   5.0e-70
E value
                   143
Match length
                   87
% identity
                   (U38550) zeta-carotene desaturase precursor [Arabidopsis
NCBI Description
                   thaliana]
                   206766
Seq. No.
                   LIB3120-007-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   q1350548
NCBI GI
BLAST score
                   245
                   8.0e-21
E value
                   111
Match length
% identity
                   (L47609) heat shock-like protein [Picea glauca]
NCBI Description
                   206767
Seq. No.
                   LIB3120-007-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1703108
BLAST score
                   292
                   3.0e-48
E value
Match length
                   96
                   100
 % identity
```

NCBI Description ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis





thaliana >gi\_2129528\_pir S68107 actin 7 - Arabidopsis

```
thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                  thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
Seq. No.
                  206768
Seq. ID
                  LIB3120-007-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                  q3158476
                  436
BLAST score
                  4.0e-43
E value
                  93
Match length
% identity
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
                  206769
Seq. No.
                  LIB3120-007-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3183185
BLAST score
                  299
                   4.0e-27
E value
Match length
                   148
% identity
                  GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG
NCBI Description
                   >gi 2224766 emb CAB09712 (Z97025) product highly similar
                   to elongation factor EF-G [Bacillus subtilis]
                   >gi 2633848 emb CAB13350 (Z99111) similar to GTP-binding
                   elongation factor [Bacillus subtilis]
Seq. No.
                   206770
Seq. ID
                   LIB3120-007-Q1-K1-B8
                   BLASTX
Method
                   q3021485
NCBI GI
BLAST score
                   143
                   4.0e-09
E value
Match length
                   41
                   71
% identity
                  (AJ224932) histone H2B-3 [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   206771
                   LIB3120-007-Q1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3023752
BLAST score
                   275
                   2.0e-24
E value
```

NCBI Description FERREDOXIN I PRECURSOR >gi\_1418982\_emb\_CAA99756\_ (Z75520) ferredoxin-I [Lycopersicon esculentum]

Seq. No. 206772

Match length

% identity

Seq. ID LIB3120-007-Q1-K1-C11

100

58

Method BLASTX
NCBI GI g120659
BLAST score 511
E value 6.0e-54
Match length 143

28371



% identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST NCBI Description >gi 81721 pir\_\_B24796 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13), chloroplast - white mustard (fragment) >gi\_829288\_emb\_CAA27845\_ (X04302) chloroplast GAPDH (233aa) [Sinapis alba] 206773 Seq. No. Seq. ID LIB3120-007-Q1-K1-C3 BLASTX Method g2764589 NCBI GI 201 BLAST score 1.0e-15 E value Match length 85 49 % identity (AJ001046) eukaryotic initiation factor 4 gamma [Homo NCBI Description sapiens] Seq. No. 206774 Seq. ID LIB3120-007-Q1-K1-C4 BLASTX Method NCBI GI q289920 580 BLAST score 3.0e-60 E value Match length 111 97 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] Seq. No. 206775 LIB3120-007-Q1-K1-C5 Seq. ID BLASTX Method q1621268 NCBI GI 150 BLAST score E value 9.0e-10 32 Match length 88 % identity (Z81012) unknown [Ricinus communis] NCBI Description Seq. No. 206776 Seq. ID LIB3120-007-Q1-K1-C6 Method BLASTX q2832625 NCBI GI BLAST score 261 9.0e-23 E value Match length 118 42 % identity (AL021711) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 206777 LIB3120-007-Q1-K1-C7 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g131772
BLAST score 362
E value 1.0e-34
Match length 86



% identity

40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) NCBI Description

>gi\_82723\_pir\_\_A30097 ribosomal protein S14 (clone MCH1) -

maize

Seq. No.

206778

Seq. ID

LIB3120-007-Q1-K1-C9

Method NCBI GI BLASTX

BLAST score

g1352821 393

E value Match length 2.0e-38

% identity

82 95

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

206779

Seq. ID Method

LIB3120-007-Q1-K1-D10

NCBI GI

BLASTX

BLAST score

g1352821

568

E value Match length 1.0e-58 108

% identity

97

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

206780

Seq. ID

LIB3120-007-Q1-K1-D11

Method NCBI GI BLAST score BLASTX g282865

E value

624 2.0e-65

Match length % identity

122 94

NCBI Description

chlorophyll a/b-binding protein - Arabidopsis thaliana >gi\_16207\_emb\_CAA39534\_ (X56062) chlorophyll A/B-binding

protein [Arabidopsis thaliana] >gi 166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.

206781

Seq. ID

LIB3120-007-Q1-K1-D12

Method NCBI GI BLASTN g18511

BLAST score E value

383

Match length

0.0e + 00

206782

% identity

423 98

NCBI Description

G.hirsutum light regulated unknown reading frame DNA

Seq. No.

Seq. ID



```
LIB3120-007-Q1-K1-D2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
                  36
BLAST score
                  7.0e-11
E value
                  36
Match length
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  206783
Seq. No.
                  LIB3120-007-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                  g3123745
NCBI GI
                  239
BLAST score
                  2.0e-20
E value
                   70
Match length
                   67
% identity
NCBI Description (AB013447) aluminum-induced [Brassica napus]
                   206784
Seq. No.
                  LIB3120-007-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                   g3738320
NCBI GI
                   387
BLAST score
                   2.0e-37
E value
                   140
Match length
                   53
% identity
                   (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
                   206785
Seq. No.
                   LIB3120-007-Q1-K1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q119748
                   638
BLAST score
                   7.0e-67
E value
                   135
Match length
                   91
% identity
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 67241_pir__PASPY fructose-bisphosphatase (EC 3.1.3.11),
                   cytosolic - spinach >gi_21245_emb_CAA43860_ (X61690)
                   fructose-bisphosphatase [Spinacia oleracea]
                   206786
Seq. No.
Seq. ID
                   LIB3120-007-Q1-K1-E12
Method
                   BLASTX
                   q478318
NCBI GI
                   204
BLAST score
E value
                   5.0e-16
                   85
Match length
                   53
% identity
                   immunophilin p59 - mouse >gi_410499_emb_CAA50231_ (X70887)
NCBI Description
                   p59 immunophilin [Mus musculus]
Seq. No.
                   206787
```

28374

LIB3120-007-Q1-K1-E5



```
BLASTX
Method
                  q2506443
NCBI GI
BLAST score
                  180
                  3.0e-13
E value
Match length
                  85
                  56
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 2117520 pir JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >qi 1402885 emb CAA66816 (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) [Arabidopsis thaliana]
                  206788
Seq. No.
Seq. ID
                  LIB3120-007-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q1644289
BLAST score
                  214
                  1.0e-17
E value
                  42
Match length
                   98
% identity
                  (X95727) chlorophyll a/b-binding protein CP26 in PS II
NCBI Description
                   [Brassica juncea]
                   206789
Seq. No.
Seq. ID
                  LIB3120-007-Q1-K1-E7
Method
                   BLASTX
                   q1352821
NCBI GI
                   584
BLAST score
                   1.0e-60
E value
                   110
Match length
                   97
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   206790
Seq. No.
                   LIB3120-007-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   a2341024
BLAST score
                   148
                   2.0e-09
E value
Match length
                   58
                   52
% identity
                   (AC000104) F19P19.1 [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 206791

Seq. ID LIB3120-007-Q1-K1-F1

MethodBLASTXNCBI GIg2191138BLAST score196E value5.0e-15



Match length % identity

(AF007269) A IG002N01.18 gene product [Arabidopsis NCBI Description

thaliana]

Seq. No.

206792

Seq. ID

LIB3120-007-Q1-K1-F2

Method NCBI GI BLAST score BLASTX q3080401 233

E value Match length

2.0e-19 64

% identity

NCBI Description

(AL022603) putative protein [Arabidopsis thaliana]

>gi 4455265 emb\_CAB36801.1\_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No.

206793

LIB3120-007-Q1-K1-F3 Seq. ID

Method BLASTX q3915095 NCBI GI BLAST score 475 9.0e-48 E value 113 Match length

% identity

TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID NCBI Description

4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi 1526537 dbj\_BAA13414\_ (D87520) cytochrome P450

(CYP73A14) [Glycyrrhiza echinata]

Seq. No.

206794 LIB3120-007-Q1-K1-F5 Seq. ID

BLASTX Method q1498332 NCBI GI BLAST score 715

7.0e-76 E value Match length 145 96 % identity

(U60499) actin [Glycine max] NCBI Description

Seq. No. 206795

LIB3120-007-Q1-K1-F8 Seq. ID

Method BLASTX q82188 NCBI GI 500 BLAST score 1.0e-50 E value 146 Match length 67 % identity

photosystem II oxygen-evolving complex protein 2 precursor NCBI Description

- common tobacco (fragment) >gi\_19896\_emb\_CAA41713 (X58910) photosystem II 23 kDa polypeptide [Nicotiana

tabacum]

Seq. No.

206796

Seq. ID

LIB3120-007-Q1-K1-G2

Method NCBI GI BLASTX q282865



BLAST score 575 E value 2.0e-59 Match length 135 % identity 82

NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana

>gi\_16207\_emb\_CAA39534\_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi\_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 206797

Seq. ID LIB3120-007-Q1-K1-G7

Method BLASTX
NCBI GI g131166
BLAST score 400
E value 6.0e-39
Match length 125
% identity 66

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi\_82100\_pir\_ S00449

photosystem I chain II precursor - tomato >gi\_170492 (M21344) photosystem I subunit II protein precursor [Lycopersicon esculentum] >gi\_226544\_prf\_\_1601516A

photosystem I reaction center II [Lycopersicon esculentum]

Seq. No. 206798

Seq. ID LIB3120-007-Q1-K1-G9

Method BLASTX
NCBI GI g1709651
BLAST score 109
E value 2.0e-10
Match length 104
% identity 39

NCBI Description PLASTOCYANIN A PRECURSOR >gi\_2117431\_pir\_\_S58209

plastocyanin a precursor - black poplar

>gi 929813\_emb\_CAA90564\_ (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 206799

Seq. ID LIB3120-007-Q1-K1-H1

Method BLASTX
NCBI GI g3885896
BLAST score 329
E value 9.0e-31
Match length 67
% identity 90

NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 206800

Seq. ID LIB3120-007-Q1-K1-H9

Method BLASTX
NCBI GI g1199772
BLAST score 339
E value 8.0e-32
Match length 131
% identity 58

NCBI Description (D83226) extensin like protein [Populus nigra]

>gi 1199774\_dbj\_BAA11855\_ (D83227) extensin like protein



## [Populus nigra]

206801 Seq. No. LIB3120-008-Q1-K1-A10 Seq. ID BLASTX Method NCBI GI q115471 BLAST score 241

2.0e-20 E value Match length 65 68 % identity

NCBI Description

CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi\_100078\_pir\_\_S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi 20673 emb CAA36792 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

206802 Seq. No.

Seq. ID LIB3120-008-Q1-K1-A3

Method BLASTX NCBI GI q625547 BLAST score 312 1.0e-28 E value 101 Match length % identity

chlorophyll a/b-binding protein type I - common tobacco NCBI Description

>qi 493723 emb CAA45523 (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

206803 Seq. No.

Seq. ID LIB3120-008-Q1-K1-A4

Method BLASTX q131397 NCBI GI 279 BLAST score 6.0e-25 E value 123 Match length % identity 53

OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD NCBI Description

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_81480\_pir\_\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi 225597 prf 1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 206804

LIB3120-008-Q1-K1-A5 Seq. ID

Method BLASTX g2565275 NCBI GI BLAST score 574 E value 2.0e-59 121 Match length % identity 85

(AF023611) Dim1p homolog [Homo sapiens] NCBI Description

206805 Seq. No.

LIB3120-008-Q1-K1-A6 Seq. ID



```
Method BLASTX
NCBI GI g3953473
BLAST score 178
E value 5.0e-13
Match length 89
% identity 51
```

NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]

Seq. No. 206806

Seq. ID LIB3120-008-Q1-K1-A7

Method BLASTX
NCBI GI g1352821
BLAST score 437
E value 5.0e-64
Match length 150
% identity 81

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206807

Seq. ID LIB3120-008-Q1-K1-A9

Method BLASTX
NCBI GI g167367
BLAST score 754
E value 2.0e-80
Match length 142
% identity 99

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 206808

Seq. ID LIB3120-008-Q1-K1-B11

Method BLASTX
NCBI GI g2879867
BLAST score 411
E value 2.0e-40
Match length 115
% identity 68

NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces

pombe]

Seq. No. 206809

Seq. ID LIB3120-008-Q1-K1-B2

Method BLASTX
NCBI GI g1352821
BLAST score 562
E value 5.0e-58
Match length 108
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
206810
Seq. No.
Seq. ID
                  LIB3120-008-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4417279
                  228
BLAST score
                  8.0e-19
E value
Match length
                  69
                  62
% identity
                  (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206811
Seq. ID
                  LIB3120-008-Q1-K1-B6
                  BLASTX
Method
NCBI GI
                  g4406372
BLAST score
                  268
                  1.0e-23
E value
                  100
Match length
% identity
                   56
                  (AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                  glomerata]
                   206812
Seq. No.
                   LIB3120-008-Q1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4115357
                   331
BLAST score
                   6.0e-31
E value
                   120
Match length
% identity
                   (AC005957) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   206813
Seq. No.
                   LIB3120-008-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q462187
BLAST score
                   701
                   3.0e-74
E value
                   139
Match length
                   96
% identity
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 282928 pir_A42906 serine
                   hydroxymethyltransferase - garden pea >gi_169158 (M87649)
                   serine hydroxymethyltransferase [Pisum sativum]
                   206814
Seq. No.
                   LIB3120-008-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g68200
NCBI GI
                   317
BLAST score
                   2.0e-29
E value
Match length
                   86
                   78
% identity
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
```

chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]



```
206815
Seq. No.
                  LIB3120-008-Q1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827888
                  196
BLAST score
                  4.0e-15
E value
                  92
Match length
                  51
% identity
                  (AF016621) ATP-dependent Clp protease proteolytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                  206816
Seq. No.
                  LIB3120-008-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  524
BLAST score
                  2.0e-53
E value
                  111
Match length
                   86
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   206817
Seq. No.
                   LIB3120-008-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g1168408
NCBI GI
                   503
BLAST score
                   5.0e-51
E value
Match length
                   131
                   77
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                   >gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea >gi 927507_emb_CAA61946_ (X89828)
                   fructose-1,6-bisphosphate aldolase [Pisum sativum]
                   206818
Seq. No.
                   LIB3120-008-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   q4210948
NCBI GI
BLAST score
                   488
                   2.0e-49
E value
                   98
Match length
                   95
% identity
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                   206819
Seq. No.
                   LIB3120-008-Q1-K1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3288821
BLAST score
                   444
                   3.0e-44
E value
Match length
                   103
% identity
                   83
NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
```



## transaminase [Arabidopsis thaliana]

```
206820
Seq. No.
                  LIB3120-008-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                  q2832669
NCBI GI
BLAST score
                  141
                   1.0e-08
E value
Match length
                  71
% identity
                   48
                   (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206821
                  LIB3120-008-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q20729
BLAST score
                   436
E value
                   3.0e-43
                   118
Match length
% identity
                   75
                   (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   206822
Seq. No.
                   LIB3120-008-Q1-K1-D12
Seq. ID
Method
                   BLASTX
                   q3107905
NCBI GI
BLAST score
                   384
                   3.0e-37
E value
                   122
Match length
% identity
                   18
                   (D85101) leaf protein [Ipomoea nil]
NCBI Description
Seq. No.
                   206823
                   LIB3120-008-Q1-K1-D2
Seq. ID
Method
                   BLASTX
                   g1754795
NCBI GI
BLAST score
                   652
                   1.0e-68
E value
Match length
                   127
% identity
                   89
                   (U59477) omega-3 fatty acid desaturase [Perilla frutescens]
NCBI Description
                   206824
Seq. No.
                   LIB3120-008-Q1-K1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1718097
                   341
BLAST score
                   1.0e-33
E value
Match length
                   119
                   59
% identity
                   VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016
                   lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                   ATPase subunit DVA41 [Dictyostelium discoideum]
```

Seq. No. 206825



```
LIB3120-008-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4115379
                   344
BLAST score
                   2.0e-32
E value
Match length
                   102
% identity
                   (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                   thaliana]
                   206826
Seq. No.
                   LIB3120-008-Q1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2623246
                   244
BLAST score
                   5.0e-21
E value
Match length
                   90
                   61
% identity
                   (AF030709) poly(A) polymerase [Pisum sativum]
NCBI Description
                   206827
Seq. No.
Seq. ID
                   LIB3120-008-Q1-K1-D6
                   BLASTX
Method
NCBI GI
                   q1439609
                                                     · de
BLAST score
                   542
                   1.0e-55
E value
                   109
Match length
                   99
% identity
                   (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                   hirsutum]
                   206828
Seq. No.
                   LIB3120-008-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   q2507458
NCBI GI
BLAST score
                   203
                   6.0e-16
E value
                   106
Match length
                   37
% identity
                   THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi 81491_pir__S20496
NCBI Description
                   thioredoxin m precursor - spinach >gi_21348_emb_CAA35826_
                   (X51462) thioredoxin M precursor (AA -67 to 114) [Spinacia
                   oleracea]
                   206829
Seq. No.
Seq. ID
                   LIB3120-008-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2339978
BLAST score
                   534
                   1.0e-54
E value
Match length
                   139
                   75
% identity
                   (Y11336) RGA1 protein [Arabidopsis thaliana]
NCBI Description
```

28383

206830

BLASTN

LIB3120-008-Q1-K1-E10

Seq. No.

Seq. ID

Method



```
q2618602
NCBI GI
BLAST score
                  41
E value
                  1.0e-13
                  126
Match length
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
                  206831
Seq. No.
                  LIB3120-008-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g4415994
NCBI GI
                  479
BLAST score
                  2.0e-48
E value
                  109
Match length
                  84
% identity
                   (AF059289) beta-tubulin 3 [Eleusine indica]
NCBI Description
                   206832
Seq. No.
Seq. ID
                  LIB3120-008-Q1-K1-E7
                   BLASTX
Method
                   q2982432
NCBI GI
                   330
BLAST score
                   5.0e-31
E value
                   76
Match length
                   79
% identity
                   (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
                   206833
Seq. No.
Seq. ID
                   LIB3120-008-Q1-K1-E8
Method
                   BLASTX
                   g1352821
NCBI GI
                   527
BLAST score
                   6.0e-54
E value
                   102
Match length
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   206834
                   LIB3120-008-Q1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1431629
BLAST score
                   272
                   4.0e-24
E value
                   72
Match length
                   71
% identity
                   (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
```

206835 Seq. No.

LIB3120-008-Q1-K1-F2 Seq. ID

BLASTX Method g231610 NCBI GI 356 BLAST score



```
E value
Match length
                  118
% identity
                  65
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 67880 pir__PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >qi 19785 emb CAA45152 (X63606) ATP synthase
                   (gamma subunit) [Nicotiana tabacum]
                  206836
Seq. No.
Seq. ID
                  LIB3120-008-Q1-K1-F3
                  BLASTX
Method
NCBI GI
                  g1928981
BLAST score
                  514
                  2.0e-52
E value
                  108
Match length
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                   206837
Seq. No.
                  LIB3120-008-Q1-K1-F5
Seq. ID
                  BLASTN
Method
                  g3242700
NCBI GI
BLAST score
                   42
                   2.0e-14
E value
                   94
Match length
                   86
% identity
                  Arabidopsis thaliana chromosome II BAC F26B6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   206838
Seq. No.
                   LIB3120-008-Q1-K1-F6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2578440
BLAST score
                   192
                   1.0e-14
E value
Match length
                   141
                   35
% identity
                   (X67425) pectinesterase [Pisum sativum]
NCBI Description
Seq. No.
                   206839
                   LIB3120-008-Q1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4210948
BLAST score
                   486
                   4.0e-49
E value
Match length
                   103
% identity
                   89
                   (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                   206840
Seq. No.
```

Seq. ID LIB3120-008-Q1-K1-G11

Method BLASTX
NCBI GI g2894603
BLAST score 201
E value 1.0e-15



```
Match length
                   39
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   206841
Seq. No.
Seq. ID
                  LIB3120-008-Q1-K1-G12
                  BLASTX
Method
                   q3413705
NCBI GI
BLAST score
                   519
E value
                   4.0e-53
                   111
Match length
```

% identity 91
NCBI Description (AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

 Seq. No.
 206842

 Seq. ID
 LIB3120-008-Q1-K1-G2

 Method
 BLASTX

 NCBI GI
 g3337361

 BLAST score
 436

BLAST score 436
E value 2.0e-43
Match length 118
% identity 66

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 206843

Seq. ID LIB3120-008-Q1-K1-G3

Method BLASTX
NCBI GI g289920
BLAST score 587
E value 5.0e-61
Match length 113
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 206844

Seq. ID LIB3120-008-Q1-K1-G6

Method BLASTX
NCBI GI g4545262
BLAST score 239
E value 4.0e-20
Match length 44
% identity 100

NCBI Description (AF118230) metallothionein-like protein [Gossypium

hirsutum]

Seq. No. 206845

Seq. ID LIB3120-008-Q1-K1-G7

Method BLASTX
NCBI GI g303736
BLAST score 297
E value 4.0e-27
Match length 62
% identity 94

NCBI Description (D12541) GTP-binding protein [Pisum sativum]

>qi 738934 prf 2001457B GTP-binding protein [Pisum



## sativum]

```
Seq. No.
                  206846
Seq. ID
                  LIB3120-008-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3914605
BLAST score
                  240
                  2.0e-20
E value
Match length
                  82
                  65
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857 (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Malus domestica]
Seq. No.
                  206847
Seq. ID
                  LIB3120-008-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  400
                  5.0e-39
E value
                  83
Match length
% identity
                  94
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  206848
Seq. ID
                  LIB3120-008-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q505482
BLAST score
                   345
                   9.0e-33
E value
                   97
Match length
% identity
                   77
NCBI Description
                   (X64349) 33 kDa polypeptide of water-oxidizing complex of
                  photosystem II [Nicotiana tabacum]
                   206849
Seq. No.
                  LIB3120-008-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2894611
BLAST score
                   228
                   8.0e-19
E value
                  81
Match length
% identity
                   62
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                  206850
Seq. No.
                  LIB3120-008-Q1-K1-H3
Seq. ID
```

BLASTX

592

g1352821

Method

NCBI GI BLAST score



3.0e-61 E value Match length 130 91 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206851

LIB3120-008-Q1-K1-H6 Seq. ID

BLASTN Method g3821780 NCBI GI BLAST score 36 1.0e-10 E value Match length 37 61 % identity

Xenopus laevis cDNA clone 27A6-1 NCBI Description

Seq. No. 206852

LIB3120-008-Q1-K1-H7 Seq. ID

BLASTX Method g3202030 NCBI GI 452 BLAST score E value 4.0e-45 137 Match length

% identity (AF069318) geranylgeranyl hydrogenase [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 206853

LIB3120-008-Q1-K1-H8 Seq. ID

BLASTX Method g2353171 NCBI GI BLAST score 190 2.0e-14 E value 82 Match length 55 % identity

(AF015542) sigma factor 1 [Arabidopsis thaliana] NCBI Description

>gi\_2443408\_dbj\_BAA22421\_ (D89993) SigA [Arabidopsis
thaliana] >gi\_2558514\_emb\_CAA74640\_ (Y14252) plastid RNA

polymerase sigma factor [Arabidopsis thaliana]

206854 Seq. No.

LIB3120-009-Q1-K1-A10 Seq. ID

Method BLASTX g1352821 NCBI GI BLAST score 535 8.0e-55 E value 99 Match length 98 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
206855
Seq. No.
                  LIB3120-009-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  g2239083
NCBI GI
                  170
BLAST score
                  5.0e-12
E value
                  103
Match length
% identity
                   45
                   (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385)
                   anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
                   206856
Seq. No.
                   LIB3120-009-Q1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567260
BLAST score
                   523
                   2.0e-53
E value
Match length
                   117
                   81
% identity
                   (AC006841) putative NADPH dependent mannose 6-phosphate
NCBI Description
                   reductase [Arabidopsis thaliana]
Seq. No.
                   206857
                   LIB3120-009-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g1084321
NCBI GI
BLAST score
                   421
E value
                   2.0e-41
                   117
Match length
                   68
% identity
                   protochlorophyllide reductase (EC 1.3.1.33) - cucumber
NCBI Description
                   >gi 2244614 dbj BAA21089_ (D50085)
                   NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]
                   206858
Seq. No.
                   LIB3120-009-Q1-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1168411
BLAST score
                   545
                   6.0e-56
E value
Match length
                   136
                   82
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   206859
Seq. No.
                   LIB3120-009-Q1-K1-A5
Seq. ID
Method
                   BLASTX
                   g1181599
NCBI GI
BLAST score
                   369
                   2.0e-35
E value
                   109
Match length
                   68
% identity
                   (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
```

28389

206860

Seq. No.



```
LIB3120-009-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  q68200
NCBI GI
BLAST score
                  553
                  5.0e-57
E value
                  137
Match length
                  82
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi 22633_emb_CAA47293_ (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
                  206861
Seq. No.
                  LIB3120-009-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
                  563
BLAST score
                  4.0e-58
E value
                  108
Match length
                   96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   206862
Seq. No.
                   LIB3120-009-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g4091810
NCBI GI
                   516
BLAST score
                   1.0e-52
E value
Match length
                   134
% identity
                   (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1
NCBI Description
                   [Arabidopsis thaliana]
                   206863
Seq. No.
Seq. ID
                   LIB3120-009-Q1-K1-B3
                   BLASTX
Method
NCBI GI
                   q20729
BLAST score
                   298
                   4.0e-27
E value
Match length
                   108
% identity
                   61
                   (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
Seq. No.
                   206864
                   LIB3120-009-Q1-K1-B5
Seq. ID
                   BLASTX
Method
                   g4455208
NCBI GI
BLAST score
                   330
                   9.0e-31
E value
Match length
                   81
```

Seq. No. 206865

% identity

NCBI Description

75

(AL035440) putative protein [Arabidopsis thaliana]

E value

Match length

% identity

130

76



```
LIB3120-009-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1352821
                  229
BLAST score
                  5.0e-19
E value
Match length
                  100
                  53
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir_RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  206866
Seq. No.
Seq. ID
                  LIB3120-009-Q1-K1-C10
                  BLASTX
Method
NCBI GI
                  g120661
                  591
BLAST score
                  2.0e-61
E value
                  127
Match length
                  93
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
                  206867
Seq. No.
                  LIB3120-009-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g3252807
NCBI GI
BLAST score
                   248
                   3.0e-21
E value
Match length
                   98
% identity
                  (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206868
                   LIB3120-009-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   q1709651
NCBI GI
                   202
BLAST score
                   6.0e-16
E value
                   95
Match length
% identity
                   PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209
NCBI Description
                   plastocyanin a precursor - black poplar
                   >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus
                   nigra]
                   206869
Seq. No.
                   LIB3120-009-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4325369
BLAST score
                   541
                   1.0e-55
```

28391

NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]



```
Seq. No.
                  206870
                  LIB3120-009-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  546
                   4.0e-56
E value
Match length
                  104
% identity
                   98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4}.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   206871
Seq. No.
                  LIB3120-009-Q1-K1-C4
Seq. ID
Method
                  BLASTN
                   q289371
NCBI GI
BLAST score
                   33
                   3.0e-09
E value
                   33
Match length
                   100
% identity
                  Brassica napus serine/threonine protein kinase (BSK1) mRNA,
NCBI Description
                   complete cds
                   206872
Seq. No.
                   LIB3120-009-Q1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q289920
BLAST score
                   177
                   4.0e-13
E value
Match length
                   62
                   61
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   206873
Seq. No.
                   LIB3120-009-Q1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1019946
BLAST score
                   302
                   4.0e-33
E value
Match length
                   88
% identity
                   85
                   (U37060) ascorbate peroxidase [Gossypium hirsutum]
NCBI Description
                   206874
Seq. No.
                   LIB3120-009-Q1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2117937
```

Method BLASTX
NCBI GI g2117937
BLAST score 253
E value 2.0e-33
Match length 135
% identity 63

NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

barley >gi\_1212996\_emb\_CAA62689\_ (X91347) UDP-glucose



## pyrophosphorylase [Hordeum vulgare]

```
Seq. No.
                  206875
Seq. ID
                  LIB3120-009-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q2388580
BLAST score
                  168
E value
                  5.0e-12
Match length
                  98
                   45
% identity
NCBI Description
                   (AC000098) Similar to Sequence 10 from patent 5477002
                   (gb 1253956). [Arabidopsis thaliana]
Seq. No.
                  206876
                  LIB3120-009-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129672
BLAST score
                  124
E value
                  1.0e-08
Match length
                   111
                   51
% identity
                  photosystem II reaction center protein, 6.1K - Arabidopsis
NCBI Description
                  thaliana >gi 950023 emb CAA62296 (X90769) component of 6.1
                   kDa polypeptide of photosystem II reaction center
                   [Arabidopsis thaliana]
                   206877
Seq. No.
Seq. ID
                  LIB3120-009-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                   q1931639
BLAST score
                   172
E value
                   3.0e-12
Match length
                   121
% identity
                   33
NCBI Description
                  (U95973) lysophospholipase isolog [Arabidopsis thaliana]
                   206878
Seq. No.
                  LIB3120-009-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3218467
BLAST score
                   176
E value
                   1.0e-12
                   118
Match length
                   36
% identity
                  (AJ006529) putative phosphatase [Gallus gallus]
NCBI Description
                  206879
Seq. No.
                  LIB3120-009-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2642217
BLAST score
                   193
E value
                   1.0e-14
Match length
                  72
                   57
% identity
NCBI Description
                  (AF030387) NOI protein [Oryza sativa]
                   206880
Seq. No.
```



```
LIB3120-009-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100203
BLAST score
                  200
                  1.0e-15
E value
Match length
                  79
                  58
% identity
                  cysteine proteinase (EC 3.4.22.-) precursor - tomato
NCBI Description
                  >gi 19195 emb CAA78403 (Z14028) pre-pro-cysteine
                  proteinase [Lycopersicon esculentum]
                  206881
Seq. No.
Seq. ID
                  LIB3120-009-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4454459
BLAST score
                  178
                   6.0e-13
E value
Match length
                  90
                   51
% identity
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                  206882
Seq. No.
                  LIB3120-009-Q1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3789952
                   570
BLAST score
                   6.0e-59
E value
                   117
Match length
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   206883
                   LIB3120-009-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g3319354
NCBI GI
BLAST score
                   298
                   3.0e-27
E value
Match length
                   88
% identity
                   72
                   (AF077407) contains similarity to sugar transporters (Pfam:
NCBI Description
                   sugar tr.hmm, score: 395.39) [Arabidopsis thaliana]
                   206884
Seq. No.
                   LIB3120-009-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115833
BLAST score
                   445
                   3.0e-44
E value
Match length
                   119
                   74
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                   a/b-binding protein Cab10A - tomato >gi_170394 (M32605)
```

Seq. No. 206885

a-binding protein [Lycopersicon esculentum]

Match length

% identity

128

42



```
LIB3120-009-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3808101
BLAST score
                  400
E value
                  4.0e-39
Match length
                  122
% identity
                  66
NCBI Description
                  (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                  206886
Seq. ID
                  LIB3120-009-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g131393
BLAST score
                  366
                  4.0e-35
E value
Match length
                  106
                  75
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi_100360_pir__S15005 photosystem II oxygen-evolving
                  complex protein 2 - common tobacco
                  >gi 19911 emb CAA39039.1 (X55354) photosystem II 23kDa
                  polypeptide [Nicotiana tabacum]
Seq. No.
                  206887
Seq. ID
                  LIB3120-009-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q2129746
BLAST score
                  225
E value
                  2.0e-18
Match length
                  88
% identity
                  56
NCBI Description
                  SUPERMAN protein - Arabidopsis thaliana >gi 1079669
                  (U38946) SUPERMAN [Arabidopsis thaliana]
                  >gi_1585427 prf 2124420A SUPERMAN gene [Arabidopsis
                  thaliana]
                  206888
Seq. No.
                  LIB3120-009-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4096662
BLAST score
                  139
E value
                  1.0e-18
Match length
                  84
                  69
% identity
NCBI Description
                  (U35026) Rab1-like small GTP-binding protein [Petunia x
                  hybrida]
Seq. No.
                  206889
Seq. ID
                  LIB3120-009-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3281846
BLAST score
                  248
E value
                  3.0e-21
```

28395

NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]



Seq. No. 206890 Seq. ID LIB3120-009-Q1-K1-F10 Method BLASTX NCBI GI g1352821 BLAST score 372 9.0e-36 E value 95 Match length % identity 75 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

206891 Seq. No.

Seq. ID LIB3120-009-Q1-K1-F11

Method BLASTX NCBI GI g4371296 BLAST score 306 E value 5.0e-28 63 Match length 94 % identity

(AC006260) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana]

206892 Seq. No.

Seq. ID LIB3120-009-Q1-K1-F12

BLASTX Method g2245118 NCBI GI BLAST score 349 5.0e-33 E value 118 Match length % identity 56

NCBI Description (297343) hypothetical protein [Arabidopsis thaliana]

206893 Seq. No.

LIB3120-009-Q1-K1-F2 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 547 3.0e-56 E value Match length 105 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206894

LIB3120-009-Q1-K1-F3 Seq. ID

Method BLASTX NCBI GI g4406530 BLAST score 321 E value 9.0e-30 97 Match length

% identity NCBI Description (AF126870) rubisco activase [Vigna radiata] Seq. No. 206895 LIB3120-009-Q1-K1-F4 Seq. ID Method BLASTX NCBI GI q2894600 BLAST score 169 E value 5.0e-12 Match length 67 49 % identity NCBI Description (AL021889) putative protein [Arabidopsis thaliana] Seq. No. 206896 Seq. ID LIB3120-009-Q1-K1-F5 BLASTX q3928543 146 3.0e-09

Method NCBI GI BLAST score E value Match length 68

% identity 50 NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No. 206897

Seq. ID LIB3120-009-Q1-K1-F7

BLASTX Method NCBI GI q1354515 BLAST score 198 E value 2.0e-15 Match length 107 48 % identity

(U55837) carbonic anhydrase [Populus tremula x Populus NCBI Description

tremuloides]

206898 Seq. No.

LIB3120-009-Q1-K1-F9 Seq. ID

Method BLASTX NCBI GI g2827755 BLAST score 272 E value 4.0e-24 Match length 95 62 % identity

INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE NCBI Description

PHOSPHOHYDROLASE) (PPASE) >gi 951323 (U31467)

pyrophosphatase [Vigna radiata]

206899 Seq. No.

LIB3120-009-Q1-K1-G11 Seq. ID

Method BLASTX NCBI GI g20729 BLAST score 346 E value 1.0e-32 106 Match length 67 % identity

(X15190) precursor (AA -68 to 337) [Pisum sativum] NCBI Description



```
Seq. No.
                   206900
                   LIB3120-009-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                   g1352821
                   503
```

NCBI GI BLAST score 4.0e-51 E value Match length 103 96 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

206901 Seq. No.

LIB3120-009-Q1-K1-G2 Seq. ID

Method BLASTX NCBI GI g2832300 BLAST score 426 4.0e-42 E value 116 Match length 72 % identity

(AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus NCBI Description

roseus]

206902 Seq. No.

LIB3120-009-Q1-K1-G4 Seq. ID

Method BLASTX NCBI GI g2146746 BLAST score 305 7.0e-28 E value 72 Match length 82 % identity

protein kinase (EC 2.7.1.-) - Arabidopsis thaliana NCBI Description

>gi 166819 (L05562) protein kinase [Arabidopsis thaliana]

206903 Seq. No.

LIB3120-009-Q1-K1-G6 Seq. ID

Method BLASTX g68200 NCBI GI BLAST score 315 4.0e-29 E value 89 Match length 76 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description

chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

206904 Seq. No.

LIB3120-009-Q1-K1-G8 Seq. ID

Method BLASTX NCBI GI g2529663 BLAST score 302 E value 2.0e-27 Match length 69 78 % identity

(AC002535) putative lysophospholipase [Arabidopsis NCBI Description

E value

Match length

% identity

8.0e-31 95

65





thaliana] >gi\_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]

Seq. No. 206905 LIB3120-009-Q1-K1-G9 Seq. ID Method BLASTX q2809246 NCBI GI BLAST score 509 8.0e-52 E value Match length 117 % identity 80 (AC002560) F2401.15 [Arabidopsis thaliana] NCBI Description Seq. No. 206906 LIB3120-009-Q1-K1-H1 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 627 1.0e-65 E value Match length 118 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 206907 Seq. No. Seq. ID LIB3120-009-Q1-K1-H10 Method BLASTX NCBI GI g2244990 BLAST score 445 3.0e-44E value 137 Match length % identity (Z97340) similarity to LIM homeobox protein -NCBI Description Caenorhabditis [Arabidopsis thaliana] 206908 Seq. No. Seq. ID LIB3120-009-Q1-K1-H11 Method BLASTX q2754849 NCBI GI BLAST score 171 8.0e-17 E value Match length 60 71 % identity (AF039000) putative serine-glyoxylate aminotransferase NCBI Description [Fritillaria agrestis] 206909 Seq. No. Seq. ID LIB3120-009-Q1-K1-H12 Method BLASTX g2565275 NCBI GI BLAST score 330



```
NCBI Description
                   (AF023611) Dimlp homolog [Homo sapiens]
                  206910
Seq. No.
                  LIB3120-009-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g1352821
NCBI GI
BLAST score
                  301
                  2.0e-27
E value
                  112
Match length
                   54
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 206911 LIB3120-009-Q1-K1-H3 Seq. ID Method BLASTX q3914940 NCBI GI 362 BLAST score

1.0e-34 E value 120 Match length % identity 64

SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR NCBI Description

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi\_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

[Spinacia oleracea]

Seq. No. 206912

LIB3120-009-Q1-K1-H4 Seq. ID

BLASTX Method NCBI GI q3785990 145 BLAST score 4.0e-09 E value 86 Match length 40 % identity

(AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 4220487 (AC006069) hypothetical protein [Arabidopsis

thaliana]

206913 Seq. No.

Seq. ID LIB3120-009-Q1-K1-H5

Method BLASTX g1688296 NCBI GI BLAST score 265 2.0e-23 E value 77 Match length 71 % identity

(U78297) plasma membrane intrinsic protein PIP3 NCBI Description

[Arabidopsis thaliana]

206914 Seq. No.

LIB3120-009-Q1-K1-H8 Seq. ID

Method BLASTX g1213629 NCBI GI BLAST score 540



```
E value
Match length
                  124
% identity
                  78
                  (X95991) pectinesterase [Prunus persica]
NCBI Description
Seq. No.
                  206915
                  LIB3120-010-Q1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q488573
                  497
BLAST score
                  2.0e-50
E value
                  99
Match length
% identity
                 (U09463) histone H3.2 [Medicago sativa]
NCBI Description
                  206916
Seq. No.
                  LIB3120-010-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  723
                   7.0e-77
E value
                   133
Match length
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   206917
Seq. No.
                  LIB3120-010-Q1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1352821
BLAST score
                   597
                   4.0e-62
E value
                   120
Match length
                   97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase \overline{(EC\ 4.1.1.39)} small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  206918
Sea. ID
                   LIB3120-010-Q1-K1-A6
Method
                   BLASTX
                   g3063695
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
                   71
Match length
                   68
% identity
                   (AL022537) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   206919
Seq. No.
```

LIB3120-010-Q1-K1-A7 Seq. ID

BLASTX Method g1352821 NCBI GI 638 BLAST score 7.0e-67 E value 118 Match length



% identity

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

206920

Seq. ID

LIB3120-010-Q1-K1-A8

Method

BLASTX

Seq. ID LIB3120-010-Q1-K3
Method BLASTX
NCBI GI g121631
BLAST score 244
E value 6.0e-21
Match length 74
% identity 66

% identity 66 NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR

>gi 72323 pir\_KNNT2S glycine-rich protein 2 - wood tobacco

>gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana

sylvestris]

Seq. No. 206921

Seq. ID LIB3120-010-Q1-K1-B1

Method BLASTX
NCBI GI g2454633
BLAST score 374
E value 7.0e-36
Match length 114
% identity 65

NCBI Description (AF019561) glutamine synthetase; GS2 [Daucus carota]

Seq. No. 206922

Seq. ID LIB3120-010-Q1-K1-B5

Method BLASTX
NCBI GI g1495366
BLAST score 196
E value 2.0e-15
Match length 82
% identity 44

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 206923

Seq. ID LIB3120-010-Q1-K1-B7

Method BLASTX
NCBI GI g119905
BLAST score 434
E value 6.0e-43
Match length 135
% identity 64

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi\_81898\_pir\_\_S04030 ferredoxin--NADP+ reductase (EC
1.18.1.2) precursor - garden pea >gi\_20722\_emb\_CAA30978\_
(X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to
308) [Pisum sativum] >gi\_226545\_prf\_\_1601517A ferredoxin

NADP reductase [Arachis hypogaea]

Seq. No. 206924

Seq. ID LIB3120-010-Q1-K1-B8



BLASTX Method NCBI GI q125887 BLAST score 167 9.0e-12 E value 93 Match length % identity

ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR NCBI Description

>gi 82092\_pir\_ S04765 LAT52 protein precursor - tomato >qi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No.

206925 Seq. ID LIB3120-010-Q1-K1-C1

Method BLASTX NCBI GI q131397 BLAST score 245 8.0e-21 E value Match length 116

% identity

OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD NCBI Description

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480\_pir \_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi 755802 emb CAA29056 (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi 225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

206926 Seq. No.

Seq. ID LIB3120-010-Q1-K1-C2

Method BLASTX NCBI GI q1352821 BLAST score 627 1.0e-65 E value 119 Match length % identity 97

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

206927 Seq. No.

LIB3120-010-Q1-K1-C3 Seq. ID

Method BLASTX NCBI GI q3914605 173 BLAST score 2.0e-12 E value 100 Match length 46 % identity

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi\_541930\_pir\_\_S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi 415852\_emb\_CAA79857\_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Method

BLASTX



```
Seq. No.
                   206928
                  LIB3120-010-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g289920
NCBI GI
                  579
BLAST score
                  5.0e-60
E value
Match length
                  119
% identity
                   92
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   206929
Seq. No.
                   LIB3120-010-Q1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2317907
BLAST score
                   549
E value
                   2.0e-56
Match length
                   134
% identity
                   81
                  (U89959) Mago Nashi-like protein [Arabidopsis thaliana]
NCBI Description
                   206930
Seq. No.
                   LIB3120-010-Q1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g289920
BLAST score
                   586
                   9.0e-61
E value
Match length
                   112
                   99
% identity
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                   hirsutum]
                   206931
Seq. No.
                   LIB3120-010-Q1-K1-D2
Seq. ID
Method
                   BLASTX
                   g3288821
NCBI GI
                   523
BLAST score
                   2.0e-53
E value
                   120
Match length
% identity
                   82
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana]
                   206932
Seq. No.
                   LIB3120-010-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4103324
BLAST score
                   611
                   1.0e-63
E value
Match length
                   128
% identity
                   93
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
                   206933
Seq. No.
                   LIB3120-010-Q1-K1-D4
Seq. ID
```



```
q1170897
NCBI GI
                  524
BLAST score
                  1.0e-53
E value
                  120
Match length
                  86
% identity
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi 1076276 pir S52039 NAD-malate dehydrogenase - cucumber
                  >gi 695311 (L31900) glyoxysomal malate dehydrogenase
                   [Cucumis sativus]
                  206934
Seq. No.
                  LIB3120-010-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g2088654
NCBI GI
BLAST score
                   448
                   1.0e-44
E value
                   102
Match length
                   85
% identity
                   (AF002109) 60S acidic ribosomal protein P0 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   206935
Seq. No.
                   LIB3120-010-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3080372
NCBI GI
                   601
BLAST score
                   1.0e-62
E value
                   142
Match length
                   76
% identity
                   (AL022580) putative pectinacetylesterase [Arabidopsis
NCBI Description
                   thaliana]
                   206936
Seq. No.
                   LIB3120-010-Q1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3859570
                   204
BLAST score
                   5.0e-16
E value
                   54
Match length
                   69
% identity
                   (AF098753) unknown [Oryza sativa]
NCBI Description
                   206937
Seq. No.
Seq. ID
                   LIB3120-010-Q1-K1-E8
                   BLASTX
Method
                   a99992
NCBI GI
BLAST score
                   161
                   6.0e-11
E value
                   60
Match length
                   24
% identity
                   protein disulfide-isomerase (EC 5.3.4.1) precursor -
NCBI Description
                   alfalfa (clone B2) >gi_166418 (M82973) putative
                   endomembrane protein; putative [Medicago sativa]
```

Seq. No. 206938

Seq. ID LIB3120-010-Q1-K1-F1

Method BLASTX



```
q4210334
NCBI GI
                  661
BLAST score
                  1.0e-69
E value
Match length
                  138
% identity
                   (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit
NCBI Description
                  [Arabidopsis thaliana]
                  206939
Seq. No.
Seq. ID
                  LIB3120-010-Q1-K1-F4
                  BLASTX
Method
                  g115833
NCBI GI
                  474
BLAST score
                  1.0e-47
E value
                  117
Match length
                  77
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                   206940
Seq. No.
                  LIB3120-010-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                   g3885515
NCBI GI
                   388
BLAST score
                   1.0e-37
E value
                   89
Match length
                   82
% identity
                   (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                   sativa]
                   206941
Seq. No.
Seq. ID
                   LIB3120-010-Q1-K1-F6
                   BLASTN
Method
                   g2924257
NCBI GI
BLAST score
                   43
                   2.0e-15
E value
                   47
Match length
                   98
% identity
NCBI Description
                   Tobacco chloroplast genome DNA
                   206942
Seq. No.
                   LIB3120-010-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   q4406530
NCBI GI
BLAST score
                   381
                   1.0e-36
E value
                   126
Match length
                   64
% identity
                   (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                   206943
Seq. No.
                   LIB3120-010-Q1-K1-G1
Seq. ID
                   BLASTX
Method
```

28406

q1170567

312

NCBI GI

BLAST score



E value 7.0e-29
Match length 65
% identity 86

NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi\_1085960\_pir\_\_S52648 INO1 protein - Citrus paradisi
>gi\_602565\_emb\_CAA83565\_ (Z32632) INO1 [Citrus x paradisi]

Seq. No. 206944

Seq. ID LIB3120-010-Q1-K1-G2

Method BLASTX
NCBI GI g2829899
BLAST score 167
E value 1.0e-11
Match length 127
% identity 37

NCBI Description (AC002311) similar to ripening-induced protein, gp AJ001449 2465015 and major#latex protein,

gp X91961 1107495 [Arabidopsis thaliana]

Seq. No. 206945

Seq. ID LIB3120-010-Q1-K1-G4

Method BLASTX
NCBI GI g542127
BLAST score 281
E value 7.0e-34
Match length 84
% identity 81

NCBI Description chlorophyll a/b-binding protein type Ib, 20K chain

precursor - barley (fragment) >gi\_544702\_bbs\_143260
(S68729) light-harvesting complex I, LHC I [Hordeum vulgare=barley, Prato, Peptide Chloroplast, 231 aa]

[Hordeum vulgare]

Seq. No. 206946

Seq. ID LIB3120-010-Q1-K1-G5

Method BLASTX
NCBI GI g132794
BLAST score 432
E value 1.0e-42
Match length 109
% identity 76

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi\_71288\_pir\_\_R5NT22

ribosomal protein L22 - common tobacco chloroplast >gi\_11866\_emb\_CAA77382\_ (Z00044) ribosomal protein L22 [Nicotiana tabacum] >gi\_225236\_prf\_\_1211235BU ribosomal

protein L22 [Nicotiana tabacum]

Seq. No. 206947

Seq. ID LIB3120-010-Q1-K1-G7

Method BLASTX
NCBI GI g166834
BLAST score 638
E value 6.0e-67
Match length 134
% identity 89

NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi\_2642155 (AC003000)





## Rubisco activase [Arabidopsis thaliana]

```
206948
Seq. No.
                  LIB3120-010-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120661
BLAST score
                  435
E value
                  4.0e-43
Match length
                  90
% identity
                  92
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                  206949
Seq. ID
                  LIB3120-010-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2702270
BLAST score
                  352
E value
                  2.0e-33
                  105
Match length
                  64
% identity
                  (AC003033) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  206950
                  LIB3120-010-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131399
BLAST score
                   414
                  1.0e-40
E value
Match length
                  96
                  80
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
NCBI Description
                  TISSUE-SPECIFIC ST-LS1 PROTEIN) >qi 82277 pir S00411
                  photosystem II 10K protein precursor - potato
                  >qi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                   tuberosum]
                   206951
Seq. No.
Seq. ID
                  LIB3120-010-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                   g20729
                   227
BLAST score
                   7.0e-19
E value
                   66
Match length
                   73
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   206952
Seq. No.
                  LIB3120-010-Q1-K1-H7
Seq. ID
Method
                   BLASTX
                   g3122785
NCBI GI
                   453
BLAST score
                   3.0e-45
E value
                   115
Match length
% identity 🚓
                  ~ 80
NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal
```

NCBI Description



## protein S14 [Lupinus luteus]

```
206953
Seq. No.
                  LIB3120-010-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115833
BLAST score
                  410
E value
                  3.0e-40
Match length
                  107
                  76
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                  206954
Seq. No.
                  LIB3120-011-Q1-K1-A1
Seq. ID
Method
                  BLASTX
                  g115784
NCBI GI
BLAST score
                  466
                  1.0e-46
E value
                  88
Match length
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB)
NCBI Description
                   (LHCP) >gi 167525 (M16058) chlorophyll a/b-binding protein
                   [Cucumis sativus]
Seq. No.
                  206955
                  LIB3120-011-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  571
E value
                   4.0e-59
                  109
Match length
                  100
% identity
NCBI Description
                  (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  206956
Seq. ID
                  LIB3120-011-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1552379
BLAST score
                  200
E value
                   2.0e-15
Match length
                  79
% identity
                   54
                  (Y08155) pectin methylesterase [Silene latifolia ssp. alba]
NCBI Description
                  206957
Seq. No.
                  LIB3120-011-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  g131385
NCBI GI
BLAST score
                   608
E value
                   3.0e-63
Match length
                  146
% identity
                   84
```

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

BLAST score

Match length

E value

742 5.0e-79

138



#### THYLAKOID MEMBRANE PROTEIN)

Seq. No. 206958 Seq. ID LIB3120-011-Q1-K1-A5 Method BLASTX NCBI GI g3914666 BLAST score 259 2.0e-22 E value Match length 61 82 % identity CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR NCBI Description >qi 2791998 emb CAA74895 (Y14566) ribosomal protein L4 [Arabidopsis thaliana] >gi 2792000 emb CAA74894 (Y14565) ribosomal protein L4 [Arabidopsis thaliana] 206959 Seq. No. Seq. ID LIB3120-011-Q1-K1-A7 Method BLASTX NCBI GI g1653230 BLAST score 173 3.0e-12 E value 61 Match length 56 % identity (D90912) hypothetical protein [Synechocystis sp.] NCBI Description 206960 Seq. No. LIB3120-011-Q1-K1-B10 Seq. ID Method BLASTX q100616 NCBI GI BLAST score 166 E value 1.0e-11 44 Match length 80 % identity ribulose-bisphosphate carboxylase activase B precursor -NCBI Description barley >gi 167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi\_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] Seq. No. 206961 Seq. ID LIB3120-011-Q1-K1-B12 Method BLASTN NCBI GI g706852 BLAST score 44 1.0e-15 E value Match length 104 % identity 86 Lycopersicon esculentum photosystem II 22 kDa component NCBI Description (psbS) gene, complete cds Seq. No. 206962 LIB3120-011-Q1-K1-B2 Seq. ID BLASTX Method NCBI GI g231688



% identity CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC NCBI Description 1.11.1.6) - upland cotton  $>gi_18488_{emb_CAA39998_{emb_N5675}}$ subunit 2 of cotton catalase [Gossypium hirsutum] 206963 Seq. No. LIB3120-011-Q1-K1-B3 Seq. ID BLASTX Method g68200 NCBI GI BLAST score 463 3.0e-46 E value

117 Match length 81 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi 22633 emb CAA47293 (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

206964 Seq. No.

LIB3120-011-Q1-K1-B4 Seq. ID

BLASTX Method NCBI GI g1651828 405 BLAST score 1.0e-39 E value 132 Match length

62 % identity

(D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.] NCBI Description

206965 Seq. No.

LIB3120-011-Q1-K1-B5 Seq. ID

BLASTX Method NCBI GI g68200 BLAST score 260 1.0e-22 E value 94 Match length 62 % identity

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description

chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

206966 Seq. No.

Seq. ID LIB3120-011-Q1-K1-B6

BLASTX Method NCBI GI q2253291 191 BLAST score 1.0e-14 E value 108 Match length % identity

(AF006067) catalase-1 [Nicotiana glutinosa] NCBI Description

Seq. No. 206967

Seq. ID LIB3120-011-Q1-K1-B7

Method BLASTX NCBI GI q3763927 BLAST score 190 3.0e-14 E value Match length 151 % identity 37

E value

Match length





```
(AC004450) putative carboxyphosphoenolpyruvate mutase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  206968
Seq. ID
                  LIB3120-011-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2980770
BLAST score
                   441
                   9.0e-44
E value
Match length
                   96
                   86
% identity
                   (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   206969
                  LIB3120-011-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                   q2494075
NCBI GI
BLAST score
                   173
E value
                   6.0e-13
Match length
                   57
% identity
                   NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
NCBI Description
                   (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE
                   DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
                   (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE)
                   >gi_1084478_pir__S43833 glyceraldehyde-3-phosphate
                   dehydrogenase (NADP+) (EC 1.2.1.9) - maize
                   >qi 474408 emb CAA53075 (X75326)
                   glyceraldehyde-3-phosphate dehydrogenase (GAPN) [Zea mays]
Seq. No.
                   206970
                   LIB3120-011-Q1-K1-C12
Seg. ID
                   BLASTX
Method
NCBI GI
                   q4164153
BLAST score
                   395
                   1.0e-38
E value
Match length
                   91
                   81
% identity
                   (AB015493) ACC oxidase [Passiflora edulis]
NCBI Description
Seq. No.
                   206971
                   LIB3120-011-Q1-K1-C3
Seq. ID
                   BLASTN
Method
                   q18058
NCBI GI
                   219
BLAST score
                   1.0e-120
E value
Match length
                   422
                   88
% identity
                   Citrus limon cistron for 26S ribosomal RNA
NCBI Description
                   206972
Seq. No.
                   LIB3120-011-Q1-K1-C5
Seq. ID
Method
                   BLASTN
                   g18058
NCBI GI
BLAST score
                   45
                   3.0e-16
```



% identity

Citrus limon cistron for 26S ribosomal RNA NCBI Description

Seq. No.

206973

Seq. ID

LIB3120-011-Q1-K1-C7

Method

BLASTX

NCBI GI

g2654094

BLAST score E value

173 2.0e-25

Match length % identity

123

NCBI Description

(AF034210) aspartate aminotransferase glyoxysomal isozyme

AAT1 precursor [Glycine max]

Seq. No.

206974

Seq. ID

LIB3120-011-Q1-K1-C8

Method

BLASTX

NCBI GI

q3914605

BLAST score

298

E value Match length 1.0e-35

% identity

134 -- 63

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 541930\_pir\_\_S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi 415852 emb CAA79857 (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No.

206975

Seq. ID

LIB3120-011-Q1-K1-C9

Method NCBI GI BLASTX g231688

BLAST score E value

687 1.0e-72

Match length

124 99

% identity NCBI Description

CATALASE ISOZYME 2 >gi\_99599\_pir\_\_S17493 catalase (EC

(X56675) 1.11.1.6) - upland cot $\overline{t}$ on > $g\overline{t}$ \_18 $\overline{t}$ 8\_emb\_CAA39998\_

subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.

206976

Seq. ID

LIB3120-011-Q1-K1-D1

Method NCBI GI BLASTX g2982432

BLAST score E value

284 2.0e-25

Match length

76 71

% identity NCBI Description

(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.

206977

Seq. ID

E value

LIB3120-011-Q1-K1-D2

Method NCBI GI BLAST score BLASTX q417544 661

2.0e-69



Match length 132 % identity 93

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi\_320209\_pir\_\_ A60695 photosystem I chain II precursor - cucumber >gi\_625966\_pir\_\_ JQ2132 photosystem I complex 20K protein precursor - cucumber >gi\_227772 prf 1710320A

photosystem I 20kD protein [Cucumis sativus]

Seq. No. 206978

Seq. ID LIB3120-011-Q1-K1-D3

Method BLASTX
NCBI GI g1168408
BLAST score 473
F value 1 0e-47

E value 1.0e-47 Match length 133 % identity 73

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi\_2118268\_pir\_\_S58168 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi\_927507\_emb\_CAA61946\_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 206979

Seq. ID LIB3120-011-Q1-K1-D4

Method BLASTX
NCBI GI g1168408
BLAST score 638
E value 8.0e-67
Match length 149
% identity 86

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1

>gi\_2118268\_pir\_\_S58168 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi\_927507\_emb\_CAA61946\_ (X89828)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 206980

Seq. ID LIB3120-011-Q1-K1-D5

Method BLASTX
NCBI GI g120661
BLAST score 698
E value 7.0e-74
Match length 147
% identity 93

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi\_170237 (M14417) glyceraldehyde-3-phosphate

dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 206981

Seq. ID LIB3120-011-Q1-K1-D9

Method BLASTX
NCBI GI g118564
BLAST score 491
E value 8.0e-50
Match length 99
% identity 92

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >qi 65955 pir DEKVG glycerate



dehydrogenase (EC 1.1.1.29) - cucumber
>gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent
hydroxypyruvate reductase [Cucumis sativus]
>gi\_18275\_emb\_CAA32764\_ (X14609) NAPH-dependent
bydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

```
hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
                  206982
Seq. No.
Seq. ID
                  LIB3120-011-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q2244868
BLAST score
                  165
E value
                  2.0e-11
Match length
                  121
% identity
                  39
                  (Z97337) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  206983
Seq. No.
Seq. ID
                  LIB3120-011-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q2654210
BLAST score
                  471
                  2.0e-47
E value
Match length
                  113
                  81
% identity
                  (AF035457) heat shock 70 protein [Spinacia oleracea]
NCBI Description
Seq. No.
                  206984
Seq. ID
                  LIB3120-011-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                   g2982458
BLAST score
                   241
                   1.0e-20
E value
Match length
                  75
                   65
% identity
                   (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                  206985
Seq. No.
                  LIB3120-011-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4115920
BLAST score
                   508
E value
                   1.0e-51
                   153
Match length
                   60
% identity
NCBI Description
                   (AF118222) similar to the subtilase family of serine
                  proteases (Pfam: PF00082, score; 45.8, E=1.1e-11, n=2)
```

[Arabidopsis thaliana]

Seq. No. 206986

Seq. ID LIB3120-011-Q1-K1-E5

Method BLASTX
NCBI GI g1632822
BLAST score 179
E value 4.0e-13
Match length 59
% identity 61

NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi 1667594





# (U77297) transmembrane protein [Oryza sativa]

```
206987
Seq. No.
                  LIB3120-011-Q1-K1-E7
Seq. ID
Method
                  BLASTX
                   g2511693
NCBI GI
BLAST score
                   398
E value
                   8.0e-39
Match length
                   107
                   73
% identity
                   (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
                   206988
Seq. No.
                   LIB3120-011-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2388710
BLAST score
                   593
E value
                   1.0e-61
Match length
                   140
% identity
                   79
                   (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                   hypochondriacus]
                   206989
Seq. No.
Seq. ID
                   LIB3120-011-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   q309673
BLAST score
                   285
                   1.0e-25
E value
Match length
                   97
% identity
                   62
                   (L19651) light harvesting protein [Pisum sativum]
NCBI Description
                   206990
Seq. No.
Seq. ID
                   LIB3120-011-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g693914
BLAST score
                   328
                   2.0e-32
E value
Match length
                   121
% identity
                   63
                   (U20983) chlorophyll a/b binding protein [Solanum
NCBI Description
                   tuberosum]
                   206991
Seq. No.
Seq. ID
                   LIB3120-011-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   g22240
BLAST score
                   642
                   2.0e-67
E value
Match length
                   133
% identity
                   93
                   (X07157) GADPH (383 AA) [Zea mays]
NCBI Description
                   206992
Seq. No.
                   LIB3120-011-Q1-K1-F2
Seq. ID
```

28416

BLASTN

Method

NCBI Description



```
NCBI GI
                  g2342495
BLAST score
                  49
                  2.0e-18
E value
Match length
                  172
                  85
% identity
                  Ananas comosus mRNA for bromelain, complete cds
NCBI Description
Seq. No.
                  206993
                  LIB3120-011-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914605
BLAST score
                  455
E value
                  2.0e-45
Match length
                  142
% identity
                  64
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857 (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Malus domestica]
Seq. No.
                  206994
                  LIB3120-011-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231562
BLAST score
                  515
                  2.0e-52
E value
Match length
                  125
% identity
                  82
                  PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR
NCBI Description
                  (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP
                  SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
                  SYNTHASE 1) >qi 166688 (M74819)
                  3-deoxy-D-arabino-heptulosonate y-phosphate synthase
                   [Arabidopsis thaliana]
                  206995
Seq. No.
                  LIB3120-011-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q99742
BLAST score
                  341
                  3.0e - 32
E value
                  96
Match length
                  72
% identity
                  2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1
NCBI Description
                  - Arabidopsis thaliana
                  206996
Seq. No.
                  LIB3120-011-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  299
                  1.0e-27
E value
Match length
                  78
                   67
% identity
```

(AC004481) ankyrin-like protein [Arabidopsis thaliana]



```
206997
Seq. No.
                  LIB3120-011-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1345979
BLAST score
                  535
E value
                  5.0e-55
Match length
                  102
                  92
% identity
NCBI Description
                  OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
                  >gi 459962 (L29215) plastid omega-6 desaturase [Glycine
                  max]
Seq. No.
                  206998
                  LIB3120-011-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2689631
BLAST score
                  314
E value
                  7.0e-29
                  69
Match length
                  94
% identity
NCBI Description (AF022389) ADP-ribosylation factor [Vigna unguiculata]
                  206999
Seq. No.
                  LIB3120-011-QT-K1-G10
Seq. ID
Method
                  BLASTX
                  g400890
NCBI GI
BLAST score
                  296
                  8.0e-27
E value
                  127
Match length
                   46
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
                  >gi 282837 pir S26953 photosystem II 22K protein precursor
                   - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
                  PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
                  photosystem II 22 kda polypeptide [spinach, Peptide, 274
                  aa] [Spinacia oleracea]
Seq. No.
                  207000
Seq. ID
                  LIB3120-011-Q1-K1-G11
                  BLASTX
Method
NCBI GI
                  g3024148
BLAST score
                  209
E value
                   3.0e-17
Match length
                  49
                   80
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1655580_emb_CAA95858_ (Z71273) S-adenosyl-L-methionine
                   synthetase 3 [Catharanthus roseus]
```

207001 Seq. No.

Seq. ID LIB3120-011-01-K1-G12

Method BLASTX NCBI GI q128692 BLAST score 379 E value 6.0e-38



Match length 95 % identity 78

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST

>gi\_66160\_pir\_\_DENTN3 NADH dehydrogenase (ubiquinone) (EC

1.6.5.3) chain 3 - common tobacco chloroplast

>gi\_11838\_emb\_CAA77358\_ (Z00044) NADH dehydrogenase ND3
subunit [Nicotiana tabacum] >gi 225206 prf 1211235AL NADH

dehydrogenase 3-like ORF 120 [Nicotiana tabacum]

Seq. No. 207002

Seq. ID LIB3120-011-Q1-K1-G2

Method BLASTX
NCBI GI g3337361
BLAST score 419
E value 3.0e-41
Match length 145
% identity 58

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 207003

Seq. ID LIB3120-011-Q1-K1-G3

Method BLASTX
NCBI GI g4335719
BLAST score 215
E value 3.0e-17
Match length 108
% identity 44

NCBI Description (AC006248) putative RING-H2 finger protein RHG1a

[Arabidopsis thaliana]

Seq. No. 207004

Seq. ID LIB3120-011-Q1-K1-G4

Method BLASTX
NCBI GI g4104058
BLAST score 155
E value 3.0e-10
Match length 76
% identity 43

NCBI Description (AF031195) blue copper-binding protein homolog [Triticum

aestivum]

Seq. No. 207005

Seq. ID LIB3120-011-Q1-K1-G5

Method BLASTX
NCBI GI g2911058
BLAST score 190
E value 2.0e-14
Match length 80
% identity 47

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 207006

Seq. ID LIB3120-011-Q1-K1-G7

Method BLASTX
NCBI GI g1750380
BLAST score 243
E value 3.0e-21



Match length % identity

NCBI Description (U80912) Eucalyptus globulus NADP- isocitrate dehydrogenase

of Eucalyptus globulus bicostata [Eucalyptus globulus]

Seq. No. 207007

Seq. ID LIB3120-011-Q1-K1-H1

Method BLASTX NCBI GI q479406 BLAST score 685 E value 2.0e-72 Match length 145 % identity 67

NCBI Description chlorophyll a/b-binding protein - garden pea

>gi\_20671\_emb\_CAA49149\_ (X69215) chlorophyll a/b-binding

protein [Pisum sativum]

Seq. No. 207008

LIB3120-011-Q1-K1-H10 Seq. ID

Method BLASTX NCBI GI g2494261 BLAST score 617 E value 2.0e-64 Match length 130 % identity 92

NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)

>gi\_99903 pir S21567 translation elongation factor Tu precursor - soybean chloroplast >gi\_18776\_emb\_CAA46864 (X66062) EF-Tu [Glycine max] >gi 448921 prf 1918220A

elongation factor Tu [Glycine max]

Seq. No. 207009

Seq. ID LIB3120-011-Q1-K1-H11

Method BLASTX NCBI GI q131385 BLAST score 404 E value 1.0e-39 Match length 108 % identity 80

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 207010

Seq. ID LIB3120-011-Q1-K1-H2

Method BLASTX NCBI GI g3158474 BLAST score 357 E value 4.0e-34 Match length 80

% identity

NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 207011

Seq. ID LIB3120-011-Q1-K1-H3

Method BLASTX NCBI GI g2864615



BLAST score 242 E value 8.0e-21 Match length 91 % identity 57

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 207012

Seq. ID LIB3120-011-Q1-K1-H4

Method BLASTX
NCBI GI g3023752
BLAST score 376
E value 4.0e-36
Match length 112
% identity 66

NCBI Description FERREDOXIN I PRECURSOR >gi\_1418982\_emb\_CAA99756 (Z75520)

ferredoxin-I [Lycopersicon esculentum]

Seq. No. 207013

Seq. ID LIB3120-011-Q1-K1-H6

Method BLASTX
NCBI GI g3158474
BLAST score 423
E value 8.0e-42
Match length 102
% identity 83

NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No.

Seq. ID LIB3120-011-Q1-K1-H8

207014

Method BLASTX
NCBI GI g115765
BLAST score 557
E value 2.0e-57
Match length 127

% identity 50

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi\_100201\_pir\_\_S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi\_19180\_emb\_CAA32197\_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_226546\_prf\_\_1601518A

chlorophyll a/b binding protein II [Lycopersicon]

esculentum]

Seq. No. 207015

Seq. ID LIB3120-011-Q1-K1-H9

Method BLASTX
NCBI GI g3287832
BLAST score 332
E value 6.0e-31
Match length 86
% identity 74

NCBI Description (+)-DELTA-CADINENE SYNTHASE (D-CADINENE SYNTHASE)

>gi\_1843647 (U88318) (+)-delta-cadinene synthase [Gossypium

hirsutum]

Seq. No. 207016

Seq. ID



```
Seq. ID
                   LIB3120-012-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2760347
BLAST score
                   389
E value
                   4.0e-38
Match length
                   82
% identity
                   16
NCBI Description
                   (U84968) ubiquitin [Arabidopsis thaliana]
Seq. No.
                   207017
Seq. ID
                   LIB3120-012-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g548852
BLAST score
                   201
E value
                   1.0e-27
Match length
                   83
% identity
                   78
NCBI Description
                   40S RIBOSOMAL PROTEIN S21 >gi 481227 pir_ S38357 ribosomal
                   protein S21 - rice >gi_303839_dbj_BAA02158 (D12633) 40S
                   subunit ribosomal protein [Oryza sativa]
Seq. No.
                   207018
Seq. ID
                   LIB3120-012-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g479406
BLAST score
                   421
E value
                   2.0e-41
Match length
                   79
% identity
                   56
NCBI Description
                   chlorophyll a/b-binding protein - garden pea
                   >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                   protein [Pisum sativum]
Seq. No.
                   207019
Seq. ID
                   LIB3120-012-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g2689720
BLAST score
                   271
E value
                   2.0e-38
Match length
                  114
                   74
% identity
NCBI Description (AF037168) DnaJ homologue [Arabidopsis thaliana]
Seq. No.
                  207020
Seq. ID
                  LIB3120-012-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q548852
BLAST score
                  219
E value
                  2.0e-18
Match length
                  54
% identity
                  76
NCBI Description
                  40S RIBOSOMAL PROTEIN S21 >gi 481227 pir_S38357 ribosomal
                  protein S21 - rice >gi_303839_dbj_BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  207021
```

28422

LIB3120-012-P1-K1-B12



```
Method
NCBI GI
                   q20729
BLAST score
                   376
E value
                   3.0e-36
Match length
                   108
% identity
                   72
NCBI Description
                   (X15190) precursor (AA -68 to 337) [Pisum sativum]
                   207022
Seq. No.
Seq. ID
                   LIB3120-012-P1-K1-B2
```

 Seq. ID
 LIB3120-012-P1-K3

 Method
 BLASTX

 NCBI GI
 g3033375

 BLAST score
 176

BLAST score 176
E value 1.0e-12
Match length 110
% identity 36
NCRL Description /ACC042

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 207023

Seq. ID LIB3120-012-P1-K1-B3

Method BLASTX
NCBI GI g3914605
BLAST score 280
E value 4.0e-25
Match length 97
% identity 61

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir\_ S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi\_415852\_emb\_CAA79857\_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 207024

Seq. ID LIB3120-012-P1-K1-B4

Method BLASTX
NCBI GI g121953
BLAST score 126
E value 2.0e-10
Match length 45
% identity 71

NCBI Description HISTONE H1 >gi\_81905\_pir\_\_S00033 histone H1.b - garden pea

>gi\_20762\_emb\_CAA29123\_ (X05636) H1 histone (AA 1-263)

[Pisum sativum]

Seq. No. 207025

Seq. ID LIB3120-012-P1-K1-B5

Method BLASTX
NCBI GI g2494076
BLAST score 428
E value 2.0e-42
Match length 92
% identity 87

NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE



(NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi\_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]

 Seq. No.
 207026

 Seq. ID
 LIB3120-012-P1-K1-C11

 Method
 BLASTX

 NCBI GI
 399600

NCBI GI g99600
BLAST score 181
E value 2.0e-13
Match length 56
% identity 95

NCBI Description chlorophyll a/b-binding protein - upland cotton

Seq. No. 207027

Seq. ID LIB3120-012-P1-K1-C12

Method BLASTX
NCBI GI 94468979
BLAST score 458
E value 6.0e-46
Match length 92
% identity 90

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 207028

Seq. ID LIB3120-012-P1-K1-C4

Method BLASTX
NCBI GI g3386596
BLAST score 458
E value 8.0e-46
Match length 114
% identity 76

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

>gi 3702346 (AC005397) unknown protein [Arabidopsis

thaliana]

Seq. No. 207029

Seq. ID LIB3120-012-P1-K1-C9

Method BLASTX
NCBI GI g585564
BLAST score 476
E value 5.0e-48
Match length 101
% identity 86

NCBI Description FERREDOXIN--NITRITE REDUCTASE PRECURSOR

>qi 81443 pir S20495 ferredoxin--nitrite reductase (EC

1.7.7.1) precursor - European white birch

>gi 17927 emb CAA42690 (X60093) ferredoxin--nitrite

reductase [Betula pendula]

Seq. No. 207030

Seq. ID LIB3120-012-P1-K1-D1

Method BLASTN
NCBI GI g18487
BLAST score 76
E value 3.0e-35
Match length 80



% identity 99

NCBI Description G. hirsutum mRNA for cotton catalase subunit

Seq. No. 207031

Seq. ID LIB3120-012-P1-K1-D11

Method BLASTX
NCBI GI g20729
BLAST score 334
E value 2.0e-31
Match length 108
% identity 67

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 207032

Seq. ID LIB3120-012-P1-K1-D2

Method BLASTX
NCBI GI g1170214
BLAST score 565
E value 6.0e-62
Match length 137
% identity 88

NCBI Description DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR

(PORPHOBILINOGEN SYNTHASE) (ALADH) >gi\_468000 (U04525) delta-aminolevulinic acid dehydratase [Glycine max]

Seq. No. 207033

Seq. ID LIB3120-012-P1-K1-D3

Method BLASTX
NCBI GI g133802
BLAST score 284
E value 2.0e-25
Match length 59
% identity 88

NCBI Description 40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)

>gi\_85845\_pir\_\_C34823 ribosomal protein S15 - African clawed frog >gi\_214737 (M33332) insulinoma protein (rig)

[Xenopus laevis]

Seq. No. 207034

Seq. ID LIB3120-012-P1-K1-D4

Method BLASTX
NCBI GI g3885511
BLAST score 363
E value 6.0e-42
Match length 115
% identity 74

NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from

barley [Medicago sativa]

Seq. No. 207035

Seq. ID LIB3120-012-P1-K1-D6

Method BLASTX
NCBI GI g2244910
BLAST score 184
E value 1.0e-13
Match length 96
% identity 43



NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 207036

Seq. ID LIB3120-012-P1-K1-E1

Method BLASTX
NCBI GI g1352821
BLAST score 325
E value 2.0e-30
Match length 66
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207037

Seq. ID LIB3120-012-P1-K1-E11

Method BLASTX
NCBI GI g1352821
BLAST score 338
E value 6.0e-32
Match length 74
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207038

Seq. ID LIB3120-012-P1-K1-E2

Method BLASTX
NCBI GI 94467134
BLAST score 258
E value 2.0e-22
Match length 117
% identity 59

NCBI Description (AL035540) protein kinase like protein [Arabidopsis

thaliana]

Seq. No. 207039

Seq. ID LIB3120-012-P1-K1-E3

Method BLASTX
NCBI GI g115833
BLAST score 502
E value 5.0e-51
Match length 121
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR

(CAB-10A) (LHCP) >gi\_100195\_pir\_\_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi\_170394 (M32605)

a-binding protein [Lycopersicon esculentum]

Seq. No. 207040

Seg. ID LIB3120-012-P1-K1-E4

Method BLASTX



q1168411 NCBI GI 384 BLAST score 1.0e-47 E value Match length 137 % identity

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.

207041

Seq. ID

LIB3120-012-P1-K1-E5

Method NCBI GI BLASTX q3892051 225

BLAST score E value

1.0e-18 57

Match length % identity

74 (AC002330) predicted NADH dehydrogenase 24 kD subunit NCBI Description

[Arabidopsis thaliana]

Seq. No.

207042

Seq. ID

LIB3120-012-P1-K1-E6

BLASTX Method NCBI GI g1352821 537 BLAST score 4.0e-55 E value 102 Match length 98 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase  $(EC \overline{4.1.1.39})$  small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

207043

LIB3120-012-P1-K1-E7 Seq. ID

BLASTX Method q1352821 NCBI GI BLAST score 445 3.0e-44E value 86 Match length 98 % identity

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb\_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

207044

Seq. ID

LIB3120-012-P1-K1-F10

BLASTX Method g266501 NCBI GI 213 BLAST score E value 4.0e-17 128 Match length 45 % identity

MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) NCBI Description

(PMI) (PHOSPHOHEXOMUTASE) >gi 1362514 pir A56239

mannose-6-phosphate isomerase (EC 5.3.1.8) - Emericella



nidulans >gi\_168072 (M85239) phosphomannose isomerase
[Emericella nidulans]

207045 Seq. No. LIB3120-012-P1-K1-F5 Seq. ID Method BLASTX g2541876 NCBI GI BLAST score 270 9.0e-24 E value 102 Match length 47 % identity (D26015) CND41, chloroplast nucleoid DNA binding protein NCBI Description [Nicotiana tabacum] 207046 Seq. No. Seq. ID LIB3120-012-P1-K1-F6 Method BLASTX NCBI GI g421969 - '\*' -BLAST score 222 2.0e-18 E value Match length 44 % identity 95 ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain NCBI Description - coffee chloroplast (fragment) >gi\_1322147\_emb\_CAA49827\_ (X70364) rbcL [Coffea arabica] 207047 Seq. No. Seq. ID LIB3120-012-P1-K1-F9 Method BLASTX g2894534 NCBI GI 352 BLAST score 2.0e-33 E value Match length 95 76 % identity (AJ224327) aquaporin [Oryza sativa] NCBI Description 207048 Seq. No. LIB3120-012-P1-K1-G1 Seq. ID BLASTX Method g118564 NCBI GI 452 BLAST score 3.0e-45E value 91 Match length 91 % identity GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE NCBI Description REDUCTASE) (HPR) (GDH) >gi\_65955\_pir\_\_DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >qi 18275 emb CAA32764 (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 207049

Seq. ID LIB3120-012-P1-K1-G10

Method BLASTX NCBI GI g228403 BLAST score 550



E value 1.0e-50
Match length 131
% identity 83

NCBI Description glycolate oxidase [Lens culinaris]

Seq. No.

207050

Seq. ID

LIB3120-012-P1-K1-G11

Method BLASTX
NCBI GI g400890
BLAST score 205
E value 3.0e-16
Match length 104

% identity 50

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi\_282837\_pir\_\_S26953 photosystem II 22K protein precursor
- spinach >gi\_21307\_emb\_CAA48557\_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi\_260917\_bbs\_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 207051

Seq. ID LIB3120-012-P1-K1-G12

Method BLASTX
NCBI GI g1168411
BLAST score 326
E value 1.0e-30
Match length 87
% identity 79

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 207052

Seq. ID LIB3120-012-P1-K1-G3

Method BLASTX
NCBI GI g125578
BLAST score 419
E value 2.0e-41
Match length 103
% identity 82

NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) >gi 167266 (M73707) phosphoribulokinase

[Mesembryanthemum crystallinum]

Seq. No. 207053

Seq. ID LIB3120-012-P1-K1-G9

Method BLASTX
NCBI GI g2950472
BLAST score 145
E value 3.0e-09
Match length 68
% identity 46

NCBI Description (AL022070) putative autophagocytosis protein

[Schizosaccharomyces pombe]

Seq. No. 207054

Seq. ID LIB3120-012-P1-K1-H1

Method BLASTX NCBI GI g3386617

Match length

% identity

81



```
BLAST score
                  2.0e-22
E value
Match length
                  79
                  70
% identity
                   (AC004665) putative cell division protein (ftsY)
NCBI Description
                   [Arabidopsis thaliana]
                  207055
Seq. No.
Seq. ID
                  LIB3120-012-P1-K1-H12
Method
                  BLASTX
                  q3037047
NCBI GI
BLAST score
                  222
                  1.0e-18
E value
                  55
Match length
                  73
% identity
                   (AF053354) 1-aminocyclopropane-1-carboxylic acid oxidase
NCBI Description
                   [Phaseolus vulgaris]
                  207056
Seq. No.
                  LIB3120-012-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2651310
BLAST score
                   246
                   3.0e-21
E value
                   51
Match length
                   88
% identity
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   207057
Seq. ID
                  LIB3120-012-P1-K1-H6
Method
                  BLASTX
                   g2281090
NCBI GI
BLAST score
                   175
                   4.0e-13
E value
Match length
                   74
% identity
                   51
NCBI Description
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   207058
Seq. ID
                   LIB3120-012-P1-K1-H8
Method
                   BLASTN
NCBI GI
                   g1465367
BLAST score
                   38
E value
                   6.0e-12
Match length
                   153
% identity
                   82
NCBI Description A.thaliana mRNA for RAP-1 protein
                   207059
Seq. No.
Seq. ID
                   LIB3120-013-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   q1170567
BLAST score
                   250
                   5.0e-22
E value
                   54
```

% identity

55



```
MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                  >gi 1085960 pir __S52648 INO1 protein - Citrus paradisi
                  >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g586004
BLAST score
                  494
E value
                  5.0e-50
                  105
Match length
                  87
% identity
                  SUPEROXIDE DISMUTASE [CU-ZN] >gi 421962 pir__S34267
NCBI Description
                  superoxide dismutase (EC 1.15.1.1) (Cu-\overline{Z}n) - sweet potato
                  >gi 542090 pir__S40404 superoxide dismutase (EC 1.15.1.1)
                   (Cu-Zn) - sweet potato >gi 311971 emb CAA51654 (X73139)
                  superoxide dismutase [Ipomoea batatas]
                  207061
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-A3
                  BLASTX
Method
                  g3650033
NCBI GI
                  214
BLAST score
                  2.0e-17
E value
                  84
Match length
                  51
% identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                  207062
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-A5
                  BLASTX
Method
NCBI GI
                   q289920
BLAST score
                   554
                   3.0e-57
E value
Match length
                   108
                   94
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   207063
Seq. No.
Seq. ID
                   LIB3120-013-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   q20729
BLAST score
                   331
                   4.0e-31
E value
                   97
Match length
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   207064
Seq. No.
                   LIB3120-013-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1354515
BLAST score
                   195
E value
                   4.0e-15
Match length
                   88
```



NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No. 207065

Seq. ID LIB3120-013-Q1-K1-A8

Method BLASTX
NCBI GI g1352821
BLAST score 306
E value 3.0e-28
Match length 81
% identity 80

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207066

Seq. ID LIB3120-013-Q1-K1-B2

Method BLASTX
NCBI GI g2879867
BLAST score 275
E value 1.0e-24
Match length 84
% identity 62

NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces

pombe]

Seq. No. 207067

Seq. ID LIB3120-013-Q1-K1-B3

Method BLASTX
NCBI GI g479406
BLAST score 503
E value 3.0e-51
Match length 106
% identity 61

NCBI Description chlorophyll a/b-binding protein - garden pea

>gi 20671 emb CAA49149 (X69215) chlorophyll a/b-binding

protein [Pisum sativum]

Seq. No. 207068

Seq. ID LIB3120-013-Q1-K1-C10

Method BLASTX
NCBI GI g4325341
BLAST score 618
E value 2.0e-64
Match length 141
% identity 77

NCBI Description (AF128393) similar to the Drosophila DES-1 protein

(GB:X94180) [Arabidopsis thaliana]

Seq. No. 207069

Seq. ID LIB3120-013-Q1-K1-C11

MethodBLASTXNCBI GIg131397BLAST score170E value3.0e-12

Seq. ID

Method



```
Match length
 % identity
                   46
 NCBI Description
                   OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
                   SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi_81480_pir__S00008 photosystem II oxygen-evolving
                   complex protein 3 precursor - spinach
                   >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                   photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                   [Spinacia oleracea]
Seq. No.
                   207070
Seq. ID
                   LIB3120-013-Q1-K1-C12
Method
                   BLASTX
NCBI GI
                   g3860247
BLAST score
                   265
E value
                   2.0e-35
Match length
                   88
% identity
                   80
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                   207071
Seq. ID
                   LIB3120-013-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   g2129538
BLAST score
                   314
E value
                   4.0e-29
Match length
                   67
% identity
                   90
                  AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
NCBI Description
                   AT103 [Arabidopsis thaliana]
Seq. No.
                   207072
Seq. ID
                   LIB3120-013-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g4538976
BLAST score
                   269
E value
                   1.0e-33
Match length
                  141
% identity
                  57
NCBI Description
                   (AL049487) sucrose-phosphate synthase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  207073
Seq. ID
                  LIB3120-013-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g4218120
BLAST score
                  422
E value
                  1.0e-41
Match length
                  119
% identity
NCBI Description
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  207074
```

28433

LIB3120-013-Q1-K1-D3

BLASTX



```
g167367
NCBI GI
BLAST score
                  369
E value
                  7.0e-36
Match length
                  75
% identity
                  95
NCBI Description
                  (L08199) peroxidase [Gossypium hirsutum]
                  207075
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2052383
BLAST score
                  325
                  1.0e-30
E value
Match length
                  69
% identity
NCBI Description
                  (U66345) calreticulin [Arabidopsis thaliana]
Seq. No.
                  207076
                  LIB3120-013-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q120669
                  229
BLAST score
                  1.0e-19
E value
                  52
Match length
% identity
                  85
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66014 pir_DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >qi 19566 emb CAA42905 (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  207077
Seq. ID
                  LIB3120-013-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q3687652
BLAST score
                  418
                  6.0e-63
E value
Match length
                  140
% identity
                  87
NCBI Description
                  (AF047352) rubisco activase precursor [Datisca glomerata]
Seq. No.
                  207078
                  LIB3120-013-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2367431
BLAST score
                  168
                  3.0e-12
E value
                  78
Match length
                  44
% identity
NCBI Description
                  (AF000403) putative cytochrome P450 [Lotus japonicus]
Seq. No.
                  207079
Seq. ID
                  LIB3120-013-Q1-K1-E5
Method
                  BLASTX
```

Method BLASTX
NCBI GI g294060
BLAST score 200
E value 2.0e-15



Match length 124 % identity 37

NCBI Description (L06467) major latex protein [Papaver somniferum]

Seq. No. 207080

Seq. ID LIB3120-013-Q1-K1-E6

Method BLASTX
NCBI GI g2335098
BLAST score 165
E value 1.0e-11
Match length 88
% identity 38

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 207081

Seq. ID LIB3120-013-Q1-K1-F10

Method BLASTX
NCBI GI g1942360
BLAST score 550
E value 1.0e-56
Match length 121
% identity 83

NCBI Description Actin-Binding Protein

Seq. No. 207082

Seq. ID LIB3120-013-Q1-K1-F12

Method BLASTX
NCBI GI g2500115
BLAST score 633
E value 3.0e-66
Match length 142
% identity 85

NCBI Description GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)

>gi 529375 dbj BAA07108 (D37870) Glutathione Reductase

precursor [Spinacia oleracea]

Seq. No. 207083

Seq. ID LIB3120-013-Q1-K1-F2

Method BLASTX
NCBI GI g4539422
BLAST score 142
E value 7.0e-12
Match length 85
% identity 59

NCBI Description (ALO49171) putative protein [Arabidopsis thaliana]

Seq. No. 207084

Seq. ID LIB3120-013-Q1-K1-F3

Method BLASTX
NCBI GI g1587206
BLAST score 348
E value 2.0e-33
Match length 136
% identity 70

NCBI Description T complex protein [Cucumis sativus]

Seq. No. 207085

Seq. No.

Seq. ID

Method

207090

BLASTX

LIB3120-013-Q1-K1-G3



```
LIB3120-013-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  295
                  6.0e-27
E value
                  84
Match length
% identity
                  76
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  207086
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1168739
                  349
BLAST score
                  3.0e-33
E value
                  97
Match length
                  68
% identity
                  CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449
NCBI Description
                 (L18901) carbonic anhydrase [Arabidopsis thaliana]
                  207087
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-F8
                  BLASTX
Method
                  g3063392
NCBI GI
BLAST score
                  372
                  9.0e-36
E value
Match length
                  103
% identity
                  75
NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]
                  207088
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q2982301
BLAST score
                  196
E value
                  3.0e-15
Match length
                  79
% identity
                  52
NCBI Description (AF051235) YGL010w-like protein [Picea mariana]
                  207089
Seq. No.
                  LIB3120-013-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3953473
                  133
BLAST score
                  9.0e-12
E value
                  73
Match length
% identity
                  64
NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]
```



NCBI GI g4406780
BLAST score 290
E value 3.0e-42
Match length 131
% identity 67

NCBI Description (AC006532) putative multispanning membrane protein

[Arabidopsis thaliana]

Seq. No. 207091

Seq. ID LIB3120-013-Q1-K1-G5

Method BLASTX
NCBI GI g3914605
BLAST score 389
E value 4.0e-38
Match length 82
% identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir\_\_S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi\_415852\_emb\_CAA79857\_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 207092

Seq. ID LIB3120-013-Q1-K1-G6

Method BLASTX
NCBI GI g3643604
BLAST score 198
E value 2.0e-15
Match length 102
% identity 5

NCBI Description (AC005395) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 207093

Seq. ID LIB3120-013-Q1-K1-G9

Method BLASTX
NCBI GI g1354515
BLAST score 200
E value 1.0e-15
Match length 112
% identity 43

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 207094

Seq. ID LIB3120-013-Q1-K1-H1

Method BLASTN
NCBI GI g289919
BLAST score 35
E value 1.0e-10
Match length 135
% identity 82

NCBI Description Gossypium hirsutum chloroplast photosystem II chlorophyll

A/B-binding protein gene, complete cds

Seq. No. 207095



```
LIB3120-013-Q1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1480014
                  228
BLAST score
                  3.0e-19
E value
                  58
Match length
% identity
                  (D78493) putative delta subunit of ATP synthase [Brassica
NCBI Description
                  rapa]
                  207096
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  g3063392
                  427
BLAST score
E value
                  4.0e-42
                  127
Match length
                  69
% identity
NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]
Seq. No.
                  207097
                  LIB3120-013-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  g1345698
NCBI GI
                  338
BLAST score
                  5.0e-32
E value
                  81
Match length
                  79
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
NCBI Description
                   (CAB-151) (LHCP) >gi_99601_pir__$20917 chlorophyll
                   a/b-binding protein - upland cotton
                  >qi 452314 emb CAA38025 (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
                   207098
Seq. No.
Seq. ID
                  LIB3120-013-Q1-K1-H7
                  BLASTX
Method
                   g505482
NCBI GI
BLAST score
                   318
                   2.0e-29
E value
                   117
Match length
                   59
% identity
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                  photosystem II [Nicotiana tabacum]
                   207099
Seq. No.
Seq. ID
                   LIB3120-013-Q1-K1-H9
Method
                   BLASTX
                   q100454
NCBI GI
                   545
BLAST score
                   6.0e-56
E value
Match length
                   136
```

% identity

photosystem II oxygen-evolving complex protein 1 - potato NCBI Description >gi 809113 emb CAA35601 (X17578) 33kDa precursor protein

of oxygen-evolving complex [Solanum tuberosum]

% identity

NCBI Description



```
207100
Seq. No.
Seq. ID .
                  LIB3120-014-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q4510345
BLAST score
                  194
E value
                  2.0e-15
                  36
Match length
                  89
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
                  207101
Seq. No.
                  LIB3120-014-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q281807
                  243
BLAST score
                  3.0e-21
E value
                  63
Match length
                  71
% identity
                  adenylosuccinate lyase - Escherichia coli
NCBI Description
                  207102
Seq. No.
                  LIB3120-014-01-K1-B6
Seq. ID
Method
                  BLASTX
                  q505482
NCBI GI
BLAST score
                  259
                  8.0e-23
E value
                  78
Match length
                  74
% identity
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                  photosystem II [Nicotiana tabacum]
                  207103
Seq. No.
                  LIB3120-014-Q1-K1-B7
Seq. ID
Method
                   BLASTX
                  g2507455
NCBI GI
BLAST score
                   488
                   2.0e-49
E value
                   116
Match length
% identity
                   FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                   SYNTHETASE) (FHS) (FTHFS) >gi 322401 pir A43350
                   formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
                   >qi 170145 (M83940) 10-formyltetrahydrofolate synthetase
                   [Spinacia oleracea]
Seq. No.
                   207104
Seq. ID
                   LIB3120-014-Q1-K1-B8
                   BLASTX
Method
NCBI GI
                   g2507455
BLAST score
                   267
E value
                   1.0e-23
Match length
                   89
```

28439

FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi\_170145 (M83940) 10-formyltetrahydrofolate synthetase

SYNTHETASE) (FHS) (FTHFS) >gi 322401 pir A43350



### [Spinacia oleracea]

```
207105
Seq. No.
Seq. ID
                  LIB3120-014-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  g2687435
BLAST score
                  97
                  1.0e-47
E value
Match length
                  141
                  92
% identity
                  Hamamelis virginiana large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  207106
Seq. ID
                  LIB3120-014-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q464849
BLAST score
                  276
                  5.0e-25
E value
Match length
                  57
                  95
% identity
                  TUBULIN ALPHA CHAIN >qi 486847 pir S36232 tubulin alpha
NCBI Description
                  chain - almond >qi 20413 emb CAA47635 (X67162)
                  alpha-tubulin [Prunus dulcis]
                  207107
Seq. No.
                  LIB3120-014-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  175
E value
                  3.0e-13
                  44
Match length
                  75
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >qi 166646 (M63931) liqht-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  207108
Seq. ID
                  LIB3120-014-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2754849
BLAST score
                  319
                  2.0e-29
E value
Match length
                  96
% identity
NCBI Description
                   (AF039000) putative serine-glyoxylate aminotransferase
                   [Fritillaria agrestis]
Seq. No.
                  207109
Seq. ID
                  LIB3120-014-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g131397
BLAST score
                  270
                  7.0e-24
E value
                  90
Match length
% identity
                  64
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
```

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)

>gi\_81480\_pir\_\_S00008 photosystem II oxygen-evolving
complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the
photosynthetic oxygen- evolving protein (OEC) [Spinacia
oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD
[Spinacia oleracea]

 Seq. No.
 207110

 Seq. ID
 LIB3120-014-Q1-K1-F6

 Method
 BLASTX

 NCBI GI
 g289920

 BLAST score
 345

BLAST score 345
E value 8.0e-33
Match length 72
% identity 92

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207111

Seq. ID LIB3120-014-Q1-K1-G4

Method BLASTX
NCBI GI g2129538
BLAST score 269
E value 9.0e-24
Match length 64
% identity 80

NCBI Description AT103 protein - Arabidopsis thaliana >gi\_1033195 (U38232)

AT103 [Arabidopsis thaliana]

Seq. No. 207112

Seq. ID LIB3120-014-Q1-K1-G6

Method BLASTN
NCBI GI g1049306
BLAST score 38
E value 5.0e-12
Match length 49
% identity 96

NCBI Description Arabidopsis thaliana actin-2 mRNA, complete cds

Seq. No. 207113

Seq. ID LIB3120-014-Q1-K1-H1

Method BLASTX
NCBI GI g1352821
BLAST score 355
E value 7.0e-34
Match length 76
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207114

Seq. ID LIB3120-014-Q1-K1-H7

Method BLASTN



```
g929812
NCBI GI
BLAST score
                  40
E value
                  2.0e-13
                  120
Match length
% identity
NCBI Description
                  P.nigra mRNA for plastocyanin a
                  207115
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  q120657
                  499
BLAST score
E value
                  1.0e-50
Match length
                  124
                  80
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi 66024 pir DEZMG3
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  maize >gi 168479 (M18976) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays] >gi 763035 emb_CAA33455 (X15408)
                  qlyceraldehyde-3-phosphate dehydrogenase [Zea mays]
                  207116
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-A12
Method
                  BLASTX
                  g1352821
NCBI GI
BLAST score
                  412
                  2.0e-40
E value
                  125
Match length
                  83
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  207117
Seq. No.
                  LIB3120-015-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q515616
BLAST score
                  300
E value
                  1.0e-45
                  114
Match length
% identity
                  (X61608) LHC II Type III chlorophyll a /b binding protein
NCBI Description
                  [Brassica napus]
Seq. No.
                  207118
Seq. ID
                  LIB3120-015-Q1-K1-A3
                  BLASTX
Method
```

NCBI GI q1354515 BLAST score 159 5.0e-11 E value Match length 81 53 % identity

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus



### tremuloides]

Seq. No. 207119 LIB3120-015-Q1-K1-A6 Seq. ID BLASTX Method NCBI GI q2765081 BLAST score 516

1.0e-52 E value 125 Match length 80 % identity

NCBI Description (Y10557) g5bf [Arabidopsis thaliana]

207120 Seq. No.

Seq. ID LIB3120-015-Q1-K1-A7

Method BLASTX g2739046 NCBI GI BLAST score 217 2.0e-17 E value Match length 62 68 % identity

(AF024652) polyphosphoinositide binding protein Ssh2p NCBI Description

[Glycine max]

207121 Seq. No.

Seq. ID LIB3120-015-Q1-K1-B1

BLASTX Method g1352821 NCBI GI 511 BLAST score 4.0e-58 E value 124 Match length

93 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

207122 Seq. No.

Seq. ID LIB3120-015-Q1-K1-B2

BLASTX Method NCBI GI q131187 166 BLAST score E value 1.0e-11 101 Match length % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description

> (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >qi 72681 pir F1SP3 photosystem I chain III precursor spinach >gi 21303 emb CAA31523 (X13133) PSI subunit IV

preprotein (AA -77 to 154) [Spinacia oleracea]

>qi 226166 prf 1413236A photosystem I reaction center IV

[Spinacia oleracea]

Seq. No. 207123

LIB3120-015-Q1-K1-B4 Seq. ID

Method BLASTX NCBI GI q3395440



```
BLAST score
                  5.0e-16
E value
Match length
                  106
% identity
                  35
NCBI Description
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  207124
                  LIB3120-015-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510345
BLAST score
                  153
E value
                  3.0e-10
Match length
                  43
                   60
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
                  207125
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3335365
BLAST score
                  238
E value
                  2.0e-20
                  69
Match length
                  75
% identity
                   (AC003028) high affinity calcium antiporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  207126
Seq. ID
                  LIB3120-015-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1352200
BLAST score
                   461
                   2.0e-46
E value
Match length
                  102
% identity
                   88
NCBI Description
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
                  >gi 480909 pir S37497 triose
                  phosphate/3-phosphoglycerate/phosphate translocator - maize
                  >gi 405635 emb CAA81349 (Z26595) triose
                  phosphate/phosphate translocator [Zea mays]
Seq. No.
                  207127
Seq. ID
                  LIB3120-015-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q4106696
BLAST score
                   257
E value
                   2.0e-22
Match length
                   66
% identity
                   76
                  (AB021872) ribosome-sedimenting protein [Pisum sativum]
NCBI Description
Seq. No.
                   207128
                  LIB3120-015-Q1-K1-C10
Seq. ID
```

Method BLASTX NCBI GI g3288821 BLAST score 429 1.0e-42 E value



```
Match length
                  89
% identity
NCBI Description
                  (AF063901) alanine:glyoxylate aminotransferase;
                  transaminase [Arabidopsis thaliana]
Seq. No.
                  207129
                  LIB3120-015-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g2738949
NCBI GI
                  473
BLAST score
                  1.0e-47
E value
                  98
Match length
                  90
% identity
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                  ananassa]
                  207130
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1199772
                  271
BLAST score
E value
                  7.0e-24
Match length
                  121
                  53
% identity
                  (D83226) extensin like protein [Populus nigra]
NCBI Description
                  >gi 1199774 dbj BAA11855 (D83227) extensin like protein
                   [Populus nigra]
Seq. No.
                  207131
                  LIB3120-015-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g217909
BLAST score
                  363
                  1.0e-34
E value
Match length
                  75
% identity
                  95
NCBI Description
                  (D14044) glycolate oxidase [Cucurbita sp.]
Seq. No.
                  207132
Seq. ID
                  LIB3120-015-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q1928981
BLAST score
                  519
E value
                  5.0e-53
Match length
                  111
% identity
                  92
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
                  207133
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-C6
Method
                  BLASTX
NCBI GI
```

Method BLASTX
NCBI GI g289920
BLAST score 527
E value 4.0e-54
Match length 103
% identity 97

BLAST score

E value Match length 207 1.0e-16

55



```
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  207134
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1084321
                  226
BLAST score
E value
                  6.0e-19
Match length
                  91
                  57
% identity
                  protochlorophyllide reductase (EC 1.3.1.33) - cucumber
NCBI Description
                  >gi 2244614 dbj BAA21089 (D50085)
                  NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]
                  207135
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4559372
BLAST score
                  217
E value
                  1.0e-17
                  58
Match length
                  76
% identity
                  (AC006585) putative CONSTANS protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  207136
Seq. ID
                  LIB3120-015-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2651308
BLAST score
                   248
E value
                   3.0e-21
Match length
                  99
                   61
% identity
                   (AC002336) putative myosin heavy chain [Arabidopsis
NCBI Description
                  thaliana]
                   207137
Seq. No.
                  LIB3120-015-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                   q119350
NCBI GI
BLAST score
                   461
                   3.0e-46
E value
Match length
                   102
                   89
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608 pir JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi 16271 emb CAA41114 (X58107) enolase
                   [Arabidopsis thaliana]
Seq. No.
                   207138
Seq. ID
                  LIB3120-015-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                   g1352821
```



```
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  207139
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3061271
                  296
BLAST score
E value
                  6.0e-27
                  101
Match length
                  56
% identity
                 (AB012863) NPCA1 [Nicotiana paniculata]
NCBI Description
                  207140
Seq. No.
                  LIB3120-015-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494415
BLAST score
                  182
                  1.0e-13
E value
                  76
Match length
                  58
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine
                  max]
                  207141
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-D3
                  BLASTX
Method
NCBI GI
                  g1439609
BLAST score
                  327
                  9.0e-33
E value
Match length
                  103
                  75
% identity
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                  hirsutum]
                  207142
Seq. No.
Seq. ID
                  LIB3120-015-Q1-K1-D5
Method
                  BLASTX
                  g3023752
NCBI GI
BLAST score
                  288
E value
                  6.0e-26
                  111
Match length
% identity
                  FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
```

Seq. No. 207143

Seq. ID LIB3120-015-Q1-K1-D6

Method BLASTX NCBI GI g3023752 BLAST score 387



2.0e-37 E value 113 Match length 68 % identity FERREDOXIN I PRECURSOR >gi 1418982 emb\_CAA99756 (Z75520) NCBI Description ferredoxin-I [Lycopersicon esculentum] 207144 Seq. No. LIB3120-015-Q1-K1-D7 Seq. ID BLASTX Method g115834 NCBI GI 329 BLAST score 5.0e-31 E value 88 Match length 70 % identity CHLOROPHYLL A-B BINDING PROTEIN CP24 10B PRECURSOR NCBI Description (CAB-10B) (LHCP) >gi 100202 pir\_\_S11878 chlorophyll a/b-binding protein Cab10B - tomato >gi\_170400 (M32606) chlorophyll b-binding protein [Lycopersicon esculentum] 207145 Seq. No. LIB3120-015-Q1-K1-D8 Seq. ID Method BLASTX NCBI GI g1053047 BLAST score 443 2.0e-44 E value Match length 90 99 % identity (U38425) histone H3 [Glycine max] >gi\_1053049 (U38426) NCBI Description histone H3 [Glycine max] >gi\_1053051 (U38427) histone H3 [Glycine max] 207146 Seq. No. LIB3120-015-Q1-K1-D9 Seq. ID BLASTX Method g289920 NCBI GI 551 BLAST score 8.0e-57 E value 108 Match length % identity 94 (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] Seq. No. 207147 Seq. ID LIB3120-015-Q1-K1-E10 BLASTX Method NCBI GI g3953473 286 BLAST score 1.0e-25 E value 119 Match length 56 % identity NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana] Seq. No. 207148 Seq. ID LIB3120-015-Q1-K1-E8

Method BLASTX

Method BLASTX NCBI GI g289920 BLAST score 558



E value 1.0e-57
Match length 101
% identity 100

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No.

207149

Seq. ID

LIB3120-015-Q1-K1-F1

Method BLASTX
NCBI GI g1352821
BLAST score 293
E value 8.0e-27
Match length 64
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207150

Seq. ID LIB3120-015-Q1-K1-F10

Method BLASTX
NCBI GI g231610
BLAST score 219
E value 6.0e-18
Match length 78
% identity 60

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi\_67880\_pir\_\_PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi\_19785\_emb\_CAA45152\_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 207151

Seq. ID LIB3120-015-Q1-K1-F11

Method BLASTX
NCBI GI, g4544457
BLAST score 299
E value 5.0e-34
Match length 116
% identity 59

NCBI Description (AC006592) putative MADS box protein [Arabidopsis thaliana]

Seq. No. 207152

Seq. ID LIB3120-015-Q1-K1-F5

Method BLASTX
NCBI GI g4138282
BLAST score 182
E value 2.0e-13
Match length 106
% identity 43

NCBI Description (AJ011576) RNA-directed RNA polymerase [Nicotiana tabacum]

Seq. No. 207153

Seq. ID LIB3120-015-Q1-K1-F7

Method BLASTX



NCBI GI g2118220 BLAST score 398 E value 4.0e-39 Match length 82 % identity 57

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi\_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>gi 3096941 emb CAA18851.1 (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi\_4539311\_emb\_CAB38812.1\_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]

Seq. No. 207154

Seq. ID LIB3120-015-Q1-K1-F8

Method BLASTX
NCBI GI g2351380
BLAST score 176
E value 9.0e-13
Match length 118
% identity 32

NCBI Description (U54559) translation initiation factor eIF3 p40 subunit

[Homo sapiens] >gi\_4503515\_ref\_NP\_003747.1\_pEIF3S3\_ UNKNOWN

Seq. No. 207155

Seq. ID LIB3120-015-Q1-K1-F9

Method BLASTN
NCBI GI g21051
BLAST score 32
E value 1.0e-08
Match length 52
% identity 90

NCBI Description P.vulgaris rbcS mRNA for small subunit of ribulose

bisphosphate carboxylase/oxygenase (clone pPvSS965)

Seq. No. 207156

Seq. ID LIB3120-015-Q1-K1-G10

Method BLASTX
NCBI GI g2494076
BLAST score 623
E value 3.0e-65
Match length 128
% identity 94

NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi\_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase

[Nicotiana plumbaginifolia]

Seq. No. 207157

Seq. ID LIB3120-015-Q1-K1-G11

Method BLASTX NCBI GI g1172974 BLAST score 345



E value 8.0e-33
Match length 70
% identity 91
NCRI Description CHIOPOR

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 >gi\_454860 (M80799)

ribosomal protein L16 [Vigna unguiculata]

Seq. No. 207158

Seq. ID LIB3120-015-Q1-K1-G12

Method BLASTN
NCBI GI g3108292
BLAST score 258
E value 1.0e-143
Match length 305
% identity 98

NCBI Description Gossypium barbadense clone pXP158 repetitive DNA sequence

Seq. No. 207159

Seq. ID LIB3120-015-Q1-K1-G2

Method BLASTX
NCBI GI g289920
BLAST score 439
E value 8.0e-44
Match length 87
% identity 94

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207160

Seq. ID LIB3120-015-Q1-K1-G6

Method BLASTX
NCBI GI g4539301
BLAST score 194
E value 2.0e-15
Match length 50
% identity 74

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 207161

Seq. ID LIB3120-015-Q1-K1-G9

Method BLASTX
NCBI GI g543939
BLAST score 458
E value 5.0e-46
Match length 104
% identity 78

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR

>gi\_541819\_pir\_\_S40210 chlorophyll a/b-binding protein CP24
precursor - spinach >gi\_437991\_emb\_CAA81105\_ (Z25886) 20
kDa protein of CP24 precursor protein [Spinacia oleracea]

Seq. No. 207162

Seq. ID LIB3120-015-Q1-K1-H10

Method BLASTX
NCBI GI g1354515
BLAST score 275
E value 2.0e-24



Match length 108 % identity 56

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 207163

Seq. ID LIB3120-015-Q1-K1-H11

Method BLASTX
NCBI GI g1346698
BLAST score 248
E value 3.0e-27
Match length 81
% identity 86

NCBI Description PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR

>gi\_21272\_emb\_CAA48479\_ (X68430) phosphoglycerate kinase

[Spinacia oleracea]

Seq. No. 207164

Seq. ID LIB3120-015-Q1-K1-H12

Method BLASTX
NCBI GI g289920
BLAST score 520
E value 5.0e-53
Match length 107
% identity 92

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207165

Seq. ID LIB3120-015-Q1-K1-H2

Method BLASTX
NCBI GI g3738261
BLAST score 486
E value 3.0e-49
Match length 100
% identity 94

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 207166

Seq. ID LIB3120-015-Q1-K1-H4

Method BLASTX
NCBI GI g2317715
BLAST score 228
E value 2.0e-19
Match length 69
% identity 65

NCBI Description (AF012942) HelD [Dictyostelium discoideum]

Seq. No. 207167

Seq. ID LIB3120-015-Q1-K1-H5

Method BLASTX
NCBI GI g3250675
BLAST score 417
E value 5.0e-41
Match length 124
% identity 65



NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 207168

Seq. ID LIB3120-015-Q1-K1-H6

Method BLASTX
NCBI GI g3335359
BLAST score 152
E value 2.0e-10
Match length 58
% identity 55

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 207169

Seq. ID LIB3120-015-Q1-K1-H8

Method BLASTX
NCBI GI g115470
BLAST score 161
E value 1.0e-11
Match length 44
% identity 70

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

DEHYDRATASE) >gi 320554 pir S28412 carbonate dehydratase

(EC 4.2.1.1) precursor - Arabidopsis thaliana

>gi 14343 emb CAA46508 (X65541) carbonic anhydrase

[Arabidopsis thaliana]

Seq. No. 207170

Seq. ID LIB3120-015-Q1-K1-H9

Method BLASTX
NCBI GI g131397
BLAST score 297
E value 5.0e-27
Match length 106
% identity 60

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_81480\_pir\_\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 207171

Seq. ID LIB3120-016-Q1-K1-A12

Method BLASTX
NCBI GI g2129559
BLAST score 417
E value 5.0e-41
Match length 137
% identity 59

NCBI Description cellulase homolog OR16pep - Arabidopsis thaliana

>gi\_1022807 (U37702) cellulase [Arabidopsis thaliana]
>gi\_3493633 (AF074092) cellulase [Arabidopsis thaliana]
>gi\_3598956 (AF074375) cellulase [Arabidopsis thaliana]
>gi\_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN

[Arabidopsis thaliana]



```
207172
Seq. No.
Seq. ID
                  LIB3120-016-Q1-K1-A3
                  BLASTX
Method
NCBI GI
                  q1351408
BLAST score
                  352
                  2.0e-33
E value
                  93
Match length
                  75
% identity
                  VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                  >gi 1076563 pir S51117 cystein proteinase - sweet orange
                  >gi 633185 emb CAA87720 (Z47793) cystein proteinase (by
                  similarity) [Citrus sinensis] >gi 1588548 prf 2208463A
                  vascular processing protease [Citrus sinensis]
                  207173
Seq. No.
                  LIB3120-016-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2494076
BLAST score
                  279
E value
                  7.0e-25
                  56
Match length
                  93
% identity
                  NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
NCBI Description
                   (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE
                   DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
                   (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi 1842115
                   (U87848) non-phosphorylating glyceraldehyde dehydrogenase
                   [Nicotiana plumbaginifolia]
Seq. No.
                   207174
                  LIB3120-016-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   q289920
NCBI GI
                   462
BLAST score
E value
                   2.0e-46
                   87
Match length
                   99
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   207175
Seq. No.
Seq. ID
                   LIB3120-016-Q1-K1-A9
                   BLASTX
Method
NCBI GI
                   g2130149
BLAST score
                   459
E value
                   3.0e-46
Match length
                   87
                   100
% identity
```

translation elongation factor eEF-1 alpha chain - maize NCBI Description

(fragment)

207176 Seq. No.

Seq. ID LIB3120-016-Q1-K1-B12

BLASTX Method NCBI GI g1346172 BLAST score 222



```
3.0e-18
E value
Match length
                  69
                  68
% identity
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)
NCBI Description
                   (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)
                  >gi 170384 (L08830) glucose-regulated protein 78
                   [Lycopersicon esculentum]
                  207177
Seq. No.
                  LIB3120-016-Q1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1709825
BLAST score
                  180
                   1.0e-28
E value
Match length
                   142
                   51
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                   207178
                   LIB3120-016-Q1-K1-B9
Seq. ID
                   BLASTX
Method
                   g4455226
NCBI GI
                   177
BLAST score
E value
                   7.0e-13
                   115
Match length
                   39
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   207179
                   LIB3120-016-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   q3335365
NCBI GI
BLAST score
                   235
                   6.0e-20
E value
Match length
                   70
                   74
% identity
                   (AC003028) high affinity calcium antiporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   207180
Seq. ID
                   LIB3120-016-Q1-K1-C10
Method
                   BLASTX
                   g228403
NCBI GI
                   320
BLAST score
E value
                   1.0e-29
                   82
Match length
                   76
% identity
NCBI Description glycolate oxidase [Lens culinaris]
Seq. No.
                   207181
                   LIB3120-016-Q1-K1-C12
Seq. ID
Method
                   BLASTX
                   q625547
NCBI GI
```

28455

230

68

1.0e-19

BLAST score

Match length

E value



% identity NCBI Description chlorophyll a/b-binding protein type I - common tobacco >qi 493723 emb CAA45523 (X64198) photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum] 207182 Seq. No.

LIB3120-016-Q1-K1-C7 Seq. ID Method BLASTX q100196 NCBI GI 341 BLAST score E value 2.0e-32 78 Match length 82 % identity

chlorophyll a/b-binding protein (cab-11) - tomato NCBI Description

Seq. No. 207183

Seq. ID LIB3120-016-Q1-K1-C9

Method BLASTX NCBI GI q1352821 BLAST score 402 E value 2.0e-39 81 Match length 98 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207184

LIB3120-016-Q1-K1-D10 Seq. ID

Method BLASTX NCBI GI a20729 BLAST score 209 E value 7.0e-17 77 Match length 61 % identity

(X15190) precursor (AA -68 to 337) [Pisum sativum] NCBI Description

Seq. No. 207185

Seq. ID LIB3120-016-Q1-K1-D3

Method BLASTX NCBI GI q1352821 BLAST score 251 5.0e-22 E value Match length 62 77 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

207186 Seq. No.

LIB3120-016-Q1-K1-D7 Seq. ID

BLASTX Method



```
NCBI GI
                   a2791423
BLAST score
                   173
                   2.0e-12
E value
                   52
Match length
% identity
                   60
NCBI Description
                  (AL021185) bcp [Mycobacterium tuberculosis]
                  207187
Seq. No.
Seq. ID
                  LIB3120-016-Q1-K1-E9
```

Method BLASTX
NCBI GI g1352821
BLAST score 147
E value 2.0e-09
Match length 76
% identity 43

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

 Seq. No.
 207188

 Seq. ID
 LIB3120-016-Q1-K1-F10

 Method
 BLASTX

 NCBI GI
 g100616

 BLAST score
 214

 E value
 1.0e-17

E value 1.0 Match length 69 % identity 62

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi\_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi\_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 207189

Seq. ID LIB3120-016-Q1-K1-F12

Method BLASTX
NCBI GI g4455251
BLAST score 258
E value 8.0e-23
Match length 59
% identity 78

NCBI Description (AL035523) magnesium-protoporphyrin IX

methyltransferase-like protein [Arabidopsis thaliana]

Seq. No. 207190

Seq. ID LIB3120-016-Q1-K1-F9

Method BLASTX
NCBI GI g3915089
BLAST score 518
E value 8.0e-53
Match length 105
% identity 91

NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)

>gi\_2144269 pir\_\_ JC5129 trans-cinnamate 4-monooxygenase (EC



1.14.13.11) A - Populus kitakamiensis >gi 1139561 dbj BAA11579 (D82815) cinnamic acid 4-hydroxylase [Populus kitakamiensis] >gi 1777370 dbj BAA11576 (D82812) cinnamic acid 4-hydroxylase [Populus kitakamiensis] 207191 LIB3120-016-Q1-K1-G11 BLASTX q282833 217 2.0e-17 57 81 phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment) NCBI Description 207192 LIB3120-016-Q1-K1-H11 BLASTX g2244888 176 4.0e-13 87 44 (Z97338) similarity to cytochrome P450 [Arabidopsis thaliana] 207193 LIB3120-016-Q1-K1-H12 BLASTX

Seq. No.

Seq. No. Seq. ID

Method

NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI

BLAST score E value

Match length

% identity NCBI Description

BLAST score

Match length % identity

Seq. ID

Method NCBI GI g2351380 143 BLAST score 3.0e-09 E value 86 Match length % identity

NCBI Description (U54559) translation initiation factor eIF3 p40 subunit

[Homo sapiens] >gi\_4503515\_ref\_NP\_003747.1\_pEIF3S3\_ UNKNOWN

Seq. No. 207194

Seq. ID LIB3120-017-Q1-K1-A1 Method BLASTX NCBI GI q3747111

BLAST score 375 E value 5.0e-36 Match length 119 60 % identity

NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No. 207195

Seq. ID LIB3120-017-Q1-K1-A10

Method BLASTX NCBI GI g3915699 BLAST score 434 E value 3.0e-4395 Match length 85 % identity

NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T



PROTEIN) >gi\_541970\_pir\_\_S40260 T-protein - garden pea >gi\_1362061\_pir\_\_S56661 glycine decarboxylase T protein precursor - garden pea >gi\_438217\_emb\_CAA81080\_(Z25861) T-protein [Pisum sativum] >gi\_3021553\_emb\_CAA10976\_(AJ222771) T protein [Pisum sativum]

Seq. No. 207196

Seq. ID LIB3120-017-Q1-K1-A11

Method BLASTX
NCBI GI g3914605
BLAST score 293
E value 5.0e-29
Match length 96
% identity 66

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi\_541930\_pir\_\_S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi\_415852\_emb\_CAA79857\_ (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 207197

Seq. ID LIB3120-017-Q1-K1-A2

Method BLASTX
NCBI GI g3023752
BLAST score 257
E value 9.0e-26
Match length 100
% identity 64

NCBI Description FERREDOXIN I PRECURSOR >gi\_1418982\_emb\_CAA99756\_ (Z75520)

ferredoxin-I [Lycopersicon esculentum]

Seq. No. 207198

Seq. ID LIB3120-017-Q1-K1-A5

Method BLASTX
NCBI GI g68200
BLAST score 292
E value 2.0e-26
Match length 109
% identity 61

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,

chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814)
fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 207199

Seq. ID LIB3120-017-Q1-K1-A6

Method BLASTX
NCBI GI g1256259
BLAST score 418
E value 4.0e-51
Match length 124
% identity 76

NCBI Description (U50900) voltage-dependent anion channel protein [Spinacia

oleracea]

Seq. No. 207200

Seq. ID LIB3120-017-Q1-K1-B1



```
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  570
                  5.0e-59
E value
Match length
                  109
%_identity
                  97
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  207201
Seq. No.
                  LIB3120-017-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g2119012
NCBI GI
BLAST score
                  145
                  1.0e-09
E value
                  40
Match length
% identity
                  72
NCBI Description
                  histone 3.3A - chicken >gi 211851 (M11667) histone 3.3A
                   [Gallus gallus]
                  207202
Seq. No.
                  LIB3120-017-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3850576
BLAST score
                  532
E value
                  2.0e-54
                  130
Match length
                  82
% identity
                   (AC005278) Strong similarity to gb U04968 nucleotide
NCBI Description
                  excision repair protein (ERCC2) from Cricetulus grisseus.
                   [Arabidopsis thaliana]
                  207203
Seq. No.
                  LIB3120-017-Q1-K1-B12
Seq. ID
Method
                  BLASTX
                  q1256259
NCBI GI
BLAST score
                   238
                   3.0e-20
E value
                  103
Match length
                   49
% identity
NCBI Description
                   (U50900) voltage-dependent anion channel protein [Spinacia
                  oleracea]
                  207204
Seq. No.
Seq. ID
                  LIB3120-017-Q1-K1-B2
                  BLASTX
Method
NCBI GI
                  q4510387
BLAST score
                   336
E value
                   1.0e-31
Match length
                   80
% identity
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
```

Seq. No. 207205

Seq. ID LIB3120-017-Q1-K1-B4

Method BLASTX NCBI GI g3063694



```
BLAST score
                  9.0e-12
E value
                  106
Match length
                   43
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                  207206
Seq. No.
                  LIB3120-017-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                   296
E value
                  8.0e-27
Match length
                  72
                   81
% identity
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                   - spinach >gi 1066153 dbj BAA07177 (D37963) cysteine
                   synthase [Spinacia oleracea]
                   207207
Seq. No.
                   LIB3120-017-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3202024
BLAST score
                   474
E value
                   8.0e-53
                   128
Match length
                   74
% identity
                   (AF069315) thylakoid-bound L-ascorbate peroxidase precursor
NCBI Description
                   [Mesembryanthemum crystallinum]
                   207208
Seq. No.
                   LIB3120-017-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2499497
BLAST score
                   614
E value
                   4.0e-64
Match length
                   142
                   87
% identity
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >qi 1161600 emb CAA88841 (Z48977) phosphoglycerate kinase
                   [Nicotiana tabacum]
                   207209
Seq. No.
Seq. ID
                   LIB3120-017-Q1-K1-B8
Method
                   BLASTX
                   g1354515
NCBI GI
BLAST score
                   498
                   1.0e-50
E value
                   121
Match length
                   77
% identity
                   (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
```

Seq. No. 207210

Seq. ID LIB3120-017-Q1-K1-B9

Method BLASTX NCBI GI g3641868 BLAST score 278

BLAST score

E value Match length 330 8.0e-31

67



```
1.0e-24
E value
Match length
                  71
% identity
                  75
                  (AJ011012) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                  207211
                  LIB3120-017-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1019946
BLAST score
                  585
E value
                  1.0e-60
Match length
                  125
% identity
                  (U37060) ascorbate peroxidase [Gossypium hirsutum]
NCBI Description
                  207212
Seq. No.
                  LIB3120-017-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2239Q85
                  166
BLAST score
                  1.0e-11
E value
                  70
Match length
                  46
% identity
                   (Z84384) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus]
                  207213
Seq. No.
Seq. ID
                  LIB3120-017-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                   g121349
BLAST score
                   382
                   3.0e-44
E value
Match length
                   98
% identity
                   86
                  GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461
                   (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza
                   sativa]
                   207214
Seq. No.
                   LIB3120-017-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g2244847
NCBI GI
                   262
BLAST score
                   5.0e-23
E value
Match length
                   81
                   60
% identity
                   (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   207215
Seq. No.
Seq. ID
                   LIB3120-017-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1352821
```



% identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi\_279581\_pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 207216 Seq. No. LIB3120-017-Q1-K1-C7 Seq. ID Method BLASTX NCBI GI q100200 BLAST score 408 7.0e-40 E value 114 Match length 69 % identity NCBI Description chlorophyll a/b-binding protein type I precursor - tomato Seq. No. 207217 LIB3120-017-Q1-K1-C8 Seq. ID Method BLASTX NCBI GI q289920 521 BLAST score E value 2.0e-53 Match length 100 98 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] Seq. No. 207218 LIB3120-017-Q1-K1-D1 Seq. ID Method BLASTN NCBI GI g3241939 BLAST score 44 1.0e-15 E value Match length 149 70 % identity Arabidopsis thaliana chromosome II BAC T26J13 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 207219 Seq. No. LIB3120-017-Q1-K1-D12 Seq. ID  ${\tt BLASTX}$ Method g1345978 NCBI GI 528 BLAST score 4.0e-54 E value 108 Match length % identity OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR NCBI Description >gi\_457631 (L29214) omega-6 desaturase [Brassica napus] 207220 Seq. No.

Seq. ID LIB3120-017-Q1-K1-D5

BLASTX Method g3953473 NCBI GI BLAST score 364 1.0e-34 E value Match length 131

E value

Match length

% identity

3.0e-42

85

98



% identity (AC002328) F2202.18 [Arabidopsis thaliana] NCBI Description 207221 Seq. No. LIB3120-017-Q1-K1-D6 Seq. ID Method BLASTX NCBI GI g1781348 455 BLAST score 1.0e-45 E value 95 Match length % identity 92 (Y10380) homologous to plastidic aldolases [Solanum NCBI Description tuberosum] 207222 Seq. No. Seq. ID LIB3120-017-Q1-K1-D9 Method BLASTX NCBI GI g303730 BLAST score 416 6.0e-41 E value 92 Match length % identity 89 (D12540) GTP-binding protein [Pisum sativum] NCBI Description >gi 738933 prf 2001457A GTP-binding protein [Pisum sativum] 207223 Seq. No. Seq. ID LIB3120-017-Q1-K1-E1 Method BLASTX NCBI GI g421826 BLAST score 234 E value 9.0e-20 81 Match length 57 % identity chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description >gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis thaliana] 207224 Seq. No. Seq. ID LIB3120-017-Q1-K1-E12 BLASTX Method NCBI GI g289920 BLAST score 370 E value 1.0e-35 Match length 84 % identity 83 (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 207225 Seq. No. LIB3120-017-Q1-K1-E2 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 427



NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207226

Seq. ID LIB3120-017-Q1-K1-E3

Method BLASTX
NCBI GI g122781
BLAST score 405
E value 9.0e-40
Match length 104
% identity 70

NCBI Description POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229)

>gi\_82210\_pir\_\_A05198 hypothetical protein 229 - common tobacco chloroplast >gi\_11844\_emb\_CAA77364\_ (Z00044)

hypothetical protein [Nicotiana tabacum]

>gi 225212 prf 1211235AT ORF 229 [Nicotiana tabacum]

Seq. No. 207227

Seq. ID LIB3120-017-Q1-K1-E5

Method BLASTX
NCBI GI g1352821
BLAST score 653
E value 1.0e-68
Match length 129
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207228

Seq. ID LIB3120-017-Q1-K1-E6

Method BLASTX
NCBI GI g2961389
BLAST score 414
E value 8.0e-41
Match length 108
% identity 69

NCBI Description (AL022141) purple acid phosphatase like protein

[Arabidopsis thaliana] >gi\_4006925\_emb\_CAB16853\_ (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]

Seq. No. 207229

Seq. ID LIB3120-017-Q1-K1-E7

Method BLASTX
NCBI GI g2501353
BLAST score 661
E value 1.0e-69
Match length 145
% identity 89

NCBI Description TRANSKETOLASE, CHLOROPLAST (TK) >gi\_1084440\_pir\_\_S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi\_664901\_emb\_CAA86607\_ (Z46646) transketolase



## [Craterostigma plantagineum]

```
      Seq. No.
      207230

      Seq. ID
      LIB3120-017-Q1-K1-E8

      Method
      BLASTX

      NCBI GI
      g4538945

      BLAST score
      205

      E value
      6.0e-18

      Match length
      97
```

56

NCBI Description (AL049483) putative thioredoxin [Arabidopsis thaliana]

 Seq. No.
 207231

 Seq. ID
 LIB3120-017-Q1-K1-E9

 Method
 BLASTX

 NCBI GI
 g1352821

BLAST score 601 E value 1.0e-62 Match length 119 % identity 92

% identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207232

Seq. ID LIB3120-017-Q1-K1-F1

Method BLASTX
NCBI GI g121689
BLAST score 328
E value 2.0e-30
Match length 57
% identity 89

NCBI Description GAST1 PROTEIN PRECURSOR >gi 100217 pir S22151 GAST1

protein - tomato >gi\_19247\_emb\_CAA44807\_ (X63093) gast1

[Lycopersicon esculentum]

Seq. No. 207233

Seq. ID LIB3120-017-Q1-K1-F10

Method BLASTX
NCBI GI g2829751
BLAST score 204
E value 6.0e-16
Match length 110
% identity 41

NCBI Description MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF)

>gi\_1850559 (U88035) macrophage migration inhibitory factor
[Brugia malayi] >gi\_2190976 (AF002699) macrophage migration

inhibitory factor [Brugia malayi]

Seq. No. 207234

Seq. ID LIB3120-017-Q1-K1-F12

MethodBLASTXNCBI GIg625547BLAST score368E value2.0e-35



```
Match length
                  74
% identity
                  chlorophyll a/b-binding protein type I - common tobacco
NCBI Description
                  >gi 493723 emb CAA45523 (X64198) photosystem I
                  light-harvesting chlorophyll a/b-binding protein [Nicotiana
                  tabacum]
                  207235
Seq. No.
Seq. ID
                  LIB3120-017-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q4512655
BLAST score
                  168
E value
                  7.0e-12
Match length
                  80
% identity
                  (AC007048) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  207236
                  LIB3120-017-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3928099
BLAST score
                  244
                  7.0e-21
E value
Match length
                  104
% identity
                  25
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
                  207237
Seq. No.
                  LIB3120-017-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  q132677
NCBI GI
BLAST score
                  130
E value
                  1.0e-10
                  103
Match length
% identity
                   51
                  50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
NCBI Description
                  >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor,
                  chloroplast - Arabidopsis thaliana >qi 16497 emb CAA77593
                   (Z11508) Plastid ribosomal protein CL15 [Arabidopsis
                   thaliana]
                   207238
Seq. No.
Seq. ID
                  LIB3120-017-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                   g4454012
BLAST score
                   183
```

E value 2.0e-13 Match length 74 51 % identity

(AL035396) Pollen-specific protein precursor like NCBI Description

[Arabidopsis thaliana]

207239 Seq. No.

Seq. ID LIB3120-017-Q1-K1-F6

BLASTX Method NCBI GI g2894593

```
BLAST score
                  1.0e-41
E value
                  118
Match length
                  71
% identity
                  (AL021889) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  207240
Seq. No.
                  LIB3120-017-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g461498
                  203
BLAST score
E value
                  2.0e-21
Match length
                  124
% identity
                  47
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                  (ALAAT-2) >gi 320619 pir S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421)
                  alanine aminotransferase [Panicum miliaceum]
Seq. No.
                  207241
Seq. ID
                  LIB3120-017-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1592672
BLAST score
                  308
E value
                  2.0e-28
Match length
                  104
% identity
                  60
NCBI Description
                  (X91921) germin1 [Arabidopsis thaliana]
                  207242
Seq. ID
                  LIB3120-017-Q1-K1-G10
Method
                  BLASTX
                  g3158474
                  313
                  8.0e-29
```

Seq. No.

NCBI GI BLAST score E value 80 Match length 80 % identity

(AF067184) aquaporin 1 [Samanea saman] NCBI Description

207243 Seq. No.

Seq. ID LIB3120-017-Q1-K1-G11

Method BLASTX g3927831 NCBI GI BLAST score 488 2.0e-49 E value 112 Match length % identity 82

(AC005727) similar to mouse ankyrin 3 [Arabidopsis NCBI Description

thaliana]

Seq. No. 207244

LIB3120-017-Q1-K1-G12 Seq. ID

Method BLASTX NCBI GI q289920 BLAST score 278 E value 4.0e-51



```
Match length
                  107
% identity
                  88
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  207245
Seq. ID
                  LIB3120-017-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3096945
BLAST score
                  417
E value
                  5.0e-41
Match length
                  102
% identity
NCBI Description
                  (AL023094) putative auxin-regulated protein [Arabidopsis
                  thaliana]
Seq. No.
                  207246
Seq. ID
                  LIB3120-017-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1345698
BLAST score
                  274
                  2.0e-24
E value
                  81
Match length
% identity
                  67
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
                   (CAB-151) (LHCP) >gi_99601_pir__$20917 chlorophyll
                  a/b-binding protein - upland cotton
                  >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
Seq. No.
                  207247
Seq. ID
                  LIB3120-017-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  276
                  2.0e-24
E value
Match length
                  96
                  60
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Oryza sativa]
Seq. No.
                  207248
                  LIB3120-017-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  278
E value
                  2.0e-53
```

Match length 138 % identity 80

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207249

Seq. ID LIB3120-017-Q1-K1-G9

Method BLASTX



```
NCBI GI
                  q118564
                  438
BLAST score
                  1.0e-43
E value
Match length
                  108
                  77
% identity
                  GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE
NCBI Description
                  REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate
                  dehydrogenase (EC 1.1.1.29) - cucumber
                  >gi 18264_emb_CAA41434 (X58542) NADH-dependent
                  hydroxypyruvate reductase [Cucumis sativus]
                  >gi 18275 emb CAA32764 (X14609) NAPH-dependent
                  hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
                  207250
Seq. No.
                  LIB3120-017-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                  q1170028
NCBI GI
BLAST score
                  187
                  4.0e-14
E value
                  43
Match length
% identity
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA
NCBI Description
                  1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1)
                 ·>gi 454357 (U03773)
                 glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis
                  thalianal
Seq. No.
                  207251
Seq. ID
                  LIB3120-017-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1709651
BLAST score
                  194
E value
                  2.0e-15
Match length
                  66
                  68
% identity
                  PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209
NCBI Description
                  plastocyanin a precursor - black poplar
                  >qi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                  nigra]
                  207252
Seq. No.
                  LIB3120-017-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2055273
BLAST score
                  665
                  5.0e-70
E value
Match length
                  142
% identity
                  87
                  (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
NCBI Description
                  207253
Seq. No.
                  LIB3120-017-Q1-K1-H6
Seq. ID
```

Method BLASTX
NCBI GI g2815246
BLAST score 121
E value 5.0e-14
Match length 55



```
% identity
NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]
                  207254
Seq. No.
                  LIB3120-017-Q1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2501011
                  271
BLAST score
E value
                  3.0e-40
                  143
Match length
                  57
% identity
                  ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
NCBI Description
                  >gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA
                  synthetase [Synechocystis sp.]
                  207255
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-A10
                  BLASTX
Method
                  g3292814
NCBI GI
BLAST score
                  167
E value
                  2.0e-15
Match length
                  95
% identity
                  53
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                  207256
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-A11
Method
                  BLASTX
                  g289920
NCBI GI
                  433
BLAST score
                  3.0e-43
E value
Match length
                  80
% identity
                  100
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  207257
Seq. No.
                  LIB3120-018-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g20729
NCBI GI
BLAST score
                  217
                  1.0e-17
E value
                  78
Match length
                   63
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
                  207258
Seq. No.
                  LIB3120-018-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2662341
BLAST score
                   466
E value
                   2.0e-64
                  133
Match length
% identity
                   95
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
```

28471

>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza
sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

% identity



## [Oryza sativa]

```
207259
Seq. No.
                  LIB3120-018-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1894771
                  151
BLAST score
                  8.0e-10
E value
                  134
Match length
% identity
                  34
                  (Z92954) product highly similar to metabolite transport
NCBI Description
                  proteins [Bacillus subtilis] >gi_2636109_emb_CAB15600.1
                   (Z99122) similar to metabolite transport protein [Bacillus
                  subtilis]
                  207260
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3757514
BLAST score
                  538
E value
                   4.0e-55
Match length
                  123
% identity
                   (AC005167) putative plasma membrane intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                  207261
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                   g1709825
BLAST score
                   371
                   1.0e-35
E value
Match length
                   132
% identity
                   66
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
                   207262
Seq. No.
Seq. ID
                   LIB3120-018-Q1-K1-B10
                   BLASTX
Method
                   g4176531
NCBI GI
                   307
BLAST score
                   4.0e-28
E value
Match length
                   142
% identity
                   45
                   (AL035263) weak similarity to chick phosphatidylcholine-ste
NCBI Description
                   rol acetyltransferase [Schizosaccharomyces pombe]
Seq. No.
                   207263
Seq. ID
                   LIB3120-018-Q1-K1-B12
                   BLASTX
Method
                   q3023752
NCBI GI
BLAST score
                   296
                   9.0e-27
E value
                   106
Match length
                   59
```

NCBI Description FERREDOXIN I PRECURSOR >gi\_1418982\_emb\_CAA99756\_ (Z75520)



## ferredoxin-I [Lycopersicon esculentum]

```
207264
Seq. No.
                  LIB3120-018-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                  g3885511
NCBI GI
                  287
BLAST score
                  7.0e-26
E value
Match length
                  75
                  75
% identity
                  (AF084200) similar to PSI-K subunit of photosystem I from
NCBI Description
                  barley [Medicago sativa]
                  207265
Seq. No.
                  LIB3120-018-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g1350956
NCBI GI
                  322
BLAST score
                  8.0e-30
E value
                  71
Match length
% identity
                   89
                  40S RIBOSOMAL PROTEIN S20 (S22)
NCBI Description
                   207266
Seq. No.
                  LIB3120-018-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                   g1709846
NCBI GI
BLAST score
                   255
                   5.0e-22
E value
                   79
Match length
                   45
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
NCBI Description
                   22 kDa component of photosystem II [Lycopersicon
                   esculentum]
                   207267
Seq. No.
                   LIB3120-018-Q1-K1-B8
Seq. ID
Method
                   BLASTX
                   q2407279
NCBI GI
BLAST score
                   439
                   6.0e-44
E value
Match length
                   89
                   93
% identity
                  (AF017362) aldolase [Oryza sativa]
NCBI Description
                   207268
Seq. No.
                   LIB3120-018-Q1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q416690
                   265
BLAST score
E value
                   4.0e-23
                   76
Match length
                   68
% identity
                   AUXIN-INDUCED PROTEIN 15A >gi_81763_pir__JQ1096
NCBI Description
                   auxin-induced protein 15A - soybean >gi_255573_bbs_113699
                   (S44172) orf 15A [Glycine max=soybeans, cv. Wayne, Peptide,
```

28473

82 aa] [Glycine max]

NCBI Description



```
207269
Seq. No.
                  LIB3120-018-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2827141
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
                  49
Match length
                  71
% identity
                   (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                  207270
Seq. No.
                  LIB3120-018-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g4415916
NCBI GI
                  323
BLAST score
                   6.0e-30
E value
                  116
Match length
                   54
% identity
                  (AC006282) putative pectin methylesterase [Arabidopsis
NCBI Description
                   thaliana]
                   207271
Seq. No.
                   LIB3120-018-Q1-K1-C12
Seq. ID
Method
                   BLASTX
                   g1354515
NCBI GI
BLAST score
                   325
                   4.0e-30
E value
                   144
Match length
                   52
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   207272
Seq. No.
                   LIB3120-018-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   q3914442
NCBI GI
                   428
BLAST score
                   2.0e-42
E value
                   97
Match length
                   84
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
                   207273
Seq. No.
                   LIB3120-018-Q1-K1-C5
Seq. ID
Method
                   BLASTX
                   q430947
NCBI GI
BLAST score
                   378
                   1.0e-36
E value
                   97
Match length
                   78
 % identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
```

[Arabidopsis thaliana]



```
Seq. No.
                  207274
                  LIB3120-018-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q117290
                  328
BLAST score
                  2.0e-30
E value
                  132
Match length
                  52
% identity
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
NCBI Description
                  (P36) (E30) >gi_100071_pir__S23774 triose
                  phosphate/3-phosphoglycerate/phosphate translocator
                  precursor - garden pea >gi_20691_emb_CAA38451_ (X54639)
                  chloroplast import receptor p36 [Pisum sativum]
                  >qi 20853 emb CAA48210 (X68077) phosphate translocator
                  [Pisum sativum] >gi_228551_prf__1805409A phosphate
                  translocator [Pisum sativum]
                  207275
Seq. No.
                  LIB3120-018-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  g131397
NCBI GI
                  261
BLAST score
                  8.0e-23
E value
Match length
                  126
% identity
                  49
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi 81480_pir__S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi 755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                   [Spinacia oleracea]
Seq. No.
                   207276
                  LIB3120-018-Q1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131176
BLAST score
                   268
E value
                   2.0e-23
                   59
Match length
                   88
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi_72683_pir__F1BH4 photosystem I chain IV precursor -
                   barley >gi 19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                   -46 to 101) [Hordeum_vulgare] >gi_226163 prf 1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum]
Seq. No.
                   207277
                   LIB3120-018-Q1-K1-D1
Seq. ID
Method
                   BLASTX
                   g115765
NCBI GI
BLAST score
                   371
```

28475

1.0e-35

90

E value Match length



```
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
NCBI Description
                   (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
                   (X14036) chlorophyll a/b-binding protein [Lycopersicon
                   esculentum] >gi_170431 (M20241) chlorophyll a/b-binding
                   protein [Lycopersicon esculentum] >gi_226546_prf__1601518A
                   chlorophyll a/b binding protein II [Lycopersicon
                   esculentum]
Seq. No.
                   207278
Seq. ID
                   LIB3120-018-Q1-K1-D11
Method
                   BLASTX
                   a1181599
NCBI GI
                   402
BLAST score
                   2.0e-39
E value
                   110
Match length
% identity
                   73
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
                   207279
Seq. No.
                   LIB3120-018-Q1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170897
                   257
BLAST score
                   2.0e-22
E value
Match length
                   61
% identity
NCBI Description
                   MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                   >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber
                   >gi_695311 (L31900) glyoxysomal malate dehydrogenase
                   [Cucumis sativus]
Seq. No.
                   207280
Seq. ID
                   LIB3120-018-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   q4263778
BLAST score
                   433
E value
                   6.0e-43
Match length
                   116
% identity
                   68
                   (AC006068) putative serine carboxypeptidase II [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   207281
                   LIB3120-018-Q1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3096945
                   440
BLAST score
E value
                   8.0e-44
                   102
Match length
% identity
                   82
                   (AL023094) putative auxin-regulated protein [Arabidopsis
NCBI Description
```

thaliana]

207282 Seq. No.

Seq. ID LIB3120-018-Q1-K1-D9



```
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                  190
                  6.0e-15
E value
Match length
                  65
% identity
                  62
                  (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
                  207283
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g133872
BLAST score
                  295
E value
                  7.0e-27
Match length
                  93
                   69
% identity
NCBI Description
                  30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
                  >gi_282838_pir_ S26494 ribosomal protein S1, chloroplast -
                  spinach >gi 322404 pir A44121 small subunit ribosomal
                  protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                  >gi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
Seq. No.
                   207284
Seq. ID
                  LIB3120-018-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                   q3914603
BLAST score
                   579
                   6.0e-60
E value
Match length
                   143
                   78
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                   PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Oryza sativa]
                  207285
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                   g421826
BLAST score
                   518
E value
                   5.0e-53
                   109
Match length
                   87
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                   >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                   thaliana]
Seq. No.
                   207286
Seq. ID
                  LIB3120-018-Q1-K1-E4
Method
                  BLASTX
NCBI GI
```

Method BLASTX
NCBI GI g3738306
BLAST score 155
E value 3.0e-10
Match length 42
% identity 69

Method

NCBI GI

E value

BLAST score

BLASTX

273

g1363479

2.0e-24



```
(AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  207287
                  LIB3120-018-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266893
BLAST score
                  438
E value
                  9.0e-44
Match length
                  88
                  97
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__$28172
                  ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis
                  sativus]
Seq. No.
                  207288
Seq. ID
                  LIB3120-018-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  253
                  4.0e-22
E value
Match length
                  57
% identity
                  95
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  207289
Seq. ID
                  LIB3120-018-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4539009
BLAST score
                  251
                  7.0e-22
E value
                  85
Match length
                  52
% identity
                  (AL049481) putative protein [Arabidopsis thaliana]
NCBI Description
                  207290
Seq. No.
∕Seq. ID
                  LIB3120-018-Q1-K1-F2
                  BLASTX
Method
NCBI GI
                  g430947
BLAST score
                  313
                   6.0e-29
E value
Match length
                  83
                  78
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   207291
Seq. No.
                  LIB3120-018-Q1-K1-F5
Seq. ID
```



```
Match length
% identity
                   66
                   photosystem I protein psaL - cucumber
NCBI Description
                   >gi 801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]
                   207292
Seq. No.
                   LIB3120-018-Q1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g267120
                   246
BLAST score
                   6.0e-21
E value
                   91
Match length
% identity
                   THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi 100070_pir__S20929
NCBI Description
                   thioredoxin f precursor - garden pea
                   >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum
                   satīvum] >gi 1388086 (U35830) thioredoxin f [Pisum sativum]
                   207293
Seq. No.
                   LIB3120-018-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g136707
NCBI GI
BLAST score
                   289
E value
                    3.0e-26
Match length
                   88
                    66
% identity
                   CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                   (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                    iron-sulfur protein precursor - garden pea
                    >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS
                    protein [Pisum sativum]
                    207294
Seq. No.
                    LIB3120-018-Q1-K1-G11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q430947
BLAST score
                    432
                    9.0e-43
E value
Match length
                    109
% identity
                    80
                    (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    207295
                    LIB3120-018-Q1-K1-G12
Seq. ID
                    BLASTX
Method
```

q1352821 NCBI GI BLAST score 349 2.0e-33 E value Match length 76 95 % identity NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi 450505 emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



207296

BLASTX

LIB3120-018-Q1-K1-G3

Seq. No.

Seq. ID

Method

```
NCBI GI
                  q3378661
BLAST score
                  239
E value
                  2.0e-20
Match length
                  96
% identity
NCBI Description
                  (Y13048) putative outward rectifying potassium channel
                  StKCO1 [Solanum tuberosum]
Seq. No.
                  207297
Seq. ID
                  LIB3120-018-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1353352
BLAST score
                  175
E value
                  8.0e-13
Match length
                  48
                  73
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                  207298
Seq. ID
                  LIB3120-018-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q123650
BLAST score
                  506
                  2.0e-51
E value
Match length
                  98
                  98
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN >gi 82245_pir__S03250 heat
NCBI Description
                  shock protein 70 (clone pMON9743) - garden petunia
                  >gi 20557 emb CAA30018 (X06932) heat shock protein 70
                   [Petunia x hybrida]
                  207299
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g120669
                   557
BLAST score
                  1.0e-57
E value
Match length
                  112
% identity
                   92
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   207300
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-G8
                  BLASTX
Method
NCBI GI
                   g4151319
BLAST score
                   288
                   3.0e-26
E value
                  81
Match length
```



```
% identity
NCBI Description
                   (AF089084) putative auxin efflux carrier protein; AtPIN1
                   [Arabidopsis thaliana]
                  207301
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1354515
BLAST score
                  180
E value
                  2.0e-13
                  73
Match length
                  58
% identity
NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
                  207302
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1592672
BLAST score
                  387
E value
                  2.0e-37
Match length
                  116
% identity
NCBI Description (X91921) germin1 [Arabidopsis thaliana]
Seq. No.
                  207303
                  LIB3120-018-Q1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2494415
BLAST score
                  337
                  6.0e-32
E value
Match length
                  87
                  83
% identity
NCBI Description
                  FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine
                  max]
                  207304
Seq. No.
Seq. ID
                  LIB3120-018-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g231610
BLAST score
                  315
E value
                  3.0e-29
Match length
                  92
% identity
                  73
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                  >gi_67880_pir_PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
```

207305 Seq. No. Seq. ID LIB3120-018-Q1-K1-H3

Method BLASTN NCBI GI g19784 BLAST score 49



E value 1.0e-18 Match length 175 % identity 85

NCBI Description N.tabacum atpC mRNA for gamma subunit of ATP synthase

Seq. No. 207306

Seq. ID LIB3120-018-Q1-K1-H7

Method BLASTX
NCBI GI g1709825
BLAST score 362
E value 9.0e-35
Match length 100
% identity 74

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi\_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No. 207307

Seq. ID LIB3120-018-Q1-K1-H8

Method BLASTX
NCBI GI g2239091
BLAST score 258
E value 2.0e-22
Match length 104
% identity 56

NCBI Description (Z84571) anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

Seq. No. 207308

Seq. ID LIB3120-018-Q1-K1-H9

Method BLASTX
NCBI GI g1352821
BLAST score 284
E value 2.0e-25
Match length 86
% identity 71

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207309

Seq. ID LIB3120-018-Q1-K2-A1

Method BLASTX
NCBI GI g3395588
BLAST score 170
E value 5.0e-12
Match length 84
% identity 44

NCBI Description (AL031179) serine-threonine protein phosphatase

[Schizosaccharomyces pombe]

Seq. No. 207310

Seq. ID LIB3120-018-Q1-K2-A2

Method BLASTX NCBI GI g20729 BLAST score 416



```
7.0e-41
E value
                  120
Match length
                  72
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                  207311
Seq. No.
                  LIB3120-018-Q1-K2-A3
Seq. ID
Method
                  BLASTX
                  g2662343
NCBI GI
                  144
BLAST score
                  4.0e-20
E value
                  106
Match length
                  57
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  207312
Seq. No.
                  LIB3120-018-Q1-K2-A4
Seq. ID
                  BLASTX
Method
                  g1894771
NCBI GI
BLAST score
                  149
                  1.0e-09
E value
                  130
Match length
                   35
% identity
                  (Z92954) product highly similar to metabolite transport
NCBI Description
                  proteins [Bacillus subtilis] >gi_2636109_emb_CAB15600.1
                   (Z99122) similar to metabolite transport protein [Bacillus
                   subtilis]
                   207313
Seq. No.
                  LIB3120-018-Q1-K2-B1
Seq. ID
Method
                   BLASTX
                   g1709825
NCBI GI
                   388
BLAST score
E value
                   1.0e-37
                   133
Match length
                   67
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                   207314
Seq. ID
                   LIB3120-018-Q1-K2-B3
Method
                   BLASTX
NCBI GI
                   g3885511
BLAST score
                   426
E value
                   5.0e-42
Match length
                   105
% identity
                   (AF084200) similar to PSI-K subunit of photosystem I from
NCBI Description
                   barley [Medicago sativa]
Seq. No.
                   207315
                   LIB3120-018-Q1-K2-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1781348
BLAST score
                   535
                   8.0e-55
E value
```

28483

2,

Match length



% identity (Y10380) homologous to plastidic aldolases [Solanum NCBI Description tuberosum] 207316 Seq. No. LIB3120-018-Q1-K2-B6 Seq. ID BLASTX Method g1350956 NCBI GI 151 BLAST score 4.0e-10 E value 56 Match length 59 % identity 40S RIBOSOMAL PROTEIN S20 (S22) NCBI Description Seq. No. 207317 LIB3120-018-Q1-K2-C2 Seq. ID BLASTX Method g117290 NCBI GI 315 BLAST score 5.0e-29 E value 130 Match length 52 % identity CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) NCBI Description (P36) (E30) >gi\_100071\_pir\_\_S23774 triose phosphate/3-phosphoglycerate/phosphate translocator precursor - garden pea >gi\_20691\_emb\_CAA38451\_ (X54639)
chloroplast import receptor p36 [Pisum sativum] >gi 20853 emb\_CAA48210\_ (X68077) phosphate translocator [Pisum sativum] >gi\_228551\_prf\_\_1805409A phosphate translocator [Pisum sativum] 207318 Seq. No. LIB3120-018-Q1-K2-C3 Seq. ID BLASTX Method g3914442 NCBI GI 469 BLAST score 4.0e-47 E value Match length 137 69 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi\_1916350 (U92504) PSI-H subunit [Brassica rapa] 207319 Seq. No. LIB3120-018-Q1-K2-C5 Seq. ID BLASTX Method q99487 NCBI GI 154 BLAST score E value 3.0e-10 88 Match length % identity 50

NCBI Description chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794\_emb\_CAA41407\_ (X58517) Type III chlorophyll

a /b-binding protein [Pinus sylvestris]

Seq. No. 207320

Seq. ID LIB3120-018-Q1-K2-C6



Method BLASTX
NCBI GI g3249081
BLAST score 225
E value 2.0e-18
Match length 79
% identity 53

NCBI Description (AC004473) Strong similarity to AROGP2 gene gb\_1762634 from

Lycopersicon esculentum. [Arabidopsis thaliana]

Seq. No. 207321

Seq. ID LIB3120-018-Q1-K2-C7

Method BLASTX
NCBI GI g131397
BLAST score 327
E value 2.0e-30
Match length 143
% identity 53

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_81480\_pir\_\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802 emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 207322

Seq. ID LIB3120-018-Q1-K2-D1

Method BLASTX
NCBI GI g115765
BLAST score 514
E value 3.0e-52
Match length 123
% identity 76

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi\_100201\_pir\_\_S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi\_19180\_emb\_CAA32197\_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_226546\_prf\_\_1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 207323

Seq. ID LIB3120-018-Q1-K2-D2

Method BLASTX
NCBI GI g1170897
BLAST score 419
E value 3.0e-41
Match length 92
% identity 89

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi\_1076276\_pir\_\_S52039 NAD-malate dehydrogenase - cucumber

>gi\_695311 (L31900) glyoxysomal malate dehydrogenase

[Cucumis sativus]

Seq. No. 207324



89

% identity

```
LIB3120-018-Q1-K2-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3096945
BLAST score
                   361
                   2.0e-34
E value
                   100
Match length
% identity
                   (AL023094) putative auxin-regulated protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   207325
Seq. ID
                   LIB3120-018-Q1-K2-D5
Method
                   BLASTX
NCBI GI
                   q2911073
BLAST score
                   194
E value
                   8.0e-15
                   70
Match length
% identity
                   56
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   207326
Seq. No.
                   LIB3120-018-Q1-K2-D6
Seq. ID
Method
                   BLASTN
                   q1350521
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
                   62
Match length
                   89
% identity
                   Picea glauca late embryogenesis abundant protein (EMB2)
NCBI Description
                   mRNA, complete cds
                   207327
Seq. No.
Seq. ID
                   LIB3120-018-Q1-K2-D7
Method
                   BLASTX
NCBI GI
                   g1706082
BLAST score
                   533
                   1.0e-54
E value
Match length
                   142
% identity
                   70
                   SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
NCBI Description
                   >gi_629787_pir__S44191 serine-type carboxypeptidase (EC
3.4.16.1) II-3 - barley >gi_619350_bbs_153536
                   CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
                   cv. Alexis, aleurone, Peptide, 516 aa]
                   >gi 474392_emb_CAA55478_ (X78877) serine carboxylase II-3
                   [Hordeum vulgare]
                   207328
Seq. No.
Seq. ID
                   LIB3120-018-Q1-K2-E3
Method
                   BLASTX
                   q445116
NCBI GI
BLAST score
                   638
                   6.0e-67
E value
                   134
Match length
```

NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]

Match length

% identity

127

36



```
Seq. No.
                  207329
Seq. ID
                  LIB3120-018-Q1-K2-E5
Method
                  BLASTX
NCBI GI
                  g100614
BLAST score
                  654
E value
                  9.0e-69
Match length
                  141
% identity
                  87
NCBI Description ribulose-bisphosphate carboxylase activase A long form
                  precursor - barley (fragment) >gi 167089 (M55446) ribulose
                  1,5-bisphosphate carboxylase activase [Hordeum vulgare]
Seq. No.
                  207330
Seq. ID
                  LIB3120-018-Q1-K2-E6
Method
                  BLASTX
NCBI GI
                  q3738306
BLAST score
                  148
E value
                  2.0e-09
Match length
                  42
                  67
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  207331
                  LIB3120-018-Q1-K2-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131393
BLAST score
                  269
E value
                  1.0e-23
Match length
                  113
% identity
                  57
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi_100360_pir__S15005 photosystem II oxygen-evolving
                  complex protein 2 - common tobacco
                  >gi_19911_emb_CAA39039.1_ (X55354) photosystem II 23kDa
                  polypeptide [Nicotiana tabacum]
Seq. No.
                  207332
Seq. ID
                  LIB3120-018-Q1-K2-F5
                  BLASTX
Method
NCBI GI
                  g1363479
BLAST score
                  465
                  1.0e-46
E value
Match length
                  126
% identity
                  75
NCBI Description photosystem I protein psaL - cucumber
                  >gi 801740 dbj BAA09047 (D50456) PsaL [Cucumis sativus]
Seq. No.
                  207333
Seq. ID
                  LIB3120-018-Q1-K2-F6
Method
                  BLASTX
NCBI GI
                  q3875463
BLAST score
                  189
E value
                  3.0e-14
```

NCBI Description (Z68341) predicted using Genefinder; Similarity to Human



SNF2alpha protein (PIR Acc. No. S45251); cDNA EST EMBL:D26678 comes from this gene; cDNA EST EMBL:D26681 comes from this gene; cDNA EST EMBL:D26680 comes from this gene; ... >gi\_3879468\_emb\_CAA92978\_ (Z68751) predicted using Genefinder; Similarity to Human SNF2alpha protein (PIR Acc. No. S45251); cDNA EST EMBL:D26678 comes from this gene; cDNA EST EMBL:D26680 comes from this gene; cDNA EST EMBL:D26680 comes from this gene;

 Seq. No.
 207334

 Seq. ID
 LIB3120-018-Q1-K2-G2

 Method
 BLASTX

 NCBI GI
 g120669

 BLAST score
 469

 E value
 4.0e-47

Match length 134 % identity 68

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 207335

Seq. ID LIB3120-018-Q1-K2-G3

Method BLASTX
NCBI GI g2181186
BLAST score 246
E value 5.0e-21
Match length 123
% identity 41

NCBI Description (X97323) outward rectifying potassium channel KCO1

[Arabidopsis thaliana] >gi\_2230761\_emb\_CAA69158\_ (Y07825)

kcol [Arabidopsis thaliana]

Seq. No. 207336

Seq. ID LIB3120-018-Q1-K2-G4

Method BLASTX
NCBI GI g1353352
BLAST score 305
E value 8.0e-28
Match length 90
% identity 71

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

Seq. No. 207337

Seq. ID LIB3120-018-Q1-K2-G5

Method BLASTX
NCBI GI g1076746
BLAST score 596
E value 6.0e-62
Match length 118
% identity 96
NCBI Description heat sho

heat shock protein 70 - rice (fragment)

>gi\_763160\_emb\_CAA47948\_ (X67711) heat shock protein 70

[Oryza sativa]



Seq. No. 207338

LIB3120-018-Q1-K2-G6 Seq. ID

BLASTX Method g120669 NCBI GI 407 BLAST score E value 2.0e-40 112 Match length % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

207339 Seq. No.

LIB3120-018-Q1-K2-G8 Seq. ID

Method BLASTX NCBI GI g4151319 BLAST score 328 1.0e-30 E value 114 Match length 66 % identity

(AF089084) putative auxin efflux carrier protein; AtPIN1 NCBI Description

[Arabidopsis thaliana]

207340 Seq. No.

LIB3120-018-Q1-K2-H2 Seq. ID

Method BLASTX q231610 NCBI GI 349 BLAST score 5.0e-33 E value 79 Match length 87 % identity

ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR NCBI Description

>gi 67880 pir\_PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi\_19785\_emb\_CAA45152\_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 207341

LIB3120-018-Q1-K2-H3 Seq. ID

Method BLASTX NCBI GI g231610 BLAST score 362 2.0e-34 E value Match length 121 % identity 64

ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR NCBI Description

>gi 67880 pir\_\_PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi\_19785\_emb\_CAA45152\_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

207342 Seq. No.

Seq. ID LIB3120-018-Q1-K2-H5

BLASTX Method



```
NCBI GI
                  g430947
                  231
BLAST score
                  2.0e-19
E value
Match length
                  95
                   55
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  207343
Seq. No.
                  LIB3120-018-Q1-K2-H7
Seq. ID
                  BLASTX
Method
                   g1709825
NCBI GI
                   267
BLAST score
                   4.0e-26
E value
Match length
                   86
                   73
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
                   207344
Seq. No.
                   LIB3120-018-Q1-K2-H8
Seq. ID
                   BLASTX
Method
                   g2239085
NCBI GI
                   291
BLAST score
                   3.0e-26
E value
                   136
Match length
                   49
% identity
                   (Z84384) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus]
                   207345
Seq. No.
                   LIB3120-019-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g4090935
NCBI GI
BLAST score
                   249
                   3.0e-21
E value
                   127
Match length
                   43
% identity
                   (AF028719) DNA polymerase type I [Rhodothermus sp. 'ITI
NCBI Description
                   518']
                   207346
Seq. No.
                   LIB3120-019-Q1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4455208
                   439
BLAST score
                   1.0e-43
E value
                   106
Match length
% identity
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   207347
 Seq. No.
                   LIB3120-019-Q1-K1-A3
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g1063400
BLAST score
                   157
```

28490

1.0e-10

E value

% identity

NCBI Description



```
Match length
% identity
                   42
                  (X92888) glycolate oxidase [Lycopersicon esculentum]
NCBI Description
                  207348
Seq. No.
                  LIB3120-019-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                  g3820978
NCBI GI
BLAST score
                  274
                  2.0e-24
E value
                  110
Match length
                   48
% identity
                  (AL031228) dJ1033B10.2 (WD40 protein BING4 (similar to S.
NCBI Description
                   cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)
                   [Homo sapiens]
                   207349
Seq. No.
                  LIB3120-019-Q1-K1-A7
Seq. ID
Method
                  BLASTX
                  g166702
NCBI GI
                   517
BLAST score
                   1.0e-52
E value
                   138
Match length
                   75
% identity
                   (M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit
NCBI Description
                   [Arabidopsis thaliana]
                   207350
Seq. No.
                   LIB3120-019-Q1-K1-A8
Seq. ID
                   BLASTX
Method
                   q461999
NCBI GI
BLAST score
                   455
                   2.0e-45
E value
                   125
Match length
% identity
                   73
NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)
Seq. No.
                   207351
Seq. ID
                   LIB3120-019-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   q1181599
BLAST score
                   369
                   2.0e-35
E value
                   108
Match length
% identity
                   69
                   (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                   207352
Seq. No.
Seq. ID
                   LIB3120-019-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   q4027897
BLAST score
                   541
                   2.0e-55
E value
Match length
                   120
```

(AF049353) alpha-expansin precursor [Nicotiana tabacum]

Seq. ID

Method



```
207353
Seq. No.
                  LIB3120-019-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  q3158474
NCBI GI
                   355
BLAST score
                  1.0e-33
E value
                  102
Match length
                   73
% identity
                  (AF067184) aquaporin 1 [Samanea saman]
NCBI Description
                   207354
Seq. No.
                  LIB3120-019-Q1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2347189
BLAST score
                   271
                   8.0e-24
E value
                   90
Match length
                   57
% identity
                   (AC002338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3150399 (AC004165) hypothetical protein [Arabidopsis
                   thaliana]
                   207355
Seq. No.
                   LIB3120-019-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g430947
NCBI GI
                   500
BLAST score
                   1.0e-50
E value
                   124
Match length
                   81
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   207356
Seq. No.
                   LIB3120-019-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g2950210
NCBI GI
                   213
BLAST score
                   2.0e-17
E value
                   54
Match length
                   76
 % identity
                   (Y14615) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
                   207357
 Seq. No.
                   LIB3120-019-Q1-K1-B5
 Seq. ID
                   BLASTX
Method
                   q4105269
 NCBI GI
                   280
 BLAST score
                   7.0e-25
 E value
                   149
 Match length
 % identity
                    46
                    (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase
 NCBI Description
                    [Rattus norvegicus]
                    207358
 Seq. No.
```

28492

LIB3120-019-Q1-K1-B7

BLASTX



```
g4558556~
NCBI GI
BLAST score
                   276
E value
                   2.0e-24
Match length
                   142
% identity
                   43
NCBI Description
                  (AC007138) predicted protein of unknown function
                   [Arabidopsis thaliana]
Seq. No.
                   207359
Seq. ID
                   LIB3120-019-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g3292817
BLAST score
                   247
                   5.0e-21
E value
                   95
Match length
                   57
% identity
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   207360
Seq. ID
                   LIB3120-019-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   q1362152
BLAST score
                   606
E value
                   4.0e-63
Match length
                   147
% identity
                   78
NCBI Description
                   ribosomal protein S6 kinase homolog (clone Aspk11) - oat
                   >qi 871986 emb CAA56313 (X79992) putative pp70 ribosomal
                   protein S6 kinase [Avena sativa]
                   207361
Seq. No.
                   LIB3120-019-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   629
E value
                   8.0e-66
Match length
                   116
                   98
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   207362
Seq. ID
                   LIB3120-019-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3063710
BLAST score
                   454
                   3.0e-45
E value
Match length
                   133
```

% identity 71

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 207363

Seq. ID LIB3120-019-Q1-K1-C4

Method BLASTX



```
q3183285
NCBI GI
BLAST score
                   143
                   7.0e-09
E value
                   124
Match length
% identity
                   HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION
NCBI Description
                   >gi_1742787_dbj_BAA15475_ (D90813) ORF_ID:o322#7; similar
to [SwissProt Accession Number Q06373] [Escherichia coli]
                   >gi 1787999 (AE000266) orf, hypothetical protein
                   [Escherichia coli]
                   207364
Seq. No.
Seq. ID
                   LIB3120-019-Q1-K1-C5
Method
                   BLASTX
                   q4559372
NCBI GI
                   282
BLAST score
                   3.0e-25
E value
                   81
Match length
                   78
% identity
NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]
                   207365
Seq. No.
                   LIB3120-019-Q1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2245068
BLAST score
                   480
                   2.0e-48
E value
                   125
Match length
% identity
                   74
NCBI Description (Z97342) serine protease homolog [Arabidopsis thaliana]
                   207366
Seq. No.
                   LIB3120-019-Q1-K1-C7
Seq. ID
Method
                   BLASTX
                   g1352821
NCBI GI
BLAST score
                   386
E value
                   2.0e-37
                   77
Match length
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   207367
Seq. No.
Seq. ID
                   LIB3120-019-Q1-K1-C8
```

Method BLASTX
NCBI GI g2191175
BLAST score 162
E value 4.0e-11
Match length 118
% identity 43

NCBI Description (AF007270) A IG002P16.24 gene product [Arabidopsis

thaliana]

Seq. No. 207368

Match length

% identity

62



```
Seq. ID
                  LIB3120-019-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q131385
BLAST score
                  565
E value
                  3.0e-58
Match length
                  135
% identity
                  84
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
Seq. No.
                  207369
Seq. ID
                  LIB3120-019-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3135611
BLAST score
                  435
                  2.0e-47
E value
Match length
                  124
% identity
                  (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
                  207370
Seq. No.
Seq. ID
                  LIB3120-019-Q1-K1-D11
Method
                  BLASTX
                  q121689
NCBI GI
BLAST score
                  395
                  2.0e-38
E value
Match length
                  89
% identity
                  71
                  GAST1 PROTEIN PRECURSOR >gi 100217 pir S22151 GAST1
NCBI Description
                  protein - tomato >gi 19247 emb CAA44807 (X63093) gast1
                   [Lycopersicon esculentum]
Seq. No.
                  207371
Seq. ID
                  LIB3120-019-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q1173347
BLAST score
                  486
E value
                  5.0e-49
Match length
                  108
% identity
                  89
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  207372
Seq. No.
Seq. ID
                  LIB3120-019-Q1-K1-D2
                  BLASTX
Method
NCBI GI
                  g4432821
BLAST score
                  143
                  8.0e-09
E value
                   48
```

28495

NCBI Description (AC006593) putative transmembrane protein [Arabidopsis



## thaliana]

```
207373
Seq. No.
                  LIB3120-019-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g3953471
NCBI GI
BLAST score
                  230
                  4.0e-19
E value
                  65
Match length
                  68
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  207374
                  LIB3120-019-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  a3850111
NCBI GI
                  238
BLAST score
E value
                  6.0e-20
Match length
                  140
                  41
% identity
                  (AL033388) hypothetical integral membrane protein, putative
NCBI Description
                  involvement in lipid metabolism [Schizosaccharomyces pombe]
Seq. No.
                  207375
                  LIB3120-019-Q1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2687434
BLAST score
                  325
E value
                  0.0e+00
                  403
Match length
% identity
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  207376
                  LIB3120-019-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266893
BLAST score
                  768
E value
                   4.0e-82
Match length
                  151
                   95
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172
                   ribulose-bisphosphate carboxylase activase - cucumber
                  >gi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis
                   sativus]
                   207377
Seq. No.
Seq. ID
                  LIB3120-019-Q1-K1-E1
                  BLASTX
Method
                   g3080400
NCBI GI
BLAST score
                   308
                   3.0e-28
E value
                   65
Match length
                   89
% identity
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
```



>gi\_4455264\_emb\_CAB36800.1\_ (AL035527) putative protein
[Arabidopsis thaliana]

Seq. No. 207378 Seq. ID LIB3120-019-Q1-K1-E10 Method BLASTX NCBI GI g1929406 BLAST score 357 7.0e-34 E value Match length 93 72 % identity NCBI Description (Z93769) protein phosphatase type 1 [Nicotiana tabacum]

Seq. No. 207379

Seq. ID LIB3120-019-Q1-K1-E11

Method BLASTX
NCBI GI g289920
BLAST score 759
E value 5.0e-81
Match length 143
% identity 99

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207380

Seq. ID LIB3120-019-Q1-K1-E12

Method BLASTX
NCBI GI g119150
BLAST score 745
E value 2.0e-79
Match length 145
% identity 97

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi\_19273\_emb\_CAA32618\_ (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

Seq. No. 207381

Seq. ID LIB3120-019-Q1-K1-E2

Method BLASTX
NCBI GI g1814407
BLAST score 657
E value 4.0e-69
Match length 138
% identity 93

NCBI Description (U84891) H+-transporting ATPase [Mesembryanthemum

crystallinum]

Seq. No. 207382

Seq. ID LIB3120-019-Q1-K1-E5

Method BLASTX
NCBI GI g2911043
BLAST score 216
E value 2.0e-17
Match length 111

% identity NCBI Description (AL021961) putative protein [Arabidopsis thaliana] 207383 Seq. No. Seq. ID LIB3120-019-Q1-K1-E7 Method BLASTX NCBI GI g134101 BLAST score 470 2.0e-47 E value Match length 117 % identity 84 NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi 72958 pir HHCSBA ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - castor bean (fragment) Seq. No. 207384 Seq. ID LIB3120-019-Q1-K1-E8 Method BLASTX NCBI GI g1352821 BLAST score 465 E value 5.0e-66 Match length 137 % identity 89 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 207385 Seq. ID LIB3120-019-Q1-K1-E9

Method BLASTX
NCBI GI g973313
BLAST score 278
E value 6.0e-25
Match length 70
% identity 77

NCBI Description (U30250) myo-inositol 1-phosphate synthase isozyme-2

[Arabidopsis thaliana]

Seq. No. 207386

Seq. ID LIB3120-019-Q1-K1-F10

Method BLASTX
NCBI GI g4454044
BLAST score 145
E value 5.0e-09
Match length 34
% identity 76

NCBI Description (AL035394) putative Ap2 domain protein [Arabidopsis

thaliana]

Seq. No. 207387

Seq. ID LIB3120-019-Q1-K1-F11

Method BLASTX NCBI GI g3511285



```
BLAST score
                  2.0e-70
E value
Match length
                  141
% identity
                  85
NCBI Description
                 (AF081534) cellulose synthase [Populus alba x Populus
                  207388
Seq. No.
Seq. ID
                  LIB3120-019-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2980793
BLAST score
                  163
E value
                  3.0e-11
Match length
                  120
% identity
                  34
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
                  207389
Seq. No.
                  LIB3120-019-Q1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1019946
BLAST score
                  698
E value
                  6.0e-74
Match length
                  133
% identity
                  98
NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]
                  207390
Seq. No.
Seq. ID
                  LIB3120-019-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1346156
BLAST score
                  681
E value
                  7.0e-72
Match length
                  148
                  91
% identity
NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR
                  (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                  (SHMT) >gi_481943 pir_ S40213 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                  >gi 437997 emb CAA81079 (Z25860) glycine
                  hydroxymethyltransferase [Flaveria pringlei]
Seq. No.
                  207391
Seq. ID
                  LIB3120-019-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q1653230
BLAST score
                  155
E value
                  3.0e-10
```

e.

Match length 59 % identity 54

NCBI Description (D90912) hypothetical protein [Synechocystis sp.]

207392 Seq. No. LIB3120-019-Q1-K1-F6 Seq. ID

Method BLASTX g1352821 NCBI GI BLAST score 631



E value 5.0e-66
Match length 118
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207393

Seq. ID LIB3120-019-Q1-K1-F8

Method BLASTX
NCBI GI g2306917
BLAST score 273
E value 3.0e-24
Match length 83
% identity 65

NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis

thaliana]

Seq. No. 207394

Seq. ID LIB3120-019-Q1-K1-G1

Method BLASTX
NCBI GI g289920
BLAST score 463
E value 9.0e-54
Match length 108
% identity 97

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207395

Seq. ID LIB3120-019-Q1-K1-G11

Method BLASTX
NCBI GI g4325338
BLAST score 486
E value 5.0e-49
Match length 108
% identity 80

NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]

Seq. No. 207396

Seq. ID LIB3120-019-Q1-K1-G12

Method BLASTX
NCBI GI g505482
BLAST score 571
E value 3.0e-59
Match length 116
% identity 93

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 207397

Seq. ID LIB3120-019-Q1-K1-G3

Method BLASTX NCBI GI g4262226 BLAST score 251

```
Match length
                   116
```

NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

207398 Seq. No.

E value

% identity

Seq. ID LIB3120-019-Q1-K1-G4

Method BLASTX NCBI GI q3834316 BLAST score 305 E value 7.0e-28 Match length 115 % identity 47

(AC005679) Similar to gb X16648 pathogenesis related NCBI Description

protein from Hordeum vulgare. EST gb Z18206 comes from

this gene. [Arabidopsis thaliana]

Seq. No. 207399

Seq. ID LIB3120-019-Q1-K1-G5

Method BLASTX NCBI GI g1353352 BLAST score 437 E value 3.0e-43Match length 137 % identity 59

(U31975) alanine aminotransferase [Chlamydomonas NCBI Description

reinhardtii]

Seq. No. 207400

Seq. ID LIB3120-019-Q1-K1-G6

Method BLASTX NCBI GI g2351378 BLAST score 201 1.0e-15 E value Match length 80 % identity 50

NCBI Description (U54558) translation initiation factor eIF3 p66 subunit

[Homo sapiens] >gi\_4200328\_emb\_CAA18440\_ (AL022313)

EIF3-P66 [Homo sapiens]

>gi 4503523 ref NP 003744.1 pEIF3S7 UNKNOWN

Seq. No. 207401

Seq. ID LIB3120-019-Q1-K1-H1

Method BLASTX NCBI GI g2499966 BLAST score 168 E value 8.0e-12 Match length 111 42 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E NCBI Description

A) >gi 632722\_bbs\_151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,

141 aa] [Nicotiana sylvestris]

207402 Seq. No.

Seq. ID LIB3120-019-Q1-K1-H10

Method BLASTX

NCBI GI g115765 BLAST score 568 E value 1.0e-58 131 Match length 49

% identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR NCBI Description

(CAB-7) >gi\_100201\_pir\_\_S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi\_19180\_emb\_CAA32197\_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi 170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_226546\_prf\_\_1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

207403 Seq. No.

Seq. ID LIB3120-019-Q1-K1-H2

Method BLASTX NCBI GI g3334200 BLAST score 576 E value 9.0e-60 Match length 112 % identity 96

NCBI Description GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE

DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) >gi\_2894362 emb CAB16918 (Z99770) P-Protein precursor

[Solanum tuberosum]

Seq. No. 207404

Seq. ID LIB3120-019-Q1-K1-H3

Method BLASTN NCBI GI g3821780 BLAST score 33 E value 4.0e-09 Match length 48

% identity 51

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 207405

Seq. ID LIB3120-019-Q1-K1-H5

BLASTN Method NCBI GI g3821780 BLAST score 33 E value 4.0e-09 Match length 37 44 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 207406

Seq. ID LIB3120-019-Q1-K1-H7

Method BLASTX NCBI GI g3298439 BLAST score 370 2.0e-35 E value Match length 101 % identity

NCBI Description (AB010878) chloroplast ribosomal protein L4 [Nicotiana

tabacum]



207407 Seq. No.

Seq. ID LIB3120-019-Q1-K1-H8

Method BLASTX NCBI GI g3892058 BLAST score 249 3.0e-21 E value Match length 106 51

NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide

[Arabidopsis thaliana]

Seq. No. 207408

% identity

Seq. ID LIB3120-019-Q1-K1-H9

Method BLASTX NCBI GI q1352821 BLAST score 549 E value 2.0e-56 Match length 111 95 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

207409 Seq. No.

Sea. ID LIB3120-020-01-K1-A1

Method BLASTX NCBI GI g1709825 BLAST score 348 E value 7.0e-33 Match length 126 % identity

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No. 207410

Seq. ID LIB3120-020-Q1-K1-A10

Method BLASTX NCBI GI g2239091 BLAST score 229 E value 6.0e-19 Match length 125 % identity

NCBI Description (Z84571) anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

207411 Seq. No.

Seq. ID LIB3120-020-Q1-K1-A11

Method BLASTX NCBI GI q3219766 BLAST score 644 E value 1.0e-67 Match length 139 90 % identity

NCBI Description ACTIN 82 >gi 1498370 (U60483) actin [Solanum tuberosum]



Seq. No. 207412

Seq. ID LIB3120-020-Q1-K1-A12

Method BLASTX
NCBI GI g1352821
BLAST score 240
E value 2.0e-20
Match length 87
% identity 61

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207413

Seq. ID LIB3120-020-Q1-K1-A2

Method BLASTX
NCBI GI g2467274
BLAST score 276
E value 2.0e-24
Match length 106
% identity 57

NCBI Description (Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 207414

Seq. ID LIB3120-020-Q1-K1-A3

Method BLASTX
NCBI GI g3335337
BLAST score 377
E value 3.0e-36
Match length 124
% identity 65

NCBI Description (AC004512) Similar to acyl carrier protein, mitochondrial

precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb\_L23574 from A. thaliana. ESTs gb\_Z30712, gb\_Z30713, gb\_Z26204, gb\_N37975 and gb\_N96330

come from this gene

Seq. No. 207415

Seq. ID LIB3120-020-Q1-K1-A4

Method BLASTX
NCBI GI g1170568
BLAST score 612
E value 6.0e-64
Match length 121
% identity 98

NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi 2147316 pir S60302 D-myo-inositol-3-phosphate synthase

(EC 5.5.1.4) - Spirodela polyrrhiza >qi 558648 emb CAA77751 (Z11693)

D-myo-inositol-3-phosphate synthase [Spirodela polyrrhiza]

Seq. No. 207416

Seq. ID LIB3120-020-Q1-K1-A5

Method BLASTX NCBI GI g115813

```
BLAST score
                  2.0e-58
E value
                  141
Match length
                  77
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                  (CAB-8) >gi 19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  207417
Seq. No.
Seq. ID
                  LIB3120-020-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g1755154
BLAST score
                  274
                  2.0e-40
E value
                  111
Match length
                  69
% identity
                  (U75188) germin-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi_1755184 (U75203) germin-like protein [Arabidopsis
                  thaliana]
                  207418
Seq. No.
                  LIB3120-020-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1572665
                  328
BLAST score
                  2.0e-30
E value
                  144
Match length
                  50
% identity
                  (U69984) kinesin-like protein K6 [Dictyostelium discoideum]
NCBI Description
                  207419
Seq. No.
                  LIB3120-020-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125578
BLAST score
                  476
                  7.0e-48
E value
Match length
                  122
                  75
% identity
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >qi 167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
                  207420
Seq. No.
                  LIB3120-020-Q1-K1-B10
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI 94567260
BLAST score 496
E value 3.0e-50
Match length 124
% identity 73

NCBI Description (AC006841) putative NADPH dependent mannose 6-phosphate

reductase [Arabidopsis thaliana]

Seq. No. 207421

Seq. ID LIB3120-020-Q1-K1-B11

Method BLASTX NCBI GI g1729927

BLAST score 333 E value 4.0e-31 Match length 120 % identity 53

NCBI Description QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE

TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi\_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No. 207422

Seq. ID LIB3120-020-Q1-K1-B2

Method BLASTX
NCBI GI g2266947
BLAST score 645
E value 9.0e-68
Match length 131
% identity 91

NCBI Description (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium

hirsutum]

Seq. No. 207423

Seq. ID LIB3120-020-Q1-K1-B3

Method BLASTX
NCBI GI g2266947
BLAST score 631
E value 4.0e-66
Match length 133
% identity 87

NCBI Description (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium

hirsutum]

Seq. No. 207424

Seq. ID LIB3120-020-Q1-K1-B4

Method BLASTX
NCBI GI g1532168
BLAST score 260
E value 1.0e-22
Match length 67
% identity 69

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 207425

Seq. ID LIB3120-020-Q1-K1-B6

Method BLASTX
NCBI GI g1616616
BLAST score 443
E value 4.0e-44
Match length 85
% identity 96

NCBI Description (Y08424) small GTP-binding protein [Nicotiana

plumbaginifolia]

Seq. No. 207426

Seq. ID LIB3120-020-Q1-K1-B7

```
Method
                   BLASTX
NCBI GI
                   a2388575
BLAST score
                   189
E value
                   3.0e-14
Match length
                   108
```

% identity NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

207427 Seq. No.

Seq. ID LIB3120-020-Q1-K1-B8

37

Method BLASTX NCBI GI q132819 BLAST score 601 E value 1.0e-62 137 Match length % identity 81

50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24) NCBI Description

>gi\_71307\_pir\_\_R5PM24 ribosomal protein L24 precursor, chloroplast - garden pea >gi\_20873\_emb\_CAA32185\_ (X14020) CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]

Seq. No. 207428

Seq. ID LIB3120-020-Q1-K1-B9

Method BLASTX NCBI GI q1352821 BLAST score 622 E value 5.0e-65 Match length 120 94 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207429

Seq. ID LIB3120-020-Q1-K1-C1

Method BLASTX NCBI GI q1084336 BLAST score 399 E value 7.0e-39 Match length 93 77 % identity

NCBI Description chlorophyll a/b-binding protein type II - Arabidopsis

thaliana >gi 541565 (U03395) PSI type II chlorophyll

a/b-binding protein [Arabidopsis thaliana]

Seq. No. 207430

Seq. ID LIB3120-020-Q1-K1-C10

Method BLASTX NCBI GI g1084321 BLAST score 262 7.0e-23 E value 125 Match length % identity 48

protochlorophyllide reductase (EC 1.3.1.33) - cucumber NCBI Description

>gi\_2244614 dbj BAA21089 (D50085)



133

96

Match length % identity

NCBI Description



## NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]

Seq. No. 207431 LIB3120-020-Q1-K1-C11 Seq. ID Method BLASTX NCBI GI g1653966 BLAST score 250 E value 2.0e-21 100 Match length 50 % identity NCBI Description (D90917) 47 kD protein [Synechocystis sp.] Seq. No. 207432 LIB3120-020-Q1-K1-C12 Seq. ID BLASTX Method q3183247 NCBI GI 271 BLAST score E value 6.0e-24 80 Match length 62 % identity PUTATIVE GTP-BINDING PROTEIN W08E3.3 NCBI Description >gi\_3880615\_emb\_CAB07131\_ (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW:P38219); cDNA EST EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777 comes from this gene; cDNA EST EMB 207433 Seq. No. Seq. ID LIB3120-020-Q1-K1-C3 Method BLASTX q3510538 NCBI GI 316 BLAST score 3.0e-29 E value Match length 74 77 % identity NCBI Description (U93167) expansin [Prunus armeniaca] 207434 Seq. No. Seq. ID LIB3120-020-Q1-K1-C4 Method BLASTX NCBI GI q1946367 BLAST score 540 E value 2.0e-55 Match length 126 % identity (U93215) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 207435 LIB3120-020-Q1-K1-C6 Seq. ID Method BLASTX NCBI GI g3334320 BLAST score 677 2.0e-71 E value

28508

ribosome-associated protein p40 [Glycine max]

40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)



354

76

93

1.0e-33

BLAST score

Match length % identity

E value

```
207436
Seq. No.
                  LIB3120-020-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g3914605
NCBI GI
                  228
BLAST score
                  6.0e-19
E value
                  97
Match length
% identity
                  53
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857 (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Malus domestica]
                  207437
Seq. No.
                  LIB3120-020-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  612
E value
                  9.0e-64
Match length
                  154
% identity
                  79
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBL Description
                  207438
Seq. No.
Seq. ID
                  LIB3120-020-Q1-K1-C9
Method
                  BLASTX
                  g2829899
NCBI GI
                  178
BLAST score
                  7.0e-13
E value
Match length
                  133
% identity
                   33
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   qp AJ001449 2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
                   207439
Seq. No.
                  LIB3120-020-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   g2702281
NCBI GI
                   496
BLAST score
                   3.0e-50
E value
                   125
Match length
                   43
% identity
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   207440
Seq. No.
                   LIB3120-020-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   g488571
NCBI GI
```





## NCBI Description (U09462) histone H3.2 [Medicago sativa]

Seq. No. 207441

Seq. ID LIB3120-020-Q1-K1-D11

Method BLASTX
NCBI GI g2827076
BLAST score 495
E value 2.0e-50
Match length 97
% identity 95

NCBI Description (AF020269) malate dehydrogenase precursor [Medicago sativa]

Seq. No. 207442

Seq. ID LIB3120-020-Q1-K1-D12

Method BLASTX
NCBI GI g4538961
BLAST score 157
E value 7.0e-14
Match length 82
% identity 60

NCBI Description (AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis

chaliana]

Seq. No. 207443

Seq. ID LIB3120-020-Q1-K1-D2

Method BLASTX
NCBI GI g4371290
BLAST score 286
E value 1.0e-25
Match length 74
% identity 65

NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

Seq. No. 207444

Seq. ID LIB3120-020-Q1-K1-D3

Method BLASTX
NCBI GI g548774
BLAST score 422
E value 1.0e-41
Match length 121
% identity 69

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal

protein L7a - rice >gi 303855 dbj BAA02156 (D12631)

ribosomal protein L7A [Oryza sativa]

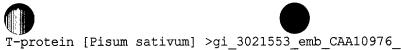
Seq. No. 207445

Seq. ID LIB3120-020-Q1-K1-D4

Method BLASTX
NCBI GI g3915699
BLAST score 297
E value 7.0e-27
Match length 62
% identity 87

NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T

PROTEIN) >gi\_541970\_pir\_\_S40260 T-protein - garden pea >gi\_1362061\_pir\_\_S56661 glycine decarboxylase T protein precursor - garden pea >gi\_438217\_emb\_CAA81080\_ (Z25861)



Seq. No. 207446

Seq. ID LIB3120-020-Q1-K1-D5

Method BLASTX
NCBI GI g2119927
BLAST score 240
E value 3.0e-20
Match length 121
% identity 53

NCBI Description translation elongation factor G, chloroplast - soybean

(AJ222771) T protein [Pisum sativum]

Seq. No. 207447

Seq. ID LIB3120-020-Q1-K1-D6

Method BLASTX
NCBI GI g3860264
BLAST score 688
E value 1.0e-72
Match length 142
% identity 86

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 207448

Seq. ID LIB3120-020-Q1-K1-D8

Method BLASTX
NCBI GI g4006881
BLAST score 298
E value 5.0e-27
Match length 134
% identity 39

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 207449

Seq. ID LIB3120-020-Q1-K1-E1

Method BLASTX
NCBI GI g2827141
BLAST score 605
E value 2.0e-63
Match length 136
% identity 85

NCBI Description (AF027173) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 207450

Seq. ID LIB3120-020-Q1-K1-E10

Method BLASTX
NCBI GI g2119927
BLAST score 665
E value 5.0e-70
Match length 137
% identity 95

NCBI Description translation elongation factor G, chloroplast - soybean

Seq. No. 207451

Seq. ID LIB3120-020-Q1-K1-E12

Method BLASTX



NCBI GI g421826 BLAST score 441 E value 9.0e-44 Match length 135 % identity 63

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis

thalianal

Seq. No. 207452

Seq. ID LIB3120-020-Q1-K1-E2

Method BLASTX
NCBI GI g1352821
BLAST score 634
E value 2.0e-66
Match length 118
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207453

Seq. ID LIB3120-020-Q1-K1-E4

Method BLASTX
NCBI GI g3176726
BLAST score 201
E value 1.0e-15
Match length 141
% identity 34

NCBI Description (AC002392) putative serine proteinase [Arabidopsis

thaliana]

Seq. No. 207454

Seq. ID LIB3120-020-Q1-K1-E5

Method BLASTX
NCBI GI g1174592
BLAST score 671
E value 9.0e-71
Match length 140
% identity 94

NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 207455

Seq. ID LIB3120-020-Q1-K1-E6

Method BLASTX
NCBI GI g1773330
BLAST score 601
E value 1.0e-62
Match length 129
% identity 92

NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No. 207456

```
Seq. ID
                  LIB3120-020-Q1-K1-E7
Method
                  BLASTN
NCBI GI
                  g2564051
BLAST score
                  34
                  1.0e-09
E value
Match length
                   58
% identity
                  90
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  207457
Seq. ID
                  LIB3120-020-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4091080
BLAST score
                  298
                   5.0e-27
E value
                  110
Match length
% identity
                   55
                  (AF045571) nucleic acid binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  207458
                  LIB3120-020-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1839188
BLAST score
                   515
                   2.0e-52
E value
Match length
                  131
% identity
                   71
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                   207459
Seq. No.
                   LIB3120-020-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3193285
BLAST score
                   168
E value
                   9.0e-12
Match length
                   97
                   34
% identity
NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
Seq. No.
                   207460
                   LIB3120-020-Q1-K1-F10
Seq. ID
Method.
                   BLASTX
NCBI GI
                   g131384
BLAST score
                   509
                   1.0e-51
E value
```

Match length 112 % identity 86

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 81934 pir S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi 20621 emb CAA33408 (X15350) precursor (AA

-81 to 248) [Pisum sativum] >gi\_344004\_dbj\_BAA02554\_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi 226937 prf 1611461A 02 evolving

complex 33kD protein [Arachis hypogaea]

BLAST score

427



```
207461
Seq. No.
Seq. ID
                  LIB3120-020-Q1-K1-F3
                  BLASTX
Method
                  g3599968
NCBI GI
BLAST score
                  222
E value
                  4.0e-18
Match length
                  48
                  92
% identity
                  (AF032123) clp protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  207462
Seq. ID
                  LIB3120-020-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q1706336
BLAST score
                  335
                  2.0e-31
E value
Match length
                  84
% identity
                  71
                  UROPORPHYRINOGEN DECARBOXYLASE >gi 1001337 dbj BAA10824
NCBI Description
                   (D64006) uroporphyrinogen decarboxylase [Synechocystis sp.]
Seq. No.
                  207463
Seq. ID
                  LIB3120-020-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g1495251
BLAST score
                  563
E value
                   4.0e-58
Match length
                  133
                  83
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  207464
                  LIB3120-020-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                   q3462351
NCBI GI
BLAST score
                   276
                   2.0e-24
E value
Match length
                   142
                   42
% identity
                  (U85647) small optic lobes homolog [Homo sapiens]
NCBI Description
                  207465
Seq. No.
Seq. ID
                  LIB3120-020-Q1-K1-F9
                  BLASTX
Method
NCBI GI
                   g508304
BLAST score
                   346
E value
                   6.0e-33
                   79
Match length
                   80
% identity
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                   207466
Seq. ID
                  LIB3120-020-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   g3288821
```

```
E value
Match length
                  104
                  79
% identity
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  207467
Seq. No.
Seq. ID
                  LIB3120-020-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  450
E value
                  6.0e-45
Match length
                  91
% identity
                  92
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  207468
Seq. ID
                  LIB3120-020-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g294062
BLAST score
                  155
E value
                  3.0e-10
Match length
                  105
                  34
% identity
                 (L06469) major latex protein [Papaver somniferum]
NCBI Description
                  207469
Seq. No.
                  LIB3120-020-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  q1871577
NCBI GI
BLAST score
                  227
                  1.0e-18
E value
                  106
Match length
                  42
% identity
                 (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                  207470
Seq. No.
Seq. ID
                  LIB3120-020-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1063400
BLAST score
                  434
                  6.0e-43
E value
                  94
Match length
                  91
% identity
NCBI Description (X92888) glycolate oxidase [Lycopersicon esculentum]
```

Seq. No. 207471

Seq. ID LIB3120-020-Q1-K1-G5

Method BLASTX
NCBI GI g1063400
BLAST score 220
E value 5.0e-18

Match length 94

% identity 56

NCBI Description (X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No. 207472

Seq. ID LIB3120-020-Q1-K1-G8

Method BLASTX
NCBI GI g4102703
BLAST score 337
E value 1.0e-31
Match length 105
% identity 70

NCBI Description (AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis

thaliana]

Seq. No. 207473

Seq. ID LIB3120-020-Q1-K1-G9

Method BLASTX
NCBI GI g730645
BLAST score 151
E value 4.0e-10
Match length 33
% identity 91

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi\_629556\_pir\_S43412 ribosomal protein S15 - Arabidopsis thaliana >gi\_313152\_emb CAA80679

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi\_313188\_emb\_CAA80681\_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi\_1903366\_gb\_AAB70449\_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788,gb ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 207474

Seq. ID LIB3120-020-Q1-K1-H1

Method BLASTX
NCBI GI g3201969
BLAST score 474
E value 1.0e-47
Match length 116
% identity 70

NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No. 207475

Seq. ID LIB3120-020-Q1-K1-H10

Method BLASTX
NCBI GI g20729
BLAST score 154
E value 2.0e-10
Match length 46
% identity 65

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 207476

Seq. ID LIB3120-020-Q1-K1-H2

Method BLASTX
NCBI GI 93128175
BLAST score 180
E value 3.0e-13

```
100
```

Match length 100 % identity 39

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 207477

Seq. ID LIB3120-020-Q1-K1-H3

Method BLASTX
NCBI GI g231688
BLAST score 383
E value 2.0e-43
Match length 113
% identity 79

NCBI Description CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC

1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No. 207478

Seq. ID LIB3120-020-Q1-K1-H4

Method BLASTX
NCBI GI g3341679
BLAST score 479
E value 3.0e-48
Match length 133
% identity 69

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 207479

Seq. ID LIB3120-020-Q1-K1-H6

Method BLASTX
NCBI GI g2493694
BLAST score 202
E value 7.0e-16
Match length 40
% identity 93

NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII

6.1 KD PROTEIN) >gi\_1076268\_pir\_\_S53025 photosystem II protein - spinach >gi\_728716 emb\_CAA59409\_ (X85038) protein

of photosystem II [Spinacia oleracea]

Seq. No. 207480

Seq. ID LIB3120-020-Q1-K1-H7

Method BLASTX
NCBI GI g3894190
BLAST score 306
E value 4.0e-30
Match length 115
% identity 56

NCBI Description (AC005662) putative RNA polymerase [Arabidopsis thaliana]

Seq. No. 207481

Seq. ID LIB3120-020-Q1-K1-H9

Method BLASTX
NCBI GI g2388578
BLAST score 210
E value 4.0e-17
Match length 77

% identity

(AC000098) Similar to Mycobacterium RlpF (gb Z84395). ESTs gb T75785, gb R30580, gb T04698 come from this gene.

[Arabidopsis thaliana]

Seq. No. 207482

NCBI Description

Seq. ID LIB3120-021-Q1-K1-A12

Method BLASTX NCBI GI g1652865 BLAST score 298 E value 5.0e-27 Match length 138 % identity 46

NCBI Description (D90909) NADH dehydrogenase [Synechocystis sp.]

207483 Seq. No.

Seq. ID LIB3120-021-Q1-K1-A4

Method BLASTX NCBI GI g2864617 BLAST score 233 E value 2.0e-19 Match length 117 % identity 45

(AL021811) H+-transporting ATP synthase chain9 - like NCBI Description

protein [Arabidopsis thaliana]

Seq. No. 207484

Seq. ID LIB3120-021-Q1-K1-A6

Method BLASTX NCBI GI g3914605 BLAST score 696 1.0e-73 E value Match length 148 90 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE NCBI Description

PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi 415852 emb CAA79857 (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

207485 Seq. No.

Seq. ID LIB3120-021-Q1-K1-A8

Method BLASTX g2459429 NCBI GI BLAST score 245 7.0e-21 E value Match length 70 % identity

(AC002332) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 207486

LIB3120-021-Q1-K1-A9 Seq. ID

Method BLASTX NCBI GI g113214 BLAST score 306 3.0e-38 E value

28518



207487

Match length % identity 76

NCBI Description

ACTIN 1 >gi\_71633\_pir\_\_ATMUM1 actin - Arabidopsis thaliana >gi\_2129521\_pir\_\_S68111 actin 1 - Arabidopsis thaliana >gi\_166582 (M20016) actin-1 [Arabidopsis thaliana]

>gi 1145693 (U39449) actin [Arabidopsis thaliana]

Seq. No.

Seq. ID

LIB3120-021-Q1-K1-B1

Method BLASTX NCBI GI q118564 BLAST score 371 E value 7.0e-36

97 Match length 73 % identity

NCBI Description

GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi\_65955\_pir\_\_DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber

>gi 18264 emb CAA41434 (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi\_18275\_emb\_CAA32764\_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No.

207488

Seq. ID

LIB3120-021-Q1-K1-B10

Method BLASTX NCBI GI q266893 BLAST score 610 E value 1.0e-63 Match length 117 % identity 99

NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 322416 pir S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi 18284 emb CAA47906 (X67674) rubisco activase [Cucumis

sativus]

Seq. No.

207489

Seq. ID

LIB3120-021-Q1-K1-B11

Method BLASTX NCBI GI g3913651 354 BLAST score E value 1.0e-33 Match length 109 % identity 64

FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR NCBI Description

(FNR) >gi 2225993 emb CAA74359 (Y14032)

ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.

207490

Seq. ID

LIB3120-021-Q1-K1-B12

Method BLASTX NCBI GI g2911073 BLAST score 493 7.0e-50 E value Match length 124 % identity 77



(AL021960) putative protein [Arabidopsis thaliana]

207491 Seq. No.

NCBI Description

LIB3120-021-Q1-K1-B2 Seq. ID

BLASTX Method g2245128 NCBI GI BLAST score 421 2.0e-41 E value 133 Match length 62 % identity

NCBI Description (Z97344) peroxidase [Arabidopsis thaliana]

Seq. No. 207492

LIB3120-021-Q1-K1-B3 Seq. ID

BLASTX Method a118564 NCBI GI 208 BLAST score E value 6.0e-17 Match length 62 68 % identity

GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE NCBI Description

REDUCTASE) (HPR) (GDH) >gi\_65955\_pir\_\_DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber

>gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi\_18275\_emb\_CAA32764\_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

207493 Seq. No.

LIB3120-021-Q1-K1-B4 Seq. ID

BLASTX Method NCBI GI q115833 642 BLAST score E value 2.0e-67 134 Match length % identity

CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR NCBI Description (CAB-10A) (LHCP) >gi 100195 pir S11877 chlorophyll

a/b-binding protein Cab10A - tomato >gi 170394 (M32605)

a-binding protein [Lycopersicon esculentum]

207494 Seq. No.

LIB3120-021-Q1-K1-B5 Seq. ID

Method BLASTX NCBI GI q118564 648 BLAST score E value 5.0e-68 Match length 147 % identity 83

GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE NCBI Description

REDUCTASE) (HPR) (GDH) >gi 65955 pir DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi 18275 emb CAA32764 (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]



Seq. No. 207495

Seq. ID LIB3120-021-Q1-K1-B7

Method BLASTX
NCBI GI g3334299
BLAST score 248
E value 2.0e-27
Match length 116
% identity 63

% identity 63
NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) >gi\_2315211\_emb\_CAA74725\_ (Y14339)

proteasome alpha subunit [Lycopersicon esculentum]

Seq. No. 207496

Seq. ID LIB3120-021-Q1-K1-B8

Method BLASTX
NCBI GI g1352821
BLAST score 620
E value 8.0e-65
Match length 125
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207497

Seq. ID LIB3120-021-Q1-K1-B9

Method BLASTX
NCBI GI g1352821
BLAST score 322
E value 5.0e-30
Match length 91
% identity 76

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207498

Seq. ID LIB3120-021-Q1-K1-C10

Method BLASTX
NCBI GI g1944319
BLAST score 198
E value 4.0e-19
Match length 95
% identity 58

NCBI Description (D31700) cysteine proteinase inhibitor [Glycine max]

>gi\_1944342\_dbj\_BAA19610\_ (D64115) cysteine proteinase

inhibitor [Glycine max]

Seq. No. 207499

Seq. ID LIB3120-021-Q1-K1-C11

Method BLASTX NCBI GI g131772 BLAST score 372

E value

Match length

% identity

2.0e-20

100

50

```
8.0e-36
E value
                  99
Match length
                  76
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  207500
Seq. No.
Seq. ID
                  LIB3120-021-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1181599
                  429
BLAST score
                  1.0e-42
E value
                  112
Match length
                  75
% identity
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                  207501
Seq. No.
                  LIB3120-021-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4239974
BLAST score
                  150
E value
                  8.0e-10
Match length
                  61
% identity
                  49
                  (AB017112) mCAC [Mus musculus]
NCBI Description
Seq. No.
                  207502
Seq. ID
                  LIB3120-021-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  g2494119
BLAST score
                  385
                  3.0e-37
E value
                  116
Match length
% identity
                  66
                  (AC002376) EST gb T04104 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  207503
Seq. No.
                  LIB3120-021-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2997591
BLAST score
                  516
E value
                  1.0e-52
Match length
                  130
                  79
% identity
NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator
                  precursor [Pisum sativum]
Seq. No.
                  207504
                  LIB3120-021-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3785991
BLAST score
                  242
```

28522

NCBI Description

```
Seq. No.
                  207505
Seq. ID
                  LIB3120-021-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1345698
BLAST score
                  675
E value
                  3.0e-71
Match length
                  134
% identity
                  94
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
                  (CAB-151) (LHCP) >gi 99601 pir S20917 chlorophyll
                  a/b-binding protein - upland cotton
                  >gi 452314 emb CAA38025 (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
Seq. No.
                  207506
Seq. ID
                  LIB3120-021-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q1354515
BLAST score
                  229
E value
                  5.0e-19
Match length
                  114
% identity
                  51
NCBI Description
                 (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
                  207507
Seq. No.
                  LIB3120-021-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3785991
BLAST score
                  366
E value
                  4.0e-35
Match length
                  125
% identity
                  59
NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  207508
Seq. ID
                  LIB3120-021-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3785991
BLAST score
                  548
E value
                  2.0e-56
Match length
                  130
% identity
NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]
                  207509
Seq. No.
                  LIB3120-021-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g400986
BLAST score
                  405
E value
                  2.0e-39
Match length
                  143
                  57
% identity
NCBI Description
                  50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
                  >gi_81947_pir__S18001 ribosomal protein L15 precursor,
```

(AC005560) putative MAP kinase [Arabidopsis thaliana]

```
hloroplast - garden pea (fragment) >gi 20867 emb CAA77595
                    (Z11510) Plastid ribosomal protein CL15 [Pisum sativum]
 Seq. No.
                   207510
 Seq. ID
                   LIB3120-021-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   q4417288
BLAST score
                   168
E value
                   9.0e-12
Match length
                   92
 % identity
                   41
NCBI Description
                  (AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.
                   207511
Seq. ID
                   LIB3120-021-Q1-K1-D8
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   222
E value
                   1.0e-121
Match length
                   421
% identity
                   43
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                   207512
                   LIB3120-021-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3894193
BLAST score
                   241
E value
                   2.0e-20
Match length
                   97
% identity
NCBI Description
                   (AC005662) putative strictosidine synthase [Arabidopsis
                   thalianal
Seq. No.
                   207513
Seq. ID
                   LIB3120-021-Q1-K1-E11
Method
                   BLASTX
NCBI GI
                   g1053047
BLAST score
                   538
E value
                   3.0e-55
Match length
                   110
% identity
                   98
NCBI Description
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
                  histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
Seq. No.
                  207514
Seq. ID
                  LIB3120-021-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1006690
BLAST score
                  639
E value
                  5.0e-67
```

Seq. No. 207515

138

87

Match length

NCBI Description

% identity

(X81787) lycopene cyclase [Nicotiana tabacum]

```
B3120-021-Q1-K1-E2
Seq. ID
Method
                  BLASTX
                  g1345674
NCBI GI
BLAST score
                  243
                  1.0e-20
E value
Match length
                  103
                  52
% identity
                  CATALASE ISOZYME 1 >gi_99598_pir__S10770 catalase (EC
NCBI Description
                  1.11.1.6) - upland cotton >gi_18484_emb_CAA36380_ (X52135)
                  catalase subunit 1 (AA 1-492) [Gossypium hirsutum]
                  207516
Seq. No.
                  LIB3120-021-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4105697
                  402
BLAST score
                  3.0e - 39
E value
Match length
                  142
% identity
                  54
                  (AF049870) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
                  207517
Seq. No.
                  LIB3120-021-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708743
BLAST score
                  143
E value
                  7.0e-09
Match length
                  102
% identity
                  32
                  (AC003952) putative Tal-1-like reverse transcriptase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  207518
                  LIB3120-021-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  757
E value
                  8.0e-81
Match length
                  145
                  98
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  207519
Seq. ID
                  LIB3120-021-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g119905
BLAST score
                  252
E value
                  1.0e-23
Match length
                  80
% identity
                  79
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                  >gi_81898_pir__S04030 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - garden pea >gi_20722_emb_CAA30978
                  (X12446) ferredoxin-NADH+ reductase preprotein (AA -52 to
                  308) [Pisum sativum] >gi_226545_prf__1601517A ferredoxin
```

28525

NADP reductase [Arachis hypogaea]



207520 Seq. No. Seq. ID LIB3120-021-Q1-K1-F1 BLASTX Method NCBI GI g289920 252 BLAST score 5.0e-22 E value 67 Match length 75 % identity (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 207521 Seq. No. Seq. ID LIB3120-021-Q1-K1-F10 Method BLASTX NCBI GI q4469011 BLAST score 607 3.0e-63 E value Match length 137 % identity 82 (AL035602) carbohydrate kinase-like protein [Arabidopsis NCBI Description thaliana] 207522 Seq. No. Seq. ID LIB3120-021-Q1-K1-F11 Method BLASTX NCBI GI q464980 BLAST score 674 4.0e-71 E value Match length 135 % identity 93 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_166422 (L06967) ubiquitin carrier protein [Medicago sativa] 207523 Seq. No. Seq. ID LIB3120-021-Q1-K1-F3 Method BLASTX NCBI GI q4218120 101 BLAST score 6.0e-10 E value Match length 68 47 % identity (AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description thaliana] 207524 Seq. No.

Seq. ID LIB3120-021-Q1-K1-F5

Method BLASTX NCBI GI g4218120 BLAST score 457 E value 1.0e-45 Match length 141 % identity 61

(AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description

thaliana]

```
Seq. No.
                  LIB3120-021-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  g100200
NCBI GI
                  392
BLAST score
E value
                  6.0e-43
Match length
                  122
                  75
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                  207526
Seq. ID
                  LIB3120-021-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q1545805
BLAST score
                  185
E value
                  2.0e-14
Match length
                  66
% identity
                  58
NCBI Description
                  (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
                  207527
Seq. No.
Seq. ID
                  LIB3120-021-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q1181599
BLAST score
                  426
E value
                  3.0e-42
Match length
                  115
% identity
                  73
NCBI Description
                  (D83007) subunit of photosystem I [Cucumis sativus]
Seq. No.
                  207528
Seq. ID
                  LIB3120-021-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3775993
BLAST score
                  257
E value
                  9.0e-23
Match length
                  74
% identity
                   69
NCBI Description
                  (AJ010460) RNA helicase [Arabidopsis thaliana]
                  207529
Seq. No.
Seq. ID
                  LIB3120-021-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3775993
BLAST score
                   639
E value
                  5.0e-67
Match length
                  136
% identity
                  92
                  (AJ010460) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  207530
Seq. No.
                  LIB3120-021-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231660
BLAST score
                  327
```

28527

2.0e-30

149

E value Match length



% identity

NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.

207531

Seq. ID

LIB3120-021-Q1-K1-H1

Method NCBI GI BLASTX

BLAST score

g125578 403

E value Match length 2.0e-39

% identity

111 73

NCBI Description

PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) >gi 167266 (M73707) phosphoribulokinase

[Mesembryanthemum crystallinum]

Seq. No.

207532

Seq. ID

LIB3120-021-Q1-K1-H12

Method NCBI GI BLASTX g4469011

BLAST score E value

358 3.0e-34

Match length % identity

103

NCBI Description

(AL035602) carbohydrate kinase-like protein [Arabidopsis

thaliana]

Seq. No.

207533

Seq. ID

LIB3120-021-01-K1-H2

Method NCBI GI BLASTX q1173345

BLAST score

170

E value Match length 3.0e-12

% identity

96

42

NCBI Description

SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi 1076403 pir S51838 sedoheptulose-1,7-biphosphatase -

Arabidopsis thaliana >gi 786466 bbs 159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa]

[Arabidopsis thaliana]

Seq. No.

207534

Seq. ID

LIB3120-021-Q1-K1-H3

Method

BLASTX q625547

NCBI GI

BLAST score

380 1.0e-36

E value · Match length

121 64

% identity NCBI Description

chlorophyll a/b-binding protein type I - common tobacco

>gi 493723 emb CAA45523 (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

Seq. No.

207535

Seq. ID

LIB3120-021-Q1-K1-H6



Method BLASTX NCBI GI q3914940 BLAST score 411 E value 3.0e-40 Match length 139 64 % identity

SEDOHEPTULOSE-1, 7-BISPHOSPHATASE CHLOROPLAST PRECURSOR NCBI Description (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE) >gi\_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

[Spinacia oleracea]

Seq. No. 207536

Seq. ID LIB3120-021-Q1-K1-H7

Method BLASTX NCBI GI q289920 BLAST score 657 4.0e-69 E value Match length 125 % identity 97

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

207537 Seq. No.

Seq. ID LIB3120-021-Q1-K1-H8

Method BLASTX q3249065 NCBI GI 556 BLAST score 3.0e-57 E value Match length 139 % identity 75

(AC004473) Similar to HAK1 gb U22945 high affinity NCBI Description

potassium transporter from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

207538 Seq. No.

Seq. ID LIB3120-022-Q1-K1-A1

Method BLASTX NCBI GI q3688182 BLAST score 226 E value 1.0e-35 Match length 102 % identity

(AL031804) P-Protein - like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 207539

LIB3120-022-Q1-K1-A2 Seq. ID

Method BLASTX NCBI GI g3355476 BLAST score 338 E value 9.0e-32 Match length 112 % identity 59

(AC004218) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 207540

LIB3120-022-Q1-K1-A5 Seq. ID

Method BLASTX

28529

```
NCBI GI
                  q4262236
                  313
BLAST score
                  7.0e-29
E value
                  89
Match length
                  72
% identity
                  (AC006200) putative ribose 5-phosphate isomerase
NCBI Description
                  [Arabidopsis thaliana]
                  207541
Seq. No.
Seq. ID
                  LIB3120-022-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3193323
BLAST score
                  563
E value
                  3.0e-58
Match length
                  119
                  92
% identity
NCBI Description
                  (AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm,
                  score: 78.35); identical to Arabidopsis 40S ribosomal
                  protein S13 (fragment) (SW: P49203A) except the first 32
                  amino acids are different [Arabidopsis thaliana]
                  207542
Seq. No.
Seq. ID
                  LIB3120-022-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3914658
                  551
BLAST score
                  9.0e-57
E value
                  124
Match length
% identity
                  80
                  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1694974 emb CAA70851 (Y09635) plastid ribosomal
                  protein [Arabidopsis thaliana]
Seq. No.
                  207543
Seq. ID
                  LIB3120-022-Q1-K1-A9
Method
                  BLASTX
                  g1354515
NCBI GI
BLAST score
                  239
                  3.0e-20
E value
                  110
Match length
                  52
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  207544
Seq. No.
Seq. ID
                  LIB3120-022-Q1-K1-B2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2662343
BLAST score 420
E value 2.0e-41
Match length 115
% identity 75

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 207545

Seq. ID LIB3120-022-Q1-K1-B4

Method BLASTX

28530



NCBI GI BLAST score 314 E value 1.0e-33 Match length 99 73 % identity

chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description

>gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis

thaliana]

207546 Seq. No.

Seq. ID LIB3120-022-Q1-K1-B5

Method BLASTX NCBI GI q125578 382 BLAST score 6.0e-37 E value Match length 101 % identity 70

NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) >gi\_167266 (M73707) phosphoribulokinase

[Mesembryanthemum crystallinum]

207547 Seq. No.

LIB3120-022-Q1-K1-B6 Seq. ID

Method BLASTX NCBI GI q2129753 586 BLAST score 7.0e-61 E value Match length 124 % identity

threonine synthase (EC 4.2.99.2) precursor - Arabidopsis NCBI Description

thaliana (fragment) >gi 1448917 (L41666) threonine synthase

[Arabidopsis thaliana]

Seq. No. 207548

LIB3120-022-Q1-K1-B8 Seq. ID

Method BLASTX NCBI GI q132944 BLAST score 558 E value 1.0e-57 Match length 111 % identity 92

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal

protein L3 (ARP2) - Arabidopsis thaliana >gi 806279

(M32655) ribosomal protein [Arabidopsis thaliana]

207549 Seq. No.

Seq. ID LIB3120-022-Q1-K1-C1

Method BLASTX NCBI GI q1345698 BLAST score 655 E value 5.0e-69 122 Match length 100 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi 99601 pir S20917 chlorophyll

a/b-binding protein - upland cotton

>gi\_452314\_emb\_CAA38025\_ (X54090) chlorophyll ab binding



## protein [Gossypium hirsutum]

207550 Seq. No. Seq. ID LIB3120-022-Q1-K1-C10 Method BLASTX NCBI GI g2851508 BLAST score 173 E value 7.0e-13 Match length 66 42 % identity NCBI Description

BI Description 60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to

ribosomal protein L21 (gb L38826). ESTs

gb\_AA395597,gb\_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi\_3482935 (AC003970) Putative ribosomal protein

L21 [Arabidopsis thaliana]

Seq. No. 207551

Seq. ID LIB3120-022-Q1-K1-C11

Method BLASTX
NCBI GI g118564
BLAST score 413
E value 1.0e-40
Match length 98
% identity 76

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi 65955 pir DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi\_18275\_emb\_CAA32764\_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 207552

Seq. ID LIB3120-022-Q1-K1-C2

Method BLASTX
NCBI GI g3023281
BLAST score 396
E value 1.0e-38
Match length 124
% identity 62

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER

>gi\_2065194\_emb\_CAA64475\_ (X95098) ammonium transporter

[Lycopersicon esculentum]

Seq. No. 207553

Seq. ID LIB3120-022-Q1-K1-C3

Method BLASTX
NCBI GI g2239085
BLAST score 154
E value 3.0e-10
Match length 70
% identity 44

NCBI Description (Z84384) anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

Seq. No. 207554

Seq. ID LIB3120-022-Q1-K1-C5



Method BLASTX
NCBI GI g3193326
BLAST score 151
E value 7.0e-10
Match length 57
% identity 61

NCBI Description (AF069299) contains similarity to transcriptional activators such as Ra-like and myc-like regulatory R

proteins [Arabidopsis thaliana]

Seq. No. 207555

Seq. ID LIB3120-022-Q1-K1-C6

Method BLASTN
NCBI GI g450504
BLAST score 50
E value 2.0e-19
Match length 96
% identity 94

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate

carboxylase, small subunit

Seq. No. 207556

Seq. ID LIB3120-022-Q1-K1-C7

Method BLASTX
NCBI GI g131385
BLAST score 137
E value 1.0e-08
Match length 65
% identity 54

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 207557

Seq. ID LIB3120-022-Q1-K1-C8

Method BLASTX
NCBI GI g3193293
BLAST score 365
E value 6.0e-35
Match length 124
% identity 68

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 207558

Seq. ID LIB3120-022-Q1-K1-D10

Method BLASTX
NCBI GI g4558665
BLAST score 427
E value 2.0e-42
Match length 106
% identity 79

NCBI Description (AC007063) putative white protein [Arabidopsis thaliana]

Seq. No. 207559

Seq. ID LIB3120-022-Q1-K1-D5

```
Method
NCBI GI
                  g4063747
BLAST score
                  358
                  4.0e-34
E value
                  94
Match length
                  74
% identity
                  (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  207560
Seq. ID
                  LIB3120-022-Q1-K1-D7
Method
                  BLASTX
                  g1346155
NCBI GI
                  269
BLAST score
                  4.0e-24
E value
                  73
Match length
                  75
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR
NCBI Description
                  (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                  (SHMT) >gi_481942_pir__S40212 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                  >gi 437995 emb CAA81078 (Z25859) glycine
                  hydroxymethyltransferase [Flaveria pringlei]
                  207561
Seq. No.
Seq. ID
                  LIB3120-022-Q1-K1-D8
                  BLASTX
Method
NCBI GI
                  q3924597
BLAST score
                  191
                  1.0e-14
E value
                  97
Match length
                  37
% identity
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                  207562
Seq. No.
Seq. ID
                  LIB3120-022-Q1-K1-D9
                  BLASTX
Method
NCBI GI
                  q167367
BLAST score
                  364
E value
                  6.0e-35
                  100
Match length
                  71
% identity
NCBI Description
                  (L08199) peroxidase [Gossypium hirsutum]
                  207563
Seq. No.
Seq. ID
                  LIB3120-022-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q131392
                  306
BLAST score
E value
                  5.0e-28
                  109
Match length
% identity
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi 81479 pir S00005 photosystem II oxygen-evolving
                  complex protein 2 precursor - spinach
```

>gi\_21265\_emb\_CAA29055\_ (X05511) 23 kDa OEC protein
[Spinacia oleracea] >gi 225596 prf 1307179A luminal



protein 23kD [Spinacia oleracea] 207564 Seq. No. Seq. ID LIB3120-022-Q1-K1-E12 Method BLASTX NCBI GI g100200 BLAST score 145 2.0e-09 E value 78 Match length % identity 45 chlorophyll a/b-binding protein type I precursor - tomato NCBI Description 207565 Seq. No. Seq. ID LIB3120-022-Q1-K1-E2 BLASTX Method NCBI GI g2501353 BLAST score 396 1.0e-38 E value 124 Match length 51 % identity NCBI Description TRANSKETOLASE, CHLOROPLAST (TK) >gi\_1084440\_pir\_\_S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi\_664901\_emb\_CAA86607\_ (Z46646) transketolase [Craterostigma plantagineum] 207566 Seq. No. Seq. ID LIB3120-022-Q1-K1-E3 Method BLASTX g133409 NCBI GI BLAST score 537 4.0e-55 E value Match length 119 % identity 87 DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN NCBI Description >gi 66962 pir RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast >gi 11860 emb CAA77376 (Z00044) RNA polymerase alpha subunit [Nicotiana tabacum] >gi 225228 prf 1211235BK RNA polymerase alpha [Nicotiana tabacum] 207567 Seq. No. Seq. ID LIB3120-022-Q1-K1-E4 Method BLASTX NCBI GI g3202030 BLAST score 588 4.0e-61 E value Match length 122 % identity 90 (AF069318) geranylgeranyl hydrogenase [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 207568

Seq. ID LIB3120-022-Q1-K1-E5

Method BLASTX
NCBI GI g1946367
BLAST score 457
E value 8.0e-46

28535



Match length 76 % identity

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No.

207569 Seq. ID LIB3120-022-Q1-K1-E6

Method BLASTX g3036796 NCBI GI

BLAST score 315 4.0e-29 E value

Match length 121 % identity 51

NCBI Description (AL022373) putative protein [Arabidopsis thaliana]

>gi 3805858 emb CAA21478 (AL031986) putative protein

[Arabidopsis thaliana]

207570 Seq. No.

Seq. ID LIB3120-022-Q1-K1-E7

Method BLASTX NCBI GI q4467098 BLAST score 360 E value 2.0e-34 Match length 126 % identity 65

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 207571

Seq. ID LIB3120-022-Q1-K1-E8

Method BLASTX NCBI GI g417060 BLAST score 225 E value 8.0e-19 Match length 86 % identity 51

NCBI Description

GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS) >gi 170637 (M94765) glutamine synthetase

[Vigna aconitifolia] >gi\_1094850\_prf\_\_2106409A Gln

synthetase [Vigna aconitifolia]

Seq. No. 207572

Seq. ID LIB3120-022-Q1-K1-F12

Method BLASTX NCBI GI g131397 BLAST score 287 8.0e-26 E value Match length 129 % identity 52

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

> SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_81480 pir S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802 emb CAA29056 (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 207573

```
Seq. ID
                  LIB3120-022-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3023752
BLAST score
                  345
                  1.0e-32
E value
Match length
                  127
                  57
% identity
                  FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
NCBI Description
                  ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                  207574
Seq. ID
                  LIB3120-022-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2137562
BLAST score
                  366
                  4.0e-35
E value
                  111
Match length
                  62
% identity
                  mouse Dhm1 protein - mouse >gi_1060921_dbj_BAA07524_
NCBI Description
                  (D38517) Dhm1 protein [Mus musculus]
Seq. No.
                  207575
Seq. ID
                  LIB3120-022-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g120659
BLAST score
                  523
E value
                  2.0e-53
Match length
                  119
                  87
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                  >gi_81721_pir__B24796 glyceraldehyde-3-phosphate
                  dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13),
                  chloroplast - white mustard (fragment)
                  >gi_829288_emb_CAA27845_ (X04302) chloroplast GAPDH (233aa)
                  [Sinapis alba]
Seq. No.
                  207576
Seq. ID
                  LIB3120-022-Q1-K1-F8
Method
                  BLASTX
                  g20729
NCBI GI
BLAST score
                  159
E value
                  2.0e-11
Match length
                  57
% identity
                  61
NCBI Description
                 (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                  207577
                  LIB3120-022-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194125
BLAST score
                  617
E value
                  2.0e-64
Match length
                  120
```

28537

(AC002062) ESTs gb R30459, gb N38441 come from this gene.

91

[Arabidopsis thaliana]

% identity

NCBI Description

```
Seq. No.
                  207578
Seq. ID
                  LIB3120-022-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2315140
BLAST score
                  380
                  7.0e-46
E value
Match length
                  101
                  94
% identity
                  (AB006187) S-adenosylmethionine synthase [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  207579
Seq. ID
                  LIB3120-022-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g266938
BLAST score
                  174
                  9.0e-21
E value
                  66
Match length
                  65
% identity
NCBI Description
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L33 >gi 336929 (M81884)
                  ribosomal protein L33 [Epifagus virginiana]
Seq. No.
                  207580
Seq. ID
                  LIB3120-022-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g114640
BLAST score
                  521
E value
                  2.0e-53
                  113
Match length
                  89
% identity
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_282923_pir__S27976 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - garden pea
                  >gi_20654_emb_CAA45150_ (X63604) ATP synthase (gamma
                  subunit) [Pisum sativum]
Seq. No.
                  207581
Seq. ID
                  LIB3120-022-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g231688
BLAST score
                  619
E value
                  9.0e-65
Match length
                  121
% identity
                  97
NCBI Description
                  CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC
                  1.11.1.6) - upland cotton >gi_18488 emb_CAA39998
                                                                      (X56675)
                  subunit 2 of cotton catalase [Gossypium hirsutum]
Seq. No.
                  207582
Seq. ID
                  LIB3120-022-Q1-K1-G4
Method
```

BLASTX NCBI GI q3242704 BLAST score 148 E value 2.0e-09 Match length 45 % identity 62

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]



Seq. No. 207583

Seq. ID LIB3120-022-Q1-K1-G5

Method BLASTX
NCBI GI g1352821
BLAST score 641
E value 3.0e-67
Match length 124
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207584

Seq. ID LIB3120-022-Q1-K1-G6

Method BLASTX
NCBI GI g289920
BLAST score 514
E value 2.0e-52
Match length 105
% identity 92

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207585

Seq. ID LIB3120-022-Q1-K1-G7

Method BLASTN
NCBI GI g4388705
BLAST score 41
E value 9.0e-14
Match length 101
% identity 85

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 207586

Seq. ID LIB3120-022-Q1-K1-G8

Method BLASTX
NCBI GI g1707998
BLAST score 586
E value 7.0e-61
Match length 126
% identity 88

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi 481944 pir S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi\_438247\_emb\_CAA81082 (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 207587

Seq. ID LIB3120-022-Q1-K1-G9

Method BLASTX NCBI GI g400992 BLAST score 208

E value 1.0e-16

Match length 65
% identity 66

NCBI Description 50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR (CL28)
>gi\_279656\_pir\_\_R5NT28 ribosomal protein L28 precursor,
chloroplast - tobacco >gi\_20016\_emb\_CAA48211\_ (X68078)
ribosomal protein CL28 [Nicotiana tabacum]

 Seq. No.
 207588

 Seq. ID
 LIB3120-022-Q1-K1-H1

 Method
 BLASTX

 NCBI GI
 g4103324

 BLAST score
 582

 E value
 2.0e-60

Match length 123 % identity 90

NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum

tuberosum]

Seq. No. 207589

Seq. ID LIB3120-022-Q1-K1-H2

Method BLASTX
NCBI GI g2677828
BLAST score 338
E value 5.0e-32
Match length 96
% identity 64

NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 207590

Seq. ID LIB3120-022-Q1-K1-H3

Method BLASTX
NCBI GI g2494415
BLAST score 557
E value 2.0e-57
Match length 119
% identity 87

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi\_515747 (L34841) fructose-1,6-bisphosphatase [Glycine

max]

Seq. No. 207591

Seq. ID LIB3120-022-Q1-K1-H4

Method BLASTX
NCBI GI g3559807
BLAST score 300
E value 1.0e-27
Match length 94
% identity 74

NCBI Description (Y15628) HCF136 protein [Arabidopsis thaliana]

Seq. No. 207592

Seq. ID LIB3120-022-Q1-K1-H5

Method BLASTX NCBI GI g1707998 BLAST score 184

```
E value
                   0e-14
Match length
                  47
% identity
                  77
NCBI Description
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                  (SHMT) >gi 481944 pir S40218 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi 438247 emb CAA81082 (Z25863) glycine
                  hydroxymethyltransferase [Solanum tuberosum]
                  207593
Seq. No.
                  LIB3120-022-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2351210
BLAST score
                  194
E value
                  3.0e-15
Match length
                  76
                  55
% identity
NCBI Description
                  (D88263) chalcone synthase [Pisum sativum]
Seq. No.
                  207594
Seq. ID
                  LIB3120-022-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3913651
BLAST score
                  409
E value
                  4.0e-40
                  96
Match length
% identity
                  80
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                  207595
Seq. ID
                  LIB3120-023-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  q4263507
BLAST score
                  154
                  2.0e-10
E value
Match length
                  95
                  34
% identity
NCBI Description
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  207596
Seq. ID
                  LIB3120-023-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  q1181599
BLAST score
                  292
E value
                  1.0e-26
```

Match length 86 % identity 67

NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]

Seq. No.

207597

Seq. ID

LIB3120-023-Q1-K1-A11

Method BLASTX NCBI GI q729409 BLAST score 304



E value Match length 85 74 % identity

NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi 478398 pir JQ2240 translation elongation factor Tu

precursor - common tobacco chloroplast

>gi 480040\_pir\_\_S36183 translation elongation factor Tu.A precursor, chloroplast - wood tobacco >gi 170344 (M94204) translation elongation factor EF-Tu [Nicotiana tabacum] >gi 459239 dbj BAA02027 (D11469) chloroplast elongation

factor TuA(EF-TuA) [Nicotiana sylvestris]

207598 Seq. No.

Seq. ID LIB3120-023-Q1-K1-A7

Method BLASTX NCBI GI g3128177 BLAST score 353 7.0e-34 E value 84 Match length 82 % identity

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

207599 Seq. No.

Seq. ID LIB3120-023-Q1-K1-A8

Method BLASTX NCBI GI q132866 BLAST score 530 2.0e-54 E value 121 Match length 87 % identity

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi 71086 pir R5NT2

ribosomal protein L2 - common tobacco chloroplast

>gi\_435269\_emb\_CAA77384\_ (Z00044) ribosomal protein L2
[Nicotiana tabacum] >gi\_1223691\_emb\_CAA77409\_ (Z00044)

ribosomal protein L2 [Nicotiana tabacum]

>gi 225238 prf 1211235BW ribosomal protein L2 [Nicotiana

tabacum]

Seq. No. 207600

Seq. ID LIB3120-023-Q1-K1-A9

Method BLASTX NCBI GI g132677 BLAST score 207 E value 2.0e-16 Match length 118 47 % identity

50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) NCBI Description

> >gi\_71241\_pir\_\_R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi\_16497\_emb\_CAA77593\_

(Z11508) Plastid ribosomal protein CL15 [Arabidopsis

thaliana]

Seq. No. 207601

Seq. ID LIB3120-023-Q1-K1-B12

Method BLASTX NCBI GI q3334201 BLAST score 242



E value 8.0e-21
Match length 70
% identity 67

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 1724106

(U79768) glycine cleavage system protein H precursor

[Mesembryanthemum crystallinum]

Seq. No. 207602

Seq. ID LIB3120-023-Q1-K1-B4

Method BLASTX
NCBI GI g131397
BLAST score 220
E value 3.0e-18
Match length 81
% identity 59

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480 pir S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi\_225597\_prf\_ 1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 207603

Seq. ID LIB3120-023-Q1-K1-B7

Method BLASTX
NCBI GI g505482
BLAST score 348
E value 4.0e-33
Match length 104
% identity 72

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 207604

Seq. ID LIB3120-023-Q1-K1-B9

Method BLASTX
NCBI GI g3023752
BLAST score 266
E value 7.0e-24
Match length 108
% identity 61

NCBI Description FERREDOXIN I PRECURSOR >gi\_1418982 emb CAA99756 (Z75520)

ferredoxin-I [Lycopersicon esculentum]

Seq. No. 207605

Seq. ID LIB3120-023-Q1-K1-C1

Method BLASTX
NCBI GI g3175990
BLAST score 302
E value 1.0e-27
Match length 59
% identity 97

NCBI Description (AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No. 207606



```
LIB3120-023-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g3063448
NCBI GI
                  344
BLAST score
                  2.0e-32
E value
Match length
                  111
                  53
% identity
NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]
Seq. No.
                  207607
                  LIB3120-023-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739375
BLAST score
                  285
                  1.0e-25
E value
Match length
                  105
% identity
                  63
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                  207608
                  LIB3120-023-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4249404
BLAST score
                  280
E value
                  4.0e-25
Match length
                  95
                  57
% identity
NCBI Description
                  (AC006072) putative nuclear protein SA-1 [Arabidopsis
                  thaliana]
                  207609
Seq. No.
                  LIB3120-023-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g2583108
NCBI GI
BLAST score
                   389
                  5.0e-38
E value
                  90
Match length
                  86
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                   207610
Seq. No.
                  LIB3120-023-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g4406530
NCBI GI
BLAST score
                   214
                  2.0e-17
E value
                  88
Match length
                  56
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
                   207611
Seq. No.
                  LIB3120-023-Q1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131384
```

6.0e-31 Match length 87

330

BLAST score

E value

28544



% identity
NCBI Description

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi\_81934\_pir\_\_S04132

photosystem II oxygen-evolving complex protein 1 precursor
- garden pea >gi\_20621\_emb\_CAA33408\_ (X15350) precursor (AA

-81 to 248) [Pisum sativum] >gi\_344004 dbj\_BAA02554\_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi\_226937 prf\_1641461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 207612

Seq. ID LIB3120-023-Q1-K1-C8

Method BLASTX
NCBI GI g2583108
BLAST score 194
E value 3.0e-15
Match length 69
% identity 59

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 207613

Seq. ID LIB3120-023-Q1-K1-D1

Method BLASTX
NCBI GI g1345698
BLAST score 643
E value 2.0e-67
Match length 132
% identity 91

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

a/b-binding protein - upland cotton

>gi\_452314\_emb\_CAA38025\_ (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 207614

Seq. ID LIB3120-023-Q1-K1-D2

Method BLASTX
NCBI GI g1658197
BLAST score 397
E value 1.0e-38
Match length 82
% identity 85

NCBI Description (U74630) calreticulin [Ricinus communis] >gi\_1763297

(U74631) calreticulin [Ricinus communis]

Seq. No. 207615

Seq. ID LIB3120-023-Q1-K1-D4

Method BLASTX
NCBI GI g131399
BLAST score 362
E value 9.0e-35
Match length 84
% identity 81

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411

photosystem II 10K protein precursor - potato



>gi\_21489\_emb\_CAA28450\_ (X04753) ST-LS1 protein [Solanum tuberosum]

Seq. No. 207616

Seq. ID LIB3120-023-Q1-K1-D6

Method BLASTX
NCBI GI g1352821
BLAST score 198
E value 5.0e-22
Match length 73
% identity 68

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207617

Seq. ID LIB3120-023-Q1-K1-D7

Method BLASTX
NCBI GI g3319882
BLAST score 290
E value 2.0e-26
Match length 76
% identity 72

NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer

arietinum]

Seq. No. 207618

Seq. ID LIB3120-023-Q1-K1-D9

Method BLASTX
NCBI GI g3983125
BLAST score 141
E value 6.0e-09
Match length 80
% identity 45

NCBI Description (AF097648) phosphate/triose-phosphate translocator

precursor [Arabidopsis thaliana]

Seq. No. 207619

Seq. ID LIB3120-023-Q1-K1-E1

Method BLASTX
NCBI GI g119150
BLAST score 343
E value 2.0e-42
Match length 94
% identity 94

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi\_19273\_emb\_CAA32618 (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

 $>gi_295810_emb_CAA37212_ (X53043)$  elongation factor 1-alpha

[Lycopersicon esculentum]

Seq. No. 207620

Seq. ID LIB3120-023-Q1-K1-E10

Method BLASTX

```
NCBI GI
                  q1709825
BLAST score
                  139
                  1.0e-08
E value
Match length
                  78
% identity
                  51
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  207621
Seq. ID
                  LIB3120-023-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q1781348
BLAST score
                  249
                  2.0e-21
E value
Match length
                  54
                  87
% identity
NCBI Description
                  (Y10380) homologous to plastidic aldolases [Solanum
                  tuberosum]
Seq. No.
                  207622
Seq. ID
                  LIB3120-023-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2191150
BLAST score
                  199
E value
                  2.0e-15
Match length
                  72
                  68
% identity
NCBI Description
                  (AF007269) similar to mitochondrial carrier family
                  [Arabidopsis thaliana]
                  207623
Seq. No.
Seq. ID
                  LIB3120-023-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q3023752
```

Method BLASTX
NCBI GI g3023752
BLAST score 238
E value 4.0e-20
Match length 83
% identity 61

NCBI Description FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)

ferredoxin-I [Lycopersicon esculentum]

Seq. No. 207624

Seq. ID LIB3120-023-Q1-K1-F11

Method BLASTX
NCBI GI g217909
BLAST score 604
E value 6.0e-63
Match length 125
% identity 95

NCBI Description (D14044) glycolate oxidase [Cucurbita sp.]

Seq. No. 207625

Seq. ID LIB3120-023-Q1-K1-F12

Method BLASTX
NCBI GI g3202030
BLAST score 430
E value 2.0e-42



Match length 135 % identity 67

NCBI Description (AF069318) geranylgeranyl hydrogenase [Mesembryanthemum

crystallinum]

Seq. No. 207626

Seq. ID LIB3120-023-Q1-K1-F2

Method BLASTX
NCBI GI g294845
BLAST score 246
E value 7.0e-21
Match length 100
% identity 49

NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar

H65-7052]

Seq. No. 207627

Seq. ID LIB3120-023-Q1-K1-F3

Method BLASTX
NCBI GI 94008010
BLAST score 243
E value 7.0e-21
Match length 86
% identity 55

NCBI Description (AF084036) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 207628

Seq. ID LIB3120-023-Q1-K1-F4

Method BLASTX
NCBI GI g1709651
BLAST score 360
E value 3.0e-34
Match length 115
% identity 62

NCBI Description PLASTOCYANIN A PRECURSOR >gi\_2117431\_pir\_\_S58209

plastocyanin a precursor - black poplar

>gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 207629

Seq. ID LIB3120-023-Q1-K1-F8

Method BLASTX
NCBI GI g3341679
BLAST score 232
E value 1.0e-19
Match length 59
% identity 81

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 207630

Seq. ID LIB3120-023-Q1-K1-G11

Method BLASTX
NCBI GI g100196
BLAST score 339
E value 3.0e-32



Match length 80 % identity 80

NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No. 207631

Seq. ID LIB3120-023-Q1-K1-G4

Method BLASTX
NCBI GI g2739168
BLAST score 292
E value 2.0e-26
Match length 106

NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana

tabacum]

Seq. No. 207632

% identity

Seq. ID LIB3120-023-Q1-K1-G7

55

Method BLASTX
NCBI GI g505482
BLAST score 305
E value 3.0e-28
Match length 85
% identity 78

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 207633

Seq. ID LIB3120-023-Q1-K1-H1

Method BLASTX
NCBI GI g1352821
BLAST score 408
E value 4.0e-40
Match length 80
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207634

Seq. ID LIB3120-023-Q1-K1-H11

Method BLASTX
NCBI GI g1352821
BLAST score 257
E value 1.0e-22
Match length 59
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207635

Seq. ID LIB3120-023-Q1-K1-H2

Method BLASTX

Seq. ID

Method

NCBI GI

```
NCBI GI
                   q4056457
BLAST score
                   361
E value
                  2.0e-34
                   97
Match length
                   68
% identity
NCBI Description
                  (AC005990) ESTs gb 234051 and gb F13722 come from this
                   gene. [Arabidopsis thaliana]
                   207636
Seq. No.
Seq. ID
                  LIB3120-023-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                   g289920
BLAST score
                   516
E value
                   5.0e-53
                   118
Match length
                   90
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   207637
Seq. No.
                   LIB3120-023-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q422337
BLAST score
                   145
                   2.0e-09
E value
                   32
Match length
                   40
% identity
                  protein disulfide-isomerase homolog precursor - fluke
NCBI Description
                   (Schistosoma mansoni) >gi 312018 emb CAA80520 (Z22933)
                   protein disulfide isomerase homologue [Schistosoma mansoni]
Seq. No.
                   207638
Seq. ID
                   LIB3120-023-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   g1389835
BLAST score
                   192
E value
                   6.0e-15
Match length
                   44
% identity
                   77
                   (U59284) Linum usitatissimum peroxidase (FLXPER3) mRNA,
NCBI Description
                   complete cds. [Linum usitatissimum]
                   207639
Seq. No.
                   LIB3120-023-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4006872
BLAST score
                   349
                   2.0e-33
E value
                   85
Match length
                   78
% identity
                   (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   207640
Seq. No.
```

28550

LIB3120-024-Q1-K1-A1

BLASTX

g289920



BLAST score 414 E value 7.0e-41 Match length 86

% identity 92

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207641

Seq. ID LIB3120-024-Q1-K1-A10

Method BLASTX
NCBI GI g2895188
BLAST score 152
E value 3.0e-10
Match length 78
% identity 26

NCBI Description (AF016011) CONSTANS homolog [Brassica napus]

Seq. No. 207642

Seq. ID LIB3120-024-Q1-K1-A11

Method BLASTX
NCBI GI g1354515
BLAST score 214
E value 2.0e-17
Match length 77
% identity 65

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 207643

Seq. ID LIB3120-024-Q1-K1-A12

Method BLASTX
NCBI GI g2388561
BLAST score 140
E value 1.0e-08
Match length 69
% identity 43

NCBI Description (AC000098) Similar to Arabidopsis hypothetical protein

PID:e326839 (gb Z97337). [Arabidopsis thaliana]

Seq. No. 207644

Seq. ID LIB3120-024-Q1-K1-A4

Method BLASTX
NCBI GI g2341032
BLAST score 460
E value 3.0e-46
Match length 93
% identity 92

NCBI Description (AC000104) EST gb ATTS0956 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 207645

Seq. ID LIB3120-024-Q1-K1-A5

Method BLASTX
NCBI GI g3641252
BLAST score 243
E value 8.0e-21
Match length 63

28551



domestica]

% identity 78
NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

Seq. No. 207646

Seq. ID LIB3120-024-Q1-K1-A7

Method BLASTX
NCBI GI g1173347
BLAST score 202
E value 2.0e-16
Match length 43
% identity 88

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi\_100803\_pir\_\_S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi\_14265\_emb\_CAA46507\_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 207647

Seq. ID LIB3120-024-Q1-K1-A8

Method BLASTX
NCBI GI g1076632
BLAST score 397
E value 1.0e-38
Match length 133
% identity 51

NCBI Description protein kinase - common tobacco >gi 506534 emb CAA50374

(X71057) protein kinase [Nicotiana tabacum]

Seq. No. 207648

Seq. ID LIB3120-024-Q1-K1-A9

Method BLASTX
NCBI GI g3763921
BLAST score 368
E value 3.0e-35
Match length 136
% identity 54

NCBI Description (AC004450) putative pirin protein [Arabidopsis thaliana]

Seq. No. 207649

Seq. ID LIB3120-024-Q1-K1-B1

Method BLASTX
NCBI GI g1709825
BLAST score 224
E value 2.0e-18
Match length 99
% identity 60

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No. 207650

Seq. ID LIB3120-024-Q1-K1-B10

Method BLASTX
NCBI GI g20729
BLAST score 324
E value 3.0e-30



Match length 107 % identity 66

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 207651

Seq. ID LIB3120-024-Q1-K1-B11

Method BLASTX
NCBI GI g4512665
BLAST score 174
E value 1.0e-12
Match length 56
% identity 61

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

>gi 4544472 gb AAD22379.1 AC006580 11 (AC006580) unknown

protein [Arabidopsis thaliana]

Seq. No. 207652

Seq. ID LIB3120-024-Q1-K1-B2

Method BLASTX
NCBI GI 94406816
BLAST score 241
E value 1.0e-20
Match length 48
% identity 92

NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 207653

Seq. ID LIB3120-024-Q1-K1-B3

Method BLASTX
NCBI GI g1617036
BLAST score 467
E value 6.0e-47
Match length 123
% identity 75

NCBI Description (Y08624) Ted2 [Vigna unguiculata]

Seq. No. 207654

Seq. ID LIB3120-024-Q1-K1-B4

Method BLASTX
NCBI GI g4406530
BLAST score 227
E value 2.0e-23
Match length 84
% identity 65

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 207655

Seq. ID LIB3120-024-Q1-K1-B5

Method BLASTN
NCBI GI g2828180
BLAST score 60
E value 4.0e-25
Match length 152
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDK4, complete sequence [Arabidopsis thaliana]

28553

44,500



Seq. ID LIB3120-024-Q1-K1-B6

BLASTX Method g2827143 NCBI GI BLAST score 493 4.0e-50 E value 100 Match length 92 % identity

(AF027174) cellulose synthase catalytic subunit NCBI Description

[Arabidopsis thaliana]

Seq. No. 207657

LIB3120-024-Q1-K1-B7 Seq. ID

BLASTX Method NCBI GI g1352821 BLAST score 341 2.0e-32 E value Match length 67 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi 450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207658

Seq. ID LIB3120-024-Q1-K1-C1

Method BLASTX g1353352 NCBI GI 202 BLAST score 5.0e-16 E value 58 Match length

% identity 71

(U31975) alanine aminotransferase [Chlamydomonas NCBI Description

reinhardtii]

207659 Seq. No.

Seq. ID LIB3120-024-Q1-K1-C12

BLASTX Method g1352821 NCBI GI BLAST score 387 E value 1.0e-37 76 Match length 96 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >qi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

207660 Seq. No.

Seq. ID LIB3120-024-Q1-K1-C6

Method BLASTX q487046 NCBI GI BLAST score 206 E value 2.0e-16 Match length 99



% identity 51

NCBI Description photosystem I chain II precursor - wood tobacco >gi\_407769 dbj\_BAA02871\_ (D13718) PSI-D1 precursor

[Nicotiana sylvestris]

Seq. No.

207661

Seq. ID

LIB3120-024-Q1-K1-C7

Method NCBI GI BLASTX q4056457

BLAST score

154

E value Match length 9.0e-11

% identity

51 61

NCBI Description

(AC005990) ESTs gb\_234051 and gb\_F13722 come from this

gene. [Arabidopsis thaliana]

Seq. No.

207662

Seq. ID

LIB3120-024-Q1-K1-C8

Method NCBI GI BLASTX g120669

BLAST score

g120669 528

E value Match length 4.0e-54

Match length % identity

104 93

NCBI Description

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.

207663

Seq. ID

LIB3120-024-Q1-K1-C9

Method NCBI GI BLASTX q1946368

BLAST score

210

E value Match length 8.0e-17 65

Match length % identity NCBI Description

(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.

207664

71

Seq. ID

LIB3120-024-Q1-K1-D11

Method

BLASTX g1352821

NCBI GI BLAST score

9133262. 547

E value

2.0e-56

Match length

112

89

% identity NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

207665

Seq. ID

LIB3120-024-Q1-K1-D2

Method

BLASTN



NCBI GI g18058
BLAST score 203
E value 1.0e-110
Match length 231
% identity 97

NCBI Description Citrus limon cistron for 26S ribosomal RNA

Seq. No. 207666

Seq. ID LIB3120-024-Q1-K1-D3

Method BLASTX
NCBI GI g120662
BLAST score 175
E value 5.0e-13
Match length 36
% identity 86

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi 81621 pir JQ1286

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - Arabidopsis thaliana >gi\_336390 (M64115) glyceraldehyde 3-phosphate dehydrogenase B subunit [Arabidopsis thaliana]

Seq. No. 207667

Seq. ID LIB3120-024-Q1-K1-D4

Method BLASTX
NCBI GI g131397
BLAST score 233
E value 8.0e-20
Match length 86
% identity 59

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480\_pir\_\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 207668

Seq. ID LIB3120-024-Q1-K1-D5

Method BLASTX
NCBI GI g2970051
BLAST score 241
E value 2.0e-20
Match length 69
% identity 64

NCBI Description (AB012110) ARG10 [Vigna radiata]

Seq. No. 207669

Seq. ID LIB3120-024-Q1-K1-D6

Method BLASTX
NCBI GI g2745849
BLAST score 196
E value 2.0e-15
Match length 58
% identity 60



(AF039201) germin-like protein; PcGER1 [Pinus caribaea] NCBI Description 207670 Seq. No. LIB3120-024-Q1-K1-D9 Seq. ID Method BLASTX NCBI GI q1170567 BLAST score 548 2.0e-56 E value Match length 111 94 % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >qi 1085960 pir S52648 INO1 protein - Citrus paradisi >qi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi] 207671 Seq. No. LIB3120-024-Q1-K1-E1 Seq. ID Method BLASTX NCBI GI g4406530 BLAST score 315 4.0e-29 E value Match length 87 75 % identity NCBI Description (AF126870) rubisco activase [Vigna radiata] 207672 Seq. No. Seq. ID LIB3120-024-Q1-K1-E10 Method BLASTX NCBI GI q121689 BLAST score 281 4.0e-25 E value Match length 88 % identity 50 GAST1 PROTEIN PRECURSOR >gi\_100217\_pir\_ S22151 GAST1 NCBI Description protein - tomato >gi\_19247\_emb\_CAA44807 (X63093) gast1 [Lycopersicon esculentum] 207673 Seq. No. LIB3120-024-Q1-K1-E12 Seq. ID BLASTX Method g1352821 NCBI GI 407 BLAST score 6.0e-40E value 79 Match length 96 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

207674 Seq. No.

Seq. ID LIB3120-024-Q1-K1-E3

Method BLASTX NCBI GI g1084321 BLAST score 273 4.0e-28 E value Match length 115



.

NCBI Description protochlorophyllide reductase (EC 1.3.1.33) - cucumber

>gi\_2244614\_dbj\_BAA21089\_ (D50085)

NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]

Seq. No. 207675

% identity

Seq. ID LIB3120-024-Q1-K1-E6

Method BLASTX
NCBI GI g100196
BLAST score 402
E value 2.0e-39
Match length 95
% identity 79

NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No. 207676

Seq. ID LIB3120-024-Q1-K1-E7

Method BLASTX
NCBI GI g625547
BLAST score 306
E value 6.0e-31
Match length 103
% identity 63

NCBI Description chlorophyll a/b-binding protein type I - common tobacco

>gi 493723 emb CAA45523 (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

Seq. No. 207677

Seq. ID LIB3120-024-Q1-K1-E8

Method BLASTX
NCBI GI g3420239
BLAST score 412
E value 1.0e-40
Match length 83
% identity 94

NCBI Description (AF059484) actin [Gossypium hirsutum]

Seq. No. 207678

Seq. ID LIB3120-024-Q1-K1-E9

Method BLASTX
NCBI GI g134101
BLAST score 564
E value 3.0e-58
Match length 116
% identity 97

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD

CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi\_72958\_pir\_\_HHCSBA ribulose-bisphosphate carboxylase

subunit-binding protein alpha chain - castor bean

(fragment)

Seq. No. 207679

Seq. ID LIB3120-024-Q1-K1-F1

Method BLASTX NCBI GI g1352821 BLAST score 447



E value 1.0e-44
Match length 85
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207680

Seq. ID LIB3120-024-Q1-K1-F10

Method BLASTX
NCBI GI g1352821
BLAST score 331
E value 3.0e-31
Match length 64
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207681

Seq. ID LIB3120-024-Q1-K1-F11

Method BLASTX
NCBI GI g121344
BLAST score 180
E value 7.0e-25
Match length 119
% identity 52

NCBI Description GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR

(GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)

>gi\_68597\_pir\_ AJPMQ2 glutamate--ammonia ligase (EC
6.3.1.2) delta precursor, chloroplast - garden pea

>gi\_169059 (M20664) glutamine synthetase (chloroplast GS2)

(EC 6.3.1.2) [Pisum sativum]

Seq. No. 207682

Seq. ID LIB3120-024-Q1-K1-F12

Method BLASTX
NCBI GI g115833
BLAST score 405
E value 1.0e-39
Match length 107
% identity 75

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR

(CAB-10A) (LHCP) >gi\_100195\_pir\_\_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi 170394 (M32605)

a-binding protein [Lycopersicon esculentum]

Seq. No. 207683

Seq. ID LIB3120-024-Q1-K1-F2

Method BLASTX
NCBI GI g2281088
BLAST score 238
E value 4.0e-20



Match length 91 % identity 54

NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog

[Arabidopsis thaliana]

Seq. No. 207684

Seq. ID LIB3120-024-Q1-K1-F3

Method BLASTX
NCBI GI g1352821
BLAST score 391
E value 3.0e-38
Match length 80
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207685

Seq. ID LIB3120-024-Q1-K1-F4

Method BLASTX
NCBI GI g3420239
BLAST score 177
E value 2.0e-13
Match length 35
% identity 94

NCBI Description (AF059484) actin [Gossypium hirsutum]

Seq. No. 207686

Seq. ID LIB3120-024-Q1-K1-F5

Method BLASTX
NCBI GI g267082
BLAST score 514
E value 2.0e-52
Match length 107
% identity 88

NCBI Description TUBULIN BETA-8 CHAIN >gi\_320189\_pir\_\_JQ1592 tubulin beta-8

chain - Arabidopsis thaliana >gi\_166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

Seq. No. 207687

Seq. ID LIB3120-024-Q1-K1-F6

Method BLASTX
NCBI GI g1352821
BLAST score 653
E value 1.0e-68
Match length 128
% identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase (Cossypium birsutum).

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207688

Seq. ID LIB3120-024-Q1-K1-F7



```
BLASTX
Method
NCBI GI
                  g3061271
BLAST score
                  159
                  1.0e-19
E value
                  95
Match length
                  53
% identity
                  (AB012863) NPCA1 [Nicotiana paniculata]
NCBI Description
                  207689
Seq. No.
                  LIB3120-024-Q1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2851508
BLAST score
                  469
                  3.0e-47
E value
                  96
Match length
% identity
                  86
                  60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                  ribosomal protein L21 (gb_L38826). ESTs
                  gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi 3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
                  207690
Seq. No.
Seq. ID
                  LIB3120-024-Q1-K1-F9
                  BLASTX
Method
                  q3695063
NCBI GI
BLAST score
                  359
                  2.0e-34
E value
                  101
Match length
                  71
% identity
                  (AF064789) rac GTPase activating protein 3 [Lotus
NCBI Description
                  japonicus]
                  207691
Seq. No.
                  LIB3120-024-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g1709651
NCBI GI
BLAST score
                  149
E value
                  9.0e-10
                  71
Match length
                   46
% identity
                  PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209
NCBI Description
                  plastocyanin a precursor - black poplar
                  >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                  nigra]
                  207692
Seq. No.
                  LIB3120-024-Q1-K1-G10
Seq. ID
Method
                  BLASTX
```

q687677 NCBI GI BLAST score 139 E value 1.0e-08 71 Match length 48 % identity

NCBI Description (U19925) unknown [Arabidopsis thaliana]

Seq. No. 207693

```
LIB3120-024-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                  g1168739
NCBI GI
                  569
BLAST score
                  6.0e-59
E value
Match length
                  120
% identity
                  CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 438449
NCBI Description
                  (L18901) carbonic anhydrase [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3120-024-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3063392
BLAST score
                  347
E value
                  7.0e-33
                  98
Match length
% identity
                  74
                  (AB012932) Ca2+/H+ exchanger [Vigna radiata]
NCBI Description
                  207695
Seq. No.
Seq. ID
                  LIB3120-024-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q4262236
BLAST score
                  251
                  2.0e-21
E value
                  71
Match length
                  72
% identity
                  (AC006200) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
                  207696
Seq. No.
Seq. ID
                  LIB3120-024-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4105561
BLAST score
                  427
                  3.0e-42
E value
Match length
                  125
% identity
                  77
                  (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
NCBI Description
                  207697
Seq. No.
                  LIB3120-024-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g1352821
NCBI GI
                   263
BLAST score
E value
                  1.0e-25
```

Match length 67 90 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi 450505 emb CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

207698 Seq. No.

Seq. ID LIB3120-024-Q1-K1-H11



Method BLASTX
NCBI GI g3873757
BLAST score 313
E value 5.0e-29
Match length 90
% identity 67

NCBI Description (Z81028) Similarity to Human ATP citrate lyase

(TR:G603074); cDNA EST EMBL:D32678 comes from this gene; cDNA EST EMBL:D37759 comes from this gene; cDNA EST

EMBL: D35374 comes from this gene; cDNA EST EMBL: D35812

comes from this

Seq. No. 207699

Seq. ID LIB3120-024-Q1-K1-H12

Method BLASTX
NCBI GI g289920
BLAST score 237
E value 2.0e-20
Match length 49
% identity 92

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207700

Seq. ID LIB3120-024-Q1-K1-H3

Method BLASTX
NCBI GI g3024127
BLAST score 443
E value 3.0e-44
Match length 88
% identity 95

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine

synthetase 2 [Catharanthus roseus]

Seq. No. 207701

Seq. ID LIB3120-024-Q1-K1-H4

Method BLASTX
NCBI GI g3822036
BLAST score 164
E value 1.0e-11
Match length 71
% identity 52

NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 207702

Seq. ID LIB3120-024-Q1-K1-H6

Method BLASTX
NCBI GI g3914473
BLAST score 249
E value 1.0e-21
Match length 73
% identity 67

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi 479684 pir S35151 photosystem I chain XI -

spinach >gi\_396275\_emb\_CAA45775\_ (X64445) subunit XI of

E value

1.0e-41





## photosystem I reaction center [Spinacia oleracea]

207703 Seq. No. Seq. ID LIB3120-024-Q1-K1-H8 Method BLASTX NCBI GI g1352821 BLAST score 233 1.0e-19 E value Match length 69 71 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 207704 Seq. No. Seq. ID LIB3120-024-Q1-K1-H9 Method BLASTX NCBI GI g1709825 BLAST score 196 3.0e-15 E value 94 Match length 57 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR NCBI Description (PSI-N) >qi 1237124 (U32176) PSI-N [Arabidopsis thaliana] 207705 Seq. No. Seq. ID LIB3120-025-Q1-K1-A10 Method BLASTX NCBI GI g3927825 BLAST score 480 2.0e-48 E value 97 Match length 92 % identity (AC005727) putative dTDP-glucose 4-6-dehydratase NCBI Description [Arabidopsis thaliana] 207706 Seq. No. Seq. ID LIB3120-025-Q1-K1-A11 Method BLASTX NCBI GI g2499967 BLAST score 213 E value 5.0e-17 Match length 115 45 % identity NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E B) >gi 632724 bbs 151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast, 143 aa] [Nicotiana sylvestris] Seq. No. 207707 Seq. ID LIB3120-025-Q1-K1-A2 Method BLASTX NCBI GI q3608147 BLAST score 422



Match length 136 % identity 65

NCBI Description (AC005314) putative chloroplast 31 kDa ribonucleoprotein

precursor [Arabidopsis thaliana]

Seq. No. 207708

Seq. ID LIB3120-025-Q1-K1-A5

Method BLASTX
NCBI GI g2494116
BLAST score 277
E value 1.0e-24
Match length 135

Match length 135 % identity 46

NCBI Description (AC002376) Similar to Synechocystis hypothetical protein

(gb\_D90915). [Arabidopsis thaliana]

Seq. No. 207709

Seq. ID LIB3120-025-Q1-K1-A6

Method BLASTX
NCBI GI g282833
BLAST score 273
E value 5.0e-24
Match length 65
% identity 86

NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)

Seq. No. 207710

Seq. ID LIB3120-025-Q1-K1-A7

Method BLASTX
NCBI GI g3608147
BLAST score 297
E value 6.0e-27
Match length 107
% identity 61

NCBI Description (AC005314) putative chloroplast 31 kDa ribonucleoprotein

precursor [Arabidopsis thaliana]

Seq. No. 207711

Seq. ID LIB3120-025-Q1-K1-A8

Method BLASTX
NCBI GI g3914666
BLAST score 230
E value 5.0e-19
Match length 60
% identity 77

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR

>gi\_2791998\_emb\_CAA74895\_ (Y14566) ribosomal protein L4
[Arabidopsis thaliana] >gi\_2792000\_emb\_CAA74894\_ (Y14565)

ribosomal protein L4 [Arabidopsis thaliana]

Seq. No. 207712

Seq. ID LIB3120-025-Q1-K1-B1

Method BLASTX
NCBI GI g131187
BLAST score 485
E value 5.0e-49
Match length 101

% identity

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

> >qi 72681 pir F1SP3 photosystem I chain III precursor spinach >gi 21303 emb CAA31523 (X13133) PSI subunit IV

preprotein (AA -77 to 154) [Spinacia oleracea]

>gi 226166 prf 1413236A photosystem I reaction center IV

[Spinacia oleracea]

207713 Seq. No.

Seq. ID LIB3120-025-Q1-K1-B10

Method BLASTX NCBI GI q4539323 310 BLAST score 2.0e-28 E value 98 Match length % identity 66

NCBI Description (AL035679) putative protein [Arabidopsis thaliana]

207714 Seq. No.

LIB3120-025-Q1-K1-B12 Seq. ID

Method BLASTX g3169182 NCBI GI 315 BLAST score 5.0e-29 E value 71 Match length % identity 85

(AC004401) unknown protein [Arabidopsis thaliana] NCBI Description

207715 Seq. No.

LIB3120-025-Q1-K1-B2 Seq. ID

BLASTX Method NCBI GI g4510375 BLAST score 187 5.0e-14 E value 95 Match length

55 % identity (AC007017) putative homeotic protein BEL1 [Arabidopsis NCBI Description

thaliana]

207716 Seq. No.

Seq. ID LIB3120-025-Q1-K1-B3

Method BLASTX NCBI GI g4539452 BLAST score 518 E value 7.0e-53 Match length 130 75 % identity

(AL049500) putative phosphoribosylanthranilate transferase NCBI Description

[Arabidopsis thaliana]

207717 Seq. No.

LIB3120-025-Q1-K1-B6 Seq. ID

Method BLASTX NCBI GI q2275202 BLAST score 519 6.0e-53 E value



Match length 147% identity 64

NCBI Description (AC002337) acyl-CoA synthetase isolog [Arabidopsis

thaliana]

Seq. No. 207718

Seq. ID LIB3120-025-Q1-K1-B8

Method BLASTX
NCBI GI g131385
BLAST score 552
E value 8.0e-57
Match length 138
% identity 80

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 207719

Seq. ID LIB3120-025-Q1-K1-C1

Method BLASTN
NCBI GI g12283
BLAST score 74
E value 2.0e-33
Match length 172
% identity 89

NCBI Description Spinach plastid psbB operon with genes for 10 kD

phosphoprotein associated with photosystem II (psbH), apocytochrome b6 and subunit 4 (petD) of cytochrome b6f

complex

Seq. No. 207720

Seq. ID LIB3120-025-Q1-K1-C10

Method BLASTN
NCBI GI g4519194
BLAST score 41
E value 1.0e-13
Match length 193
% identity 80

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHM17, complete sequence

Seq. No. 207721

Seq. ID LIB3120-025-Q1-K1-C11

Method BLASTX
NCBI GI g3080428
BLAST score 404
E value 2.0e-39
Match length 104
% identity 71

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 207722

Seq. ID LIB3120-025-Q1-K1-C2

Method BLASTX
NCBI GI g1352821
BLAST score 480
E value 2.0e-48



Match length 100 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. LIB3120-025-Q1-K1-C3 Seq. ID

207723

BLASTN Method NCBI GI q3821780 BLAST score 36 9.0e-11 E value 45 Match length

NCBI Description Xenopus laevis cDNA clone 27A6-1

207724 Seq. No.

% identity

Seq. ID LIB3120-025-Q1-K1-C6

65

Method BLASTX NCBI GI g1168410 BLAST score 534 1.0e-54 E value Match length 129 % identity 81

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2 NCBI Description

>qi 2118267 pir S58167 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi 927505\_emb CAA61947\_ (X89829)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 207725

LIB3120-025-Q1-K1-C8 Seq. ID

Method BLASTX g2191135 NCBI GI BLAST score 161 6.0e-11 E value 80 Match length % identity 36

(AF007269) A IG002N01.14 gene product [Arabidopsis NCBI Description

thaliana]

207726 Seq. No.

Seq. ID LIB3120-025-Q1-K1-D1

BLASTX Method NCBI GI g2511691 BLAST score 480 E value 2.0e-48 Match length 143 66 % identity

(Z99953) cysteine proteinase precursor [Phaseolus vulgaris] NCBI Description

Seq. No. 207727

LIB3120-025-Q1-K1-D11 Seq. ID

Method BLASTX NCBI GI q4417203 BLAST score 698

E value 6.0e-74
Match length 144
% identity 90

NCBI Description (AB006386) maturase [Tilia kiusiana]

Seq. No. 207728

Seq. ID LIB3120-025-Q1-K1-D12

Method BLASTX
NCBI GI g3122673
BLAST score 514
E value 2.0e-52
Match length 130
% identity 77

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi\_2245027\_emb\_CAB10447\_

(Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 207729

Seq. ID LIB3120-025-Q1-K1-D3

Method BLASTX
NCBI GI g120669
BLAST score 575
E value 2.0e-59
Match length 134
% identity 82

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 207730

Seq. ID LIB3120-025-Q1-K1-D4

Method BLASTX
NCBI GI g3929333
BLAST score 255
E value 4.0e-22
Match length 120
% identity 44

NCBI Description CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD)

(PHENYLUREA DEALKYLASE) >qi 2370230 emb CAA71054 (Y09920)

7-ethoxycoumarin O-deethylase [Helianthus tuberosus]

Seq. No. 207731

Seq. ID LIB3120-025-Q1-K1-D6

Method BLASTX
NCBI GI g1352821
BLAST score 152
E value 5.0e-10
Match length 29
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207732

```
LIB3120-025-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3763932
BLAST score
                  252
E value
                  9.0e-34
Match length
                  125
% identity
                  60
NCBI Description
                  (AC004450) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  207733
Seq. ID
                  LIB3120-025-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g136707
BLAST score
                  452
E value
                  4.0e-45
Match length
                  125
% identity
                  70
NCBI Description
                  CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
                  (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 280397 pir S26199
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  iron-sulfur protein precursor - garden pea
                  >gi 20832 emb CAA45151 (X63605) chloroplast Rieske FeS
                  protein [Pisum sativum]
Seq. No.
                  207734
                  LIB3120-025-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2880051
BLAST score
                  223
E value
                  4.0e-36
Match length
                  103
% identity
                  74
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  207735
Seq. ID
                  LIB3120-025-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1946367
BLAST score
                  202
E value
                  9.0e-16
                  103
Match length
                  36
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  207736
                  LIB3120-025-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3202030
BLAST score
                  370
E value
                  2.0e-35
```

Match length 121

% identity 65 NCBI Description

(AF069318) geranylgeranyl hydrogenase [Mesembryanthemum

crystallinum]

207737 Seq. No.

Seq. ID LIB3120-025-Q1-K1-E3



```
Method
                  BLASTX
NCBI GI
                  g4115561
BLAST score
                  260
E value
                  1.0e-22
Match length
                  118
                  46
% identity
                  (AB013597) UDP-glucose:anthocyanin 5-O-glucosyltransferase
NCBI Description
                  homologue [Perilla frutescens]
Seq. No.
                  207738
Seq. ID
                  LIB3120-025-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  618
                  2.0e-64
E value
Match length
                  126
                  94
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  207739
Seq. ID
                  LIB3120-025-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  407
E value
                  9.0e-40
Match length
                  128
                  71
% identity
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  207740
Seq. ID
                  LIB3120-025-Q1-K1-E7
Method
                  BLASTX
                  g3024362
NCBI GI
BLAST score
                  191
E value
                  1.0e-14
Match length
                  66
% identity
                  62
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE G2B >gi 2118317 pir $60042
                  phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese
                  aspen x large-toothed aspen >gi 1109641 dbj BAA07860
                  (D43802) phenylalanine ammonia-lyase [Populus
                  kitakamiensis]
Seq. No.
                  207741
Seq. ID
                  LIB3120-025-Q1-K1-E8
```

Method BLASTX NCBI GI g2129538 BLAST score 337 E value 1.0e-31 Match length 71 % identity 89

NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)

AT103 [Arabidopsis thaliana]



```
207742
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3024362
BLAST score
                  397
                  1.0e-38
E value
Match length
                  106
                  74
% identity
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE G2B >gi 2118317 pir S60042
                  phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese
                  aspen x large-toothed aspen >gi 1109641 dbj BAA07860
                  (D43802) phenylalanine ammonia-lyase [Populus
                  kitakamiensis]
                  207743
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g231688
BLAST score
                  704
                  1.0e-74
E value
Match length
                  127
% identity
                  99
                  CATALASE ISOZYME 2, >gi 99599 pir S17493 catalase (EC
NCBI Description
                  1.11.1.6) - upland cotton >gi 18488 emb CAA39998
                                                                      (X56675)
                  subunit 2 of cotton catalase [Gossypium hirsutum]
Seq. No.
                  207744
Seq. ID
                  LIB3120-025-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2833386
BLAST score
                  371
E value
                  1.0e-35
Match length
                  98
                  79
% identity
                  RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR
NCBI Description
                  (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E)
                  >gi_2129493 pir S62724 ribulose-phosphate 3-epimerase (EC
                  5.1.3.1) precursor - spinach >gi 1162980 (L42328)
                  ribulose-5-phosphate 3-epimerase [Spinacia oleracea]
                  >gi 3264788 (AF070941) ribulose-phosphate 3-epimerase
                  [Spinacia oleracea] >gi_1587969_prf__2207382A
                  D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]
Seq. No.
                  207745
Seq. ID
                  LIB3120-025-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q487046
BLAST score
                  310
                  3.0e-30
E value
                  127
Match length
% identity
                  55
```

NCBI Description

[Nicotiana sylvestris]

photosystem I chain II precursor - wood tobacco
>gi\_407769\_dbj\_BAA02871\_ (D13718) PSI-D1 precursor



```
LIB3120-025-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543939
                  652
BLAST score
                  2.0e-68
E value
Match length
                  140
                  82
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR
NCBI Description
                  >gi 541819 pir S40210 chlorophyll a/b-binding protein CP24
                  precursor - spinach >gi 437991 emb CAA81105 (Z25886) 20
                  kDa protein of CP24 precursor protein [Spinacia oleracea]
                  207747
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  464
                  1.0e-46
E value
                  109
Match length
% identity
                  83
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
Seq. No.
                  207748
                  LIB3120-025-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3355468
BLAST score
                  468
                  5.0e-47
E value
                  108
Match length
                  91
% identity
NCBI Description
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
                  thaliana]
                  207749
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-F6
                  BLASTX
Method
NCBI GI
                  q1168411
BLAST score
                  351
                  3.0e-33
E value
                  93
Match length
                  80
% identity
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                  207750
Seq. ID
                  LIB3120-025-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q4309738
BLAST score
                  433
E value
                  7.0e-43
                  103
Match length
% identity
                  80
                  (AC006439) putative tubby protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB3120-025-Q1-K1-G1

Method BLASTX



```
g2501062
NCBI GI
                   183
BLAST score
                   1.0e-13
E value
Match length
                   52
% identity
                   62
                  THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
NCBI Description
                  >gi 1001722 dbj BAA10559 (D64004) threonyl-tRNA synthetase
                   [Synechocystis sp.]
Seq. No.
                   207752
Seq. ID
                  LIB3120-025-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                   q4191774
BLAST score
                   263
                   5.0e-48
E value
                   127
Match length
                   77
% identity
NCBI Description
                   (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
                   thaliana]
                   207753
Seq. No.
                   LIB3120-025-Q1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131385
BLAST score
                   461
                   4.0e-46
E value
                   130
Match length
                   74
% identity
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN)
Seq. No.
                   207754
Seq. ID
                   LIB3120-025-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g1703129
BLAST score
                   524
                   1.0e-53
E value
Match length
                   97
                   99
% identity
                   ACTIN 11 >gi_2129522_pir___S68109 actin 11 - Arabidopsis
NCBI Description
                   thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis
                   thaliana]
                   207755
Seq. No.
Seq. ID
                   LIB3120-025-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g3869088
                   546
BLAST score
                   4.0e-56
E value
                   104
Match length
                   100
% identity
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
```

Seq. ID LIB3120-025-Q1-K1-H1

Method BLASTX

NCBI GI

q68200

```
NCBI GI
                  q4204697
                  346
BLAST score
                  9.0e-33
E value
                  77
Match length
% identity
                  81
                  (AF117063) putative inositol polyphosphate 5-phosphatase
NCBI Description
                  At5P2 [Arabidopsis thaliana]
                  207757
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  264
                  5.0e-23
E value
Match length
                  98
% identity
                  48
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                  207758
Seq. No.
                  LIB3120-025-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  605
E value
                  4.0e-63
Match length
                  130
% identity
                  89
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                  - spinach >gi 1066153 dbj_BAA07177_ (D37963) cysteine
                  synthase [Spinacia oleracea]
                  207759
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-H4
                  BLASTX
Method
                  g1703129
NCBI GI
                  543
BLAST score
                   8.0e-56
E value
                  102
Match length
                   98
% identity
                  ACTIN 11 >gi 2129522 pir S68109 actin 11 - Arabidopsis
NCBI Description
                  thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis
                  thaliana]
                  207760
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                   g2117700
BLAST score
                   567
                  1.0e-58
E value
                  113
Match length
                   91
% identity
NCBI Description transketolase (EC 2.2.1.1) precursor - potato (fragment)
                  207761
Seq. No.
Seq. ID
                  LIB3120-025-Q1-K1-H8
Method
                  BLASTX
```

```
BLAST score
E value
                   1.0e-43
Match length
                   108
% identity
                   83
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.
                   207762
Seq. ID
                   LLB3120-026-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   325
E value
                   2.0e-30
Match length
                   65
% identity
                   95
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   207763
Seq. ID
                   LIB3120-026-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2689720
BLAST score
                   337
E value
                   1.0e-31
Match length
                  115
% identity
                   59
NCBI Description
                  (AF037168) DnaJ homologue [Arabidopsis thaliana]
Seq. No.
                  207764
                  LIB3120-026-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g505482
BLAST score
                  514
E value
                  2.0e-52
Match length
                  112
% identity
NCBI Description
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
                  photosystem II [Nicotiana tabacum]
Seq. No.
                  207765
Seq. ID
                  LIB3120-026-Q1-K1-A3
Method
                  BLASTX
                  q3650033
                  353
                  1.0e-33
```

NCBI GI BLAST score E value Match length 78 % identity

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 207766

Seq. ID LIB3120-026-Q1-K1-A5

Method BLASTX NCBI GI g1352821



BLAST score E value 5.0e-11 Match length 43 % identity 72

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207767

Seq. ID LIB3120-026-Q1-K1-A6

Method BLASTX NCBI GI q2281338 BLAST score 489 E value 2.0e-49 117 Match length % identity 78

(U83621) putative pectate lyase [Arabidopsis thaliana] NCBI Description

207768 Seq. No.

LIB3120-026-Q1-K1-A7 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 167 3.0e-12 E value Match length 46 76 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207769

Seq. ID LIB3120-026-Q1-K1-A9

Method BLASTX NCBI GI g1352821 BLAST score 539 E value 3.0e-55 Match length 105 95 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

207770 Seq. No.

Seq. ID LIB3120-026-Q1-K1-B10

Method BLASTX NCBI GI q1352821 649 BLAST score E value 3.0e-68 122 Match length 96 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR





(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
Seq. No.
                  207771
Seq. ID
                  LIB3120-026-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1684851
BLAST score
                  186
E value
                  3.0e-14
                  80
Match length
% identity
                  51
NCBI Description
                  (U77935) DnaJ-like protein [Phaseolus vulgaris]
                  207772
Seq. No.
Seq. ID
                  LIB3120-026-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  430
E value
                  2.0e-42
Match length
                  105
% identity
                  80
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  207773
Seq. ID
                  LIB3120-026-Q1-K1-B2
```

Method BLASTX NCBI GI g68200

BLAST score 262 7.0e-23 E value Match length 75 % identity 75

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 207774

LIB3120-026-Q1-K1-B4 Seq. ID

Method BLASTX NCBI GI g2244979 BLAST score 329 8.0e-31 E value Match length 105 % identity 64

NCBI Description (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis

thaliana]

Seq. No. 207775

Seq. ID LIB3120-026-Q1-K1-B5

Method BLASTX NCBI GI g4220534 BLAST score 275 E value 3.0e-24



Match length % identity 69

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 207776

Seq. ID LIB3120-026-Q1-K1-B6

Method BLASTN g18487 NCBI GI BLAST score 83

E value 8.0e-39 Match length 103 % identity 95

NCBI Description G. hirsutum mRNA for cotton catalase subunit

Seq. No. 207777

Seq. ID LIB3120-026-Q1-K1-B7

Method BLASTX NCBI GI g2642648 BLAST score 551 E value 8.0e-57 Match length 111 95 % identity

NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3

> [Spinacia oleracea] >gi 2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi 2660770 (AF034617)

cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 207778

Seq. ID LIB3120-026-Q1-K1-B8

Method BLASTX NCBI GI g2833386 BLAST score 226 E value 1.0e-18 Match length 71 % identity 70

RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR NCBI Description

(PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi 2129493 pir S62724 ribulose-phosphate 3-epimerase (EC

5.1.3.1) precursor - spinach >gi\_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea]

>gi 3264788 (AF070941) ribulose-phosphate 3-epimerase

[Spinacia oleracea] >gi 1587969 prf 2207382A

D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No. 207779

Seq. ID LIB3120-026-Q1-K1-B9

Method BLASTX NCBI GI g1352821 BLAST score 510 E value 7.0e-52 104 Match length 90 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase  $\overline{\text{(EC 4.1.1.39)}}$  small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
207780
Seq. No.
Seq. ID
                  LIB3120-026-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1076800
BLAST score
                  433
E value
                  4.0e-44
                  108
Match length
% identity
                  86
                  L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                  maize >qi 600116 emb CAA84406 (Z34934) cytosolic ascorbate
                  peroxidase [Zea mays] >gi 1096503 prf 2111423A ascorbate
                  peroxidase [Zea mays]
                  207781
Seq. No.
Seq. ID
                  LIB3120-026-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g131392
BLAST score
                  359
                  2.0e-34
E value
Match length
                  93
                  74
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi 81479_pir__S00005 photosystem II oxygen-evolving
                  complex protein 2 precursor - spinach
                  >gi 21265 emb CAA29055 (X05511) 23 kDa OEC protein
                  [Spinacia oleracea] >gi 225596 prf 1307179A luminal
                  protein 23kD [Spinacia oleracea]
Seq. No.
                  207782
Seq. ID
                  LIB3120-026-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4539422
BLAST score
                  384
E value
                  3.0e - 37
Match length
                  115
% identity
                  67
NCBI Description
                  (AL049171) putative protein [Arabidopsis thaliana]
Seq. No.
                  207783
                  LIB3120-026-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982318
BLAST score
                  287
                  2.0e-26
E value
Match length
                  62
                  82
% identity
NCBI Description
                  (AF051244) probable 60S ribosomal protein L15 [Picea
                  mariana]
Seq. No.
                  207784
```

Seq. ID LIB3120-026-Q1-K1-C6 Method BLASTX

NCBI GI g1771778
BLAST score 508
E value 1.0e-51



Match length 12 % identity 77

NCBI Description (X99320) 23 kDa oxygen evolving protein of photosystem II

[Solanum tuberosum]

Seq. No. 207785

Seq. ID LIB3120-026-Q1-K1-D1

Method BLASTX
NCBI GI g131385
BLAST score 529
E value 4.0e-54
Match length 130
% identity 82

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 207786

Seq. ID LIB3120-026-Q1-K1-D11

Method BLASTX
NCBI GI g3738261
BLAST score 545
E value 5.0e-56
Match length 127
% identity 86

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 207787

Seq. ID LIB3120-026-Q1-K1-D3

Method BLASTX
NCBI GI g1168446
BLAST score 152
E value 6.0e-10
Match length 123
% identity 33

NCBI Description AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)

>gi\_1073840\_pir\_\_F64132 aminopeptidase N (pepN) homolog Haemophilus influenzae (strain Rd KW20) >gi\_1574460
(U32835) aminopeptidase N (pepN) [Haemophilus influenzae

Rd]

Seq. No. 207788

Seq. ID LIB3120-026-Q1-K1-D5

Method BLASTX
NCBI GI g543565
BLAST score 288
E value 9.0e-26
Match length 90
% identity 58

NCBI Description hypothetical 10.0K protein - Zinnia elegans

>gi\_493721\_dbj\_BAA06462\_ (D30802) TED4 [Zinnia elegans]
>gi\_641903 (U19266) putative nonspecific lipid transfer;

auxin induced gene [Zinnia elegans]

Seq. No. 207789

Seq. ID LIB3120-026-Q1-K1-D7



Method BLASTX
NCBI GI g4204267
BLAST score 159
E value 8.0e-11
Match length 37
% identity 81

NCBI Description (AC005223) 55585 [Arabidopsis thaliana]

Seq. No. 207790

Seq. ID LIB3120-026-Q1-K1-D8

Method BLASTX
NCBI GI g1170507
BLAST score 625
E value 2.0e-65
Match length 132
% identity 90

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)

>gi\_100276\_pir\_\_S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi\_19699\_emb\_CAA43514\_ (X61206)
nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 207791

Seq. ID LIB3120-026-Q1-K1-E1

Method BLASTX
NCBI GI g118564
BLAST score 594
E value 8.0e-62
Match length 121
% identity 93

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi\_65955\_pir\_\_DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent
hydroxypyruvate reductase [Cucumis sativus]
>gi\_18275\_emb\_CAA32764\_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 207792

Seq. ID LIB3120-026-Q1-K1-E10

Method BLASTX
NCBI GI g2191197
BLAST score 446
E value 3.0e-44
Match length 122
% identity 72

NCBI Description (AF007271) contains similarity to Synechococcus PCC7942

chromosomal region used as basis of neutral siteII

recombinational cloning vector (PID:g1174192) [Arabidopsis

thaliana]

Seq. No. 207793

Seq. ID LIB3120-026-Q1-K1-E11

Method BLASTX NCBI GI g464986 BLAST score 617 E value 2.0e-64



Match length % identity NCBI Description 98

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana

>qi 297884 emb CAA78714 (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi\_600391\_emb\_CAA51201\_ (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi\_4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

207794 Seq. No.

LIB3120-026-Q1-K1-E12 Seq. ID

BLASTX Method g132091 NCBI GI BLAST score 331 3.0e-42 E value 106 Match length 80

% identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN F1 PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT F1) >gi\_68065\_pir\_\_RKRPF1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (gene rbcSF1) - rape >gi\_17852\_emb\_CAA39402\_ (X55937) ribulose bisphosphate carboxylase /oxygenase

small subunit [Brassica napus]

207795 Seq. No.

LIB3120-026-Q1-K1-E2 Seq. ID BLASTX Method q1352821 NCBI GI

BLAST score 579 5.0e-60 E value Match length 119 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

207796 Seq. No.

LIB3120-026-Q1-K1-E6 Seq. ID

BLASTX Method NCBI GI g4432823 BLAST score 174 2.0e-12 E value Match length 148 % identity 39

(AC006593) hypothetical protein [Arabidopsis thaliana] NCBI Description

207797 Seq. No.

LIB3120-026-Q1-K1-E9 Seq. ID

BLASTX Method g1935912 NCBI GI



BLAST score 220 E value 4.0e-18 Match length 90 % identity 49

NCBI Description (U77346) LLS1 [Zea mays]

Seq. No. 207798

Seq. ID LIB3120-026-Q1-K1-F1

Method BLASTX
NCBI GI g21491
BLAST score 162
E value 3.0e-11
Match length 46
% identity 67

NCBI Description (X04401) ST-LS1 protein (AA 1-138) [Solanum tuberosum]

Seq. No. 207799

Seq. ID LIB3120-026-Q1-K1-F10

Method BLASTX
NCBI GI g1071913
BLAST score 368
E value 3.0e-35
Match length 132
% identity 64

NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial

- spinach >qi 1066153 dbj BAA07177 (D37963) cysteine

synthase [Spinacia oleracea]

Seq. No. 207800

Seq. ID LIB3120-026-Q1-K1-F12

Method BLASTX
NCBI GI g1352821
BLAST score 569
E value 7.0e-59
Match length 117
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207801

Seq. ID LIB3120-026-Q1-K1-F2

Method BLASTX
NCBI GI g1354515
BLAST score 228
E value 7.0e-19
Match length 131
% identity 43

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 207802

Seq. ID LIB3120-026-Q1-K1-F3

Method BLASTX NCBI GI q3738306

BLAST score 7.0e-09 E value 52 Match length 52 % identity

(AC005309) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

207803

Seq. ID

LIB3120-026-Q1-K1-F6

BLASTX Method q2384671 NCBI GI BLAST score 362 4.0e-44 E value Match length 130 % identity

(AF012657) putative potassium transporter AtKT2p NCBI Description

[Arabidopsis thaliana]

Seq. No.

207804

Seq. ID

LIB3120-026-Q1-K1-F8

Method BLASTX q417103 NCBI GI BLAST score 503 E value 6.0e-59 Match length 123 % identity

HISTONE H3.2, MINOR >gi\_282871 pir\_\_S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa]  $>gi_488567$  ( $\overline{U}09460$ ) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

207805 Seq. No.

LIB3120-026-Q1-K1-G10 Seq. ID

Method BLASTX q3128217 NCBI GI BLAST score 169 6.0e-12 E value 68 Match length 54 % identity

(AC004077) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 3337374 (AC004481) hypothetical protein [Arabidopsis

thaliana]

```
207806
Seq. No.
                  LIB3120-026-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g3947719
NCBI GI
                  250
BLAST score
E value
                  2.0e-21
                  53
Match length.
                  94
% identity
                  (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                  >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
                   [Prunus persica] >gi 3947723_emb_CAA10103_ (AJ012655)
                  ribosomal protein S28 [Prunus persica]
                  207807
Seq. No.
                  LIB3120-026-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914430
                   240
BLAST score
                   2.0e-20
E value
Match length
                   63
                   75
% identity
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi 2285800_dbj BAA21650_ (D78172) 265 proteasome beta
                   subunit [Spinacia oleracea]
Seq. No.
                   207808
                   LIB3120-026-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3090403
BLAST score
                   220
                   5.0e-18
E value
Match length
                   73
% identity
                   66
                   (AJ005671) cytochrome b6f complex subunit [Arabidopsis
NCBI Description
                   thaliana]
                   207809
Seq. No.
                   LIB3120-026-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g3108053
NCBI GI
                   433
BLAST score
                   4.0e-60
E value
                   125
Match length
                   96
% identity
                   (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
NCBI Description
                   mays]
                   207810
Seq. No.
                   LIB3120-026-Q1-K1-G6
Seq. ID
```

Method BLASTX
NCBI GI g2191138
BLAST score 209
E value 1.0e-16
Match length 108
% identity 46

NCBI Description (AF007269) A\_IG002N01.18 gene product [Arabidopsis



ea. No. 207811

Seq. No. 207811 Seq. ID LIB3120-026-Q1-K1-G8

Method BLASTX
NCBI GI g1168411
BLAST score 270
E value 7.0e-24

Match length 77 % identity 74

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 207812

Seq. ID LIB3120-026-Q1-K1-G9

Method BLASTX
NCBI GI g115812
BLAST score 615
E value 3.0e-64
Match length 118
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-7) (LHCP) >gi\_100312\_pir\_\_S14650 chlorophyll

a/b-binding protein - common tobacco

>gi 19837\_emb\_CAA41187\_ (X58229) chlorophyll a /b binding

protein [Nicotiana tabacum]

Seq. No. 207813

Seq. ID LIB3120-026-Q1-K1-H10

Method BLASTX
NCBI GI g3668086
BLAST score 314
E value 7.0e-29
Match length 89
% identity 66

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 207814

Seq. ID LIB3120-026-Q1-K1-H11

Method BLASTX
NCBI GI g1352821
BLAST score 452
E value 3.0e-45
Match length 92
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207815

Seq. ID LIB3120-026-Q1-K1-H12

Method BLASTX
NCBI GI g1352821
BLAST score 370
E value 8.0e-36
Match length 79



```
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  207816
Seq. ID
                  LIB3120-026-Q1-K1-H3
Method
                  BLASTN
NCBI GI
                  g450504
BLAST score
                  44
                  4.0e-16
E value
Match length
                  124
% identity
                  84
NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate
                  carboxylase, small subunit
Seq. No.
                  207817
Seq. ID
                  LIB3120-026-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  531
E value
                  2.0e-54
Match length
                  102
% identity
                  97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  207818
Seq. ID
                  LIB3120-026-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g418507
BLAST score
                  235
E value
                  1.0e-19
                  112
Match length
                  42
% identity
NCBI Description S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE
                  METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical
                  protein f161 - Escherichia coli >gi 305032 (L19201)
                  ORF_f161 [Escherichia coli] >gi_1336002 (U56082)
                  S-adenosylmethionine: 2-demethylmenaquinone
                  methyltransferase [Escherichia coli] >gi 1790364 (AE000467)
                  menaquinone biosynthesis, unknown [Escherichia coli]
Seq. No.
                  207819
Seq. ID
                  LIB3120-026-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  363
```

E value 6.0e - 35

Match length 73 % identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR





(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

 Seq. No.
 207820

 Seq. ID
 LIB3120-026-Q1-K1-H8

 Method
 BLASTX

 NCBI GI
 g133872

 BLAST score
 315

 E value
 2.0e-40

E value 2.06
Match length 133
% identity 65

NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)

>gi\_282838\_pir\_\_S26494 ribosomal protein S1, chloroplast spinach >gi\_322404\_pir\_\_A44121 small subunit ribosomal
protein CS1, CS-S2 - spinach >gi\_18060\_emb\_CAA46927\_
(X66135) ribosomal protein S1 [Spinacia oleracea]
>gi\_170143 (M82923) chloroplast ribosomal protein S1

[Spīnacia oleracea]

Seq. No. 207821

Seq. ID LIB3120-026-Q1-K1-H9

Method BLASTX
NCBI GI g2494076
BLAST score 309
E value 1.0e-28
Match length 68
% identity 85

NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi\_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase

[Nicotiana plumbaginifolia]

Seq. No. 207822

Seq. ID LIB3120-027-Q1-K1-A2

Method BLASTX
NCBI GI g2791423
BLAST score 197
E value 4.0e-15
Match length 69
% identity 54

NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]

Seq. No. 207823

Seq. ID LIB3120-027-Q1-K1-A3

Method BLASTX
NCBI GI g543905
BLAST score 546
E value 4.0e-56
Match length 140
% identity 71

NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi\_347459 (L22162)

brassinosteroid-regulated protein [Glycine max]

```
Seq. No.
                  LIB3120-027-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g1439609
NCBI GI
                  609
BLAST score
E value
                  2.0e-63
Match length
                  123
                  55
% identity
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  207825
                  LIB3120-027-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006878
                  228
BLAST score
E value
                  9.0e-19
Match length
                  94
                  50
% identity
                  (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                  207826
Seq. No.
Seq. ID
                  LIB3120-027-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  q3913239
BLAST score
                  283
                  3.0e-25
E value
                  128
Match length
% identity
                  51
                  PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP
NCBI Description
                  SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like
                  protein [Oryza sativa]
                  207827
Seq. No.
Seq. ID
                  LIB3120-027-Q1-K1-B1
                  BLASTX
Method
                  q2809246
NCBI GI
                  308
BLAST score
                  1.0e-28
E value
                  86
Match length
% identity
                  63
                  (AC002560) F2401.15 [Arabidopsis thaliana]
NCBI Description
                  207828
Seq. No.
Seq. ID
                  LIB3120-027-Q1-K1-B3
Method
                  BLASTX
                  g4512709
NCBI GI
BLAST score
                  245
                  6.0e-21
E value
Match length
                  58
                  79
% identity
                   (AC006569) putative photosystem I reaction center subunit
NCBI Description
                  IV precursor [Arabidopsis thaliana]
                  207829
Seq. No.
Seq. ID
                  LIB3120-027-Q1-K1-B5
Method
                  BLASTX
```

28590

NCBI GI g126896 BLAST score 648 E value 5.0e-68 Match length 142 % identity 89

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi\_319831\_pir\_\_DEPUMW malate dehydrogenase (EC 1.1.1.37)

precursor, mitochondrial - watermelon

>gi\_18297\_emb\_CAA35239\_ (X17362) precursor protein (AA -27

to 320) [Citrullus lanatus]

Seq. No. 207830

Seq. ID LIB3120-027-Q1-K1-B7

Method BLASTX
NCBI GI g1352821
BLAST score 614
E value 5.0e-64
Match length 118
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207831

Seq. ID LIB3120-027-Q1-K1-B8

Method BLASTX
NCBI GI g285317
BLAST score 451
E value 6.0e-45
Match length 141
% identity 68

NCBI Description dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea

Seq. No. 207832

Seq. ID LIB3120-027-Q1-K1-C2

Method BLASTX
NCBI GI g1755156
BLAST score 408
E value 7.0e-40
Match length 129
% identity 62

NCBI Description (U75189) germin-like protein [Arabidopsis thaliana]

>gi\_1755158 (U75190) germin-like protein [Arabidopsis
thaliana] >gi\_1755170 (U75196) germin-like protein
[Arabidopsis thaliana] >gi\_1755172 (U75197) germin-like
protein [Arabidopsis thaliana] >gi\_1755180 (U75201)
germin-like protein [Arabidopsis thaliana] >gi\_1755190
(U75206) germin-like protein [Arabidopsis thaliana]
>gi\_1934728 (U95035) germin-like protein [Arabidopsis
thaliana] >gi\_4154285 (AF090733) germin-like protein 1

[Arabidopsis thaliana]

Seq. No. 207833

Seq. ID LIB3120-027-Q1-K1-C3

Method BLASTX



NCBI GI g1352821
BLAST score 254
E value 3.0e-22
Match length 65
% identity 80

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207834

Seq. ID LIB3120-027-Q1-K1-C4

Method BLASTX
NCBI GI g322752
BLAST score 190
E value 3.0e-14
Match length 102
% identity 40

NCBI Description auxin-independent growth promoter - Nicotiana tabacum

>gi 559921 emb CAA56570 (X80301) axi 1 [Nicotiana tabacum]

Seq. No. 207835

Seq. ID LIB3120-027-Q1-K1-C6

Method BLASTX
NCBI GI g115470
BLAST score 460
E value 5.0e-49
Match length 140
% identity 70

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

DEHYDRATASE) >gi 320554 pir S28412 carbonate dehydratase

(EC 4.2.1.1) precursor - Arabidopsis thaliana

>gi\_14343\_emb\_CAA46508\_ (X65541) carbonic anhydrase

[Arabidopsis thaliana]

Seq. No. 207836

Seq. ID LIB3120-027-Q1-K1-C7

Method BLASTX
NCBI GI g1352821
BLAST score 635
E value 2.0e-66
Match length 119
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_(X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207837

Seq. ID LIB3120-027-Q1-K1-C8

Method BLASTX
NCBI GI g730922
BLAST score 373
E value 7.0e-36
Match length 130



Seq. No. 207838

Seq. ID LIB3120-027-Q1-K1-D3

Method BLASTX
NCBI GI g289920
BLAST score 596
E value 6.0e-62
Match length 126
% identity 88

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207839

Seq. ID LIB3120-027-Q1-K1-D4

Method BLASTX
NCBI GI g1169534
BLAST score 294
E value 1.0e-26
Match length 64
% identity 89

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_542019\_pir\_\_S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >qi 433609 emb CAA82232 (Z28386) enolase [Ricinus

communis]

Seq. No. 207840

Seq. ID LIB3120-027-Q1-K1-D6

Method BLASTX
NCBI GI g549063
BLAST score 405
E value 2.0e-39
Match length 120
% identity 67

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 207841

Seq. ID LIB3120-027-Q1-K1-D7

Method BLASTX
NCBI GI g400890
BLAST score 154
E value 4.0e-10
Match length 111
% identity 32

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi\_282837\_pir\_\_S26953-photosystem II 22K protein precursor
- spinach >gi\_21307\_emb\_CAA48557\_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi\_260917\_bbs\_119338 (S49864)

photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

 Seq. No.
 207842

 Seq. ID
 LIB3120-027-Q1-K1-D8

 Method
 BLASTX

 NCBI GI
 g1181599

BLAST score 501 E value 9.0e-51 Match length 153 % identity 65

NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]

Seq. No. 207843

Seq. ID LIB3120-027-Q1-K1-E1

Method BLASTX
NCBI GI g4406812
BLAST score 169
E value 3.0e-12
Match length 89
% identity 43

NCBI Description (AC006201) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 207844

Seq. ID LIB3120-027-Q1-K1-E4

Method BLASTX
NCBI GI g3901268
BLAST score 169
E value 7.0e-12
Match length 143
% identity 30

NCBI Description (AF060173) SV2 related protein [Rattus norvegicus]

Seq. No. 207845

Seq. ID LIB3120-027-Q1-K1-E5

Method BLASTX
NCBI GI g2565305
BLAST score 748
E value 9.0e-80
Match length 151
% identity 94

NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x

Triticum sp.]

Seq. No. 207846

Seq. ID LIB3120-027-Q1-K1-E8

Method BLASTX
NCBI GI g4406530
BLAST score 446
E value 2.0e-44
Match length 122
% identity 75

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 207847

Seq. ID LIB3120-027-Q1-K1-F1



```
Method
NCBI GI
                  q3063643
                  398
BLAST score
                  1.0e-38
E value
                  97
Match length
                  82
% identity
                   (AF056622) putative Cu/Zn superoxide dismutase precursor
NCBI Description
                   [Vitis vinifera]
                  207848
Seq. No.
Seq. ID
                  LIB3120-027-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q559964
                  201
BLAST score
                  1.0e-15
E value
Match length
                  146
                  38
% identity
NCBI Description
                  (J05282) insect-type dehydrogenase [Pseudomonas cepacia]
                  207849
Seq. No.
                  LIB3120-027-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115833
BLAST score
                   527
E value
                  7.0e-54
Match length
                  129
                   78
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi 100195 pir S11877 chlorophyll
                   a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                   a-binding protein [Lycopersicon esculentum]
                   207850
Seq. No.
Seq. ID
                   LIB3120-027-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   q1946690
BLAST score
                   511
E value
                   5.0e-52
Match length
                   126
% identity
                   75
                  (U94495) glutathione peroxidase [Arabidopsis thaliana]
NCBI Description
                   207851
Seq. No.
                   LIB3120-027-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q3319882
NCBI GI
BLAST score
                   285
                   1.0e-25
E value
                   71
Match length
                   82
% identity
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
```

207852 Seq. No.

Seq. ID LIB3120-027-Q1-K1-F8

BLASTX Method NCBI GI g4206195

28595

```
BLAST score 223
E value 1.0e-36
Match length 86
% identity 85
```

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] >gi 4262169 gb AAD14469 (AC005275) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 207853

Seq. ID LIB3120-027-Q1-K1-G1

Method BLASTX
NCBI GI 94406812
BLAST score 503
E value 5.0e-51
Match length 127
% identity 73

NCBI Description (AC006201) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 207854

Seq. ID LIB3120-027-Q1-K1-G2

Method BLASTX
NCBI GI g886100
BLAST score 550
E value 1.0e-56
Match length 129
% identity 82

NCBI Description (U27347) putative water channel protein; plasmalemma

intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No. 207855

Seq. ID LIB3120-027-Q1-K1-G4

Method BLASTX
NCBI GI g1354515
BLAST score 316
E value 4.0e-29
Match length 142
% identity 50

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 207856

Seq. ID LIB3120-027-Q1-K1-G5

Method BLASTX
NCBI GI g730922
BLAST score 524
E value 2.0e-53
Match length 149
% identity 69

NCBI Description T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)

(TCP20) (HTR3) >gi\_627402\_pir\_\_S48087 chaperonin TCP20 - human >gi\_517065 (L27706) chaperonin-like protein [Homo sapiens] >gi\_4502643\_ref\_NP\_001753.1\_pCCT6\_ chaperonin

containing T-complex subunit

Seq. No. 207857

Seq. No.

207862

```
LIB3120-027-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  q470373
NCBI GI
                  247
BLAST score
                  5.0e-21
E value
Match length
                  146
                  39
% identity
NCBI Description (U00047) ZK418.5 gene product [Caenorhabditis elegans]
                  207858
Seq. No.
                  LIB3120-027-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  244
                  1.0e-40
E value
Match length
                  91
                  97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  207859
                  LIB3120-027-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129931
                  257
BLAST score
                  2.0e-22
E value
                  94
Match length
                  59
% identity
NCBI Description lycopene beta-cyclase - tomato
Seq. No.
                  207860
Seq. ID
                  LIB3120-027-Q1-K1-H3
Method
                  BLASTX
                  g2493146
NCBI GI
                  310
BLAST score
                  2.0e-28
E value
Match length
                  93
                  70
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148
NCBI Description
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                   [Gossypium hirsutum] >gi 4519415_dbj_BAA75542.1_ (AB024275)
                   vacuolar H+-ATPase c subunit [Citrus unshiu]
                  207861
Seq. No.
Seq. ID
                  LIB3120-027-Q1-K1-H5
                  BLASTX
Method
                  g20729
NCBI GI
                  526
BLAST score
                  1.0e-53
E value
                  149
Match length
                  73
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
```

28597



```
LIB3120-027-Q1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3550663
                  277
BLAST score
                  1.0e-24
E value
Match length
                  130
% identity
                  51
                  (AJ007739) w-3 desaturase [Solanum tuberosum]
NCBI Description
Seq. No.
                  207863
                  LIB3120-027-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1531672
BLAST score
                   610
E value
                  1.0e-63
Match length
                  118
% identity
                  97
                  (U68461) actin [Striga asiatica]
NCBI Description
                   207864
Seq. No.
                  LIB3120-027-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2754849
BLAST score
                   692
E value
                   4.0e-73
Match length
                   155
                   83
% identity
NCBI Description
                   (AF039000) putative serine-glyoxylate aminotransferase
                   [Fritillaria agrestis]
Seq. No.
                   207865
Seq. ID
                  LIB3120-028-Q1-K1-A3
Method
                  BLASTX
                   g100200
NCBI GI
                   477
BLAST score
                   3.0e-48
E value
                   96
Match length
                   92
% identity
                  chlorophyll a/b-binding protein type I precursor - tomato
NCBI Description
                   207866
Seq. No.
Seq. ID
                   LIB3120-028-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                   g2706450
BLAST score
                   341
                   5.0e-32
E value
                   86
Match length
                   81
% identity
                  (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                  pyrophosphatase [Solanum tuberosum]
Seq. No.
                   207867
                  LIB3120-028-Q1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1788928
BLAST score
                   270
```

28598

9.0e-24

E value



```
Match length
                   42
% identity
                   (AE000344) quinolinate synthetase, B protein [Escherichia
NCBI Description
                  coli]
                   207868
Seq. No.
                  LIB3120-028-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1871577
BLAST score
                   236
                   1.0e-19
E value
Match length
                   95
% identity
                   49
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                   207869
Seq. No.
                   LIB3120-028-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352821
                   695
BLAST score
                   2.0e-73
E value
                   137
Match length
% identity
                   97
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase \overline{(EC\ 4.1.1.39)} small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   207870
Seq. No.
                   LIB3120-028-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1181599
BLAST score
                   566
E value
                   2.0e-58
                   146
Match length
                   77
% identity
                   (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                   207871
Seq. No.
                   LIB3120-028-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   g4539324
NCBI GI
BLAST score
                   161
                   6.0e-11
E value
                   126
Match length
% identity
                   38
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                   207872
Seq. No.
                   LIB3120-028-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g1771778
NCBI GI
                   479
BLAST score
```

28599

3.0e-48

111

84

E value

Match length

% identity

```
(X99320) 23 kDa oxygen evolving protein of photosystem II
NCBI Description
                  [Solanum tuberosum]
                  207873
Seq. No.
                  LIB3120-028-Q1-K1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3133272
BLAST score
                  33
E value
                  5.0e-09
Match length
                  115
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T17H7,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  207874
Seq. No.
Seq. ID
                  LIB3120-028-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q3738257
BLAST score
                  164
                   6.0e-12
E value
                  36
Match length
                  92
% identity
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
                   207875
Seq. No.
                  LIB3120-028-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3914940
BLAST score
                   258
                   2.0e-22
E value
Match length
                   123
                   47
% identity
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                   >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase
                   [Spinacia oleracea]
Seq. No.
                   207876
                   LIB3120-028-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g4432855
NCBI GI
BLAST score
                   416
                   7.0e-41
E value
                   131
Match length
                   68
% identity
                   (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
                   207877
Seq. No.
                   LIB3120-028-Q1-K1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1532135
BLAST score
                   298
                   2.0e-27
E value
                   74
Match length
                   76
% identity
                  (U49442) chloroplast mRNA-binding protein CSP41 precursor
NCBI Description
```



## [Spinacia oleracea]

```
207878
Seq. No.
                  LIB3120-028-Q1-K1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g12216
BLAST score
                   39
                   1.0e-12
E value
Match length
                   55
% identity
                   93
NCBI Description
                  Sinapis alba chloroplast rps16 gene
Seq. No.
                   207879
                  LIB3120-028-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2618688
BLAST score
                   282
E value
                   2.0e-25
Match length
                   66
% identity
                   79
NCBI Description
                  (AC002510) putative esterase D [Arabidopsis thaliana]
Seq. No.
                   207880
Seq. ID
                  LIB3120-028-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                   q1354515
BLAST score
                   355
E value
                   1.0e-33
Match length
                   134
% identity
                   56
                   (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
                   207881
Seq. No.
Seq. ID
                  LIB3120-028-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                   g125578
BLAST score
                   468
                   6.0e-47
E value
                   94
Match length
                   94
% identity
NCBI Description
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                   (PRK) >gi 167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
                   207882
Seq. No.
Seq. ID
                  LIB3120-028-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   q2501578
BLAST score
                   303
E value
                   7.0e-28
```

Match length 86 % identity 76

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047

ethylene-responsive protein 1 - Para rubber tree

>gi\_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]



```
207883
Seq. No.
                   LIB3120-028-Q1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4235430
BLAST score
                   377
                   3.0e-36
E value
Match length
                   149
                   52
% identity
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
                   207884
Seq. No.
                   LIB3120-028-Q1-K1-E6
Seq. ID
Method
                   BLASTX
                   g1352821
NCBI GI
BLAST score
                   371
                   9.0e-36
E value
Match length
                   73
% identity
                   97
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   207885
                   LIB3120-028-Q1-K1-E7
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2687434
                   133
BLAST score
                   9.0e-69
E value
                   238
Match length
                   90
% identity
                   Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
Seq. No.
                   207886
                   LIB3120-028-Q1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q461550
BLAST score
                   208
                   1.0e-16
E value
                   98
Match length
                   58
% identity
                   ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_81635_pir__B39732 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma-1 chain precursor, chloroplast -
                   Arabidopsis thaliana >gi 166632 (M61741) ATP synthase
                   gamma-subunit [Arabidopsis thaliana]
                   207887
Seq. No.
                   LIB3120-028-Q1-K1-F1
Seq. ID
                   BLASTX
Method
```

NCBI GI 9430947
BLAST score 355
E value 9.0e-34
Match length 105

28602



% identity 72

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 207888

Seq. ID LIB3120-028-Q1-K1-F11

Method BLASTX
NCBI GI g70647
BLAST score 128
E value 9.0e-18

Match length 60 % identity 25

NCBI Description ubiquitin precursor - Phytophthora infestans

>gi\_3176\_emb\_CAA39250 (X55717) ubiquitin [Phytophthora

infestans]

Seq. No. 207889

Seq. ID LIB3120-028-Q1-K1-F3

Method BLASTX
NCBI GI g1352821
BLAST score 233
E value 2.0e-19
Match length 98
% identity 53

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207890

Seq. ID LIB3120-028-Q1-K1-F5

Method BLASTX
NCBI GI g115765
BLAST score 609
E value 2.0e-63
Match length 147
% identity 50

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi\_100201\_pir\_\_S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi\_19180\_emb\_CAA32197\_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_226546\_prf\_\_1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 207891

Seq. ID LIB3120-028-Q1-K1-F6

Method BLASTX
NCBI GI g430947
BLAST score 427
E value 3.0e-42
Match length 106
% identity 80

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

NCBI Description



```
207892
Seq. No.
                  LIB3120-028-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g2880047
NCBI GI
BLAST score
                  150
                  1.0e-09
E value
Match length
                  67
                  49
% identity
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  207893
                  LIB3120-028-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q430947
BLAST score
                  275
                  2.0e-24
E value
Match length
                  115
                  55
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  207894
                  LIB3120-028-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q430947
BLAST score
                   241
E value
                   1.0e-23
Match length
                   104
                   62
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   207895
Seq. No.
                   LIB3120-028-Q1-K1-H5
Seq. ID
Method
                   BLASTX
                   q1352821
NCBI GI
                   626
BLAST score
                   2.0e-65
E value
                   118
Match length
                   97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   207896
Seq. No.
                   LIB3120-028-Q1-K1-H6
Seq. ID
Method
                   BLASTX
                   q430947
NCBI GI
                   328
BLAST score
                   1.0e-30
E value
                   85
Match length
                   79
% identity
```

28604

[Arabidopsis thaliana]

(U01103) PSI type III chlorophyll a/b-binding protein

Seq. ID



```
207897
Seq. No.
                  LIB3120-028-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363479
BLAST score
                  477
                  6.0e-48
E value
Match length
                  121
                  79
% identity
NCBI Description
                  photosystem I protein psaL - cucumber
                  >gi 801740 dbj BAA09047 (D50456) PsaL [Cucumis sativus]
Seq. No.
                  207898
Seq. ID
                  LIB3120-029-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1877480
BLAST score
                  187
E value
                  3.0e-14
Match length
                  66
% identity
                  59
                  (U89270) short-chain alcohol dehydrogenase [Tripsacum
NCBI Description
                  dactyloides]
                  207899
Seq. No.
                  LIB3120-029-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g309673
BLAST score
                  347
                  4.0e-33
E value
                  93
Match length
                  76
% identity
                  (L19651) light harvesting protein [Pisum sativum]
NCBI Description
                  207900
Seq. No.
Seq. ID
                  LIB3120-029-Q1-K1-C10
                  BLASTX
Method
                                - J: -
                  q3608485
NCBI GI
BLAST score
                   488
                  2.0e-49
E value
                  103
Match length
                  89
% identity
                  (AF088915) proteasome beta subunit [Petunia x hybrida]
NCBI Description
                  207901
Seq. No.
Seq. ID
                  LIB3120-029-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q1351279
BLAST score
                  374
                  5.0e-36
E value
Match length
                  106
                   69
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                  >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase
                   [Petunia x hybrida]
Seq. No.
                  207902
```

28605

LIB3120-029-Q1-K1-E11



Method BLASTX
NCBI GI g100196
BLAST score 367
E value 3.0e-35
Match length 88
% identity 78

NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No. 207903

Seq. ID LIB3120-029-Q1-K1-F10

Method BLASTX
NCBI GI 94406530
BLAST score 250
E value 2.0e-21
Match length 83
% identity 65

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 207904

Seq. ID LIB3120-030-Q1-K1-A1

Method BLASTX
NCBI GI g1352821
BLAST score 594
E value 1.0e-61
Match length 111
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207905

Seq. ID LIB3120-030-Q1-K1-A11

Method BLASTX
NCBI GI g2407800
BLAST score 147
E value 2.0e-09
Match length 43
% identity 72

NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 207906

Seq. ID LIB3120-030-Q1-K1-A2

Method BLASTX
NCBI GI g2117355
BLAST score 144
E value 6.0e-09
Match length 125
% identity 46

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain precursor - potato >gi 587562 emb CAA56520 (X80236)

mitochondrial processing peptidase [Solanum tuberosum]

Seq. No. 207907

Seq. ID LIB3120-030-Q1-K1-A3

Method BLASTX



```
g3600032
NCBI GI
                  185
BLAST score
                   9.0e-14
E value
                   89
Match length
                   49
% identity
                   (AF080119) contains similarity to tropomyosin (Pfam:
NCBI Description
                  Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:
                  ATP-synt B.hmm, score: 10.89) [Arabidopsis thaliana]
Seq. No.
                   207908
                  LIB3120-030-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                   q3702368
NCBI GI
                   489
BLAST score
                   2.0e-49
E value
Match length
                   128
                   73
% identity
                   (AJ001855) alpha subunit of F-actin capping protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   207909
Seq. ID
                   LIB3120-030-Q1-K1-A7
Method
                   BLASTX.
NCBI GI
                   g1170567
BLAST score
                   605
E value
                   6.0e-63
Match length
                   125
                   88
% identity
                   MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                   >gi 1085960 pir S52648 INO1 protein - Citrus paradisi
                   >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                   207910
                   LIB3120-030-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   q1709846
NCBI GI
                   289
BLAST score
                   6.0e-26
E value
Match length
                   140
                   40
% identity
                   PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
NCBI Description
                   22 kDa component of photosystem II [Lycopersicon
                   esculentum]
                   207911
Seq. No.
                   LIB3120-030-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   g131187
NCBI GI
                   377
BLAST score
                   3.0e-36
E value
                   146
Match length
```

58 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi\_72681\_pir\_\_F1SP3 photosystem I chain III precursor -

spinach >gi 21303 emb CAA31523 (X13133) PSI subunit IV

preprotein (AA -77 to 154) [Spinacia oleracea]



>gi\_226166\_prf\_\_1413236A photosystem I reaction center IV
[Spinacia oleracea]

 Seq. No.
 207912

 Seq. ID
 LIB3120-030-Q1-K1-B1

 Method
 BLASTX

 NCBI GI
 g629602

 BLAST score
 524

 BLAST score
 100-53

E value 1.0e-53 Match length 126 % identity 76

NCBI Description probable imbibition protein - wild cabbage

>gi\_488787\_emb\_CAA55893\_ (X79330) putative imbibition

protein [Brassica oleracea]

Seq. No. 207913

Seq. ID LIB3120-030-Q1-K1-B10

Method BLASTX
NCBI GI g131399
BLAST score 370
E value 1.0e-35
Match length 90
% identity 78

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277\_pir\_\_S00411

photosystem II 10K protein precursor - potato

>gi\_21489\_emb\_CAA28450\_ (X04753) ST-LS1 protein [Solanum

tuberosum]

Seq. No. 207914

Seq. ID LIB3120-030-Q1-K1-B12

Method BLASTX
NCBI GI g2129770
BLAST score 186
E value 4.0e-14
Match length 60
% identity 62

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -

Arabidopsis thaliana >gi\_1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 207915

Seq. ID LIB3120-030-Q1-K1-B2

Method BLASTX
NCBI GI g1709846
BLAST score 224
E value 3.0e-18
Match length 61
% identity 44

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi\_706853 (U04336)

22 kDa component of photosystem II [Lycopersicon

esculentum]

Seq. No. 207916

Seq. ID LIB3120-030-Q1-K1-B4

Seq. ID

Method

NCBI GI

BLASTX

g1352821

```
Method
NCBI GI
                  q1169586
                   158
BLAST score
E value
                   1.0e-10
Match length
                   139
                   33
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   (CY-F1) >gi 542079 pir S41287 fructose-bisphosphatase (EC
                   3.1.3.11) - potato >gi 440591 emb CAA54265 (X76946)
                   fructose-1,6-bisphosphatase [Solanum tuberosum]
Seq. No.
                   207917
Seq. ID
                   LIB3120-030-Q1-K1-B6
                   BLASTX
Method
                   q1652467
NCBI GI
                   205
BLAST score
E value
                   4.0e-16
                   65
Match length
                   60
% identity
                  (D90905) hypothetical protein [Synechocystis sp.]
NCBI Description
                   207918
Seq. No.
Seq. ID
                   LIB3120-030-Q1-K1-B8
                   BLASTX
Method
                   q100200
NCBI GI
                   562
BLAST score
E value
                   6.0e-58
Match length
                   137
                   62
% identity
                   chlorophyll a/b-binding protein type I precursor - tomato
NCBI Description
Seq. No.
                   207919
                   LIB3120-030-Q1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244779
BLAST score
                   180
                   3.0e-13
E value
                   101
Match length
% identity
                   44
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   207920
Seq. No.
Seq. ID
                   LIB3120-030-Q1-K1-C10
Method
                   BLASTX
                   g4572671
NCBI GI
BLAST score
                   302
E value
                   1.0e-27
                   97
Match length
                   64
% identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   207921
Seq. No.
                   LIB3120-030-Q1-K1-C12
```

28609



BLAST score 4.0e-35 E value Match length 80 % identity 94

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207922

Seq. ID LIB3120-030-Q1-K1-C3

Method BLASTX NCBI GI q4160346 BLAST score 245 8.0e-21 E value Match length 97 % identity 52

(AL035216) nucleolar protein involved in pre-rRNA NCBI Description

processing [Schizosaccharomyces pombe]

Seq. No. 207923

Seq. ID LIB3120-030-Q1-K1-C6

Method BLASTX NCBI GI q456209 BLAST score 198 E value 3.0e-15 Match length 116 % identity 37

NCBI Description (X75856) TEGT [Rattus norvegicus]

207924 Seq. No.

Seq. ID LIB3120-030-Q1-K1-C9

Method BLASTX NCBI GI g120669 BLAST score 519 6.0e-53 E value Match length 106 % identity 92

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>qi 66014 pir DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

207925 Seq. No.

Seq. ID LIB3120-030-Q1-K1-D1

Method BLASTX NCBI GI q3068713 BLAST score 606 4.0e-63 E value 137 Match length % identity

(AF049236) unknown [Arabidopsis thaliana] NCBI Description

207926 Seq. No.

Seq. ID LIB3120-030-Q1-K1-D10



Method BLASTX
NCBI GI g3176072
BLAST score 487
E value 2.0e-49
Match length 101
% identity 87

NCBI Description (AJ002485) protein phosphatase 1, catalytic beta subunit

[Medicago sativa]

Seq. No. 207927

Seq. ID LIB3120-030-Q1-K1-D11

Method BLASTX
NCBI GI g2541876
BLAST score 323
E value 5.0e-30
Match length 126
% identity 52

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 207928

Seq. ID LIB3120-030-Q1-K1-D12

Method BLASTX
NCBI GI g2129770
BLAST score 160
E value 4.0e-11
Match length 52
% identity 60

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -

Arabidopsis thaliana >gi\_1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 207929

Seq. ID LIB3120-030-Q1-K1-D2

Method BLASTX
NCBI GI g131397
BLAST score 343
E value 3.0e-32
Match length 151
% identity 54

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_81480\_pir\_\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi 225597 prf 1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 207930

Seq. ID LIB3120-030-Q1-K1-D3

Method BLASTX
NCBI GI g2440044
BLAST score 570
E value 6.0e-59



55

% identity
NCBI Description

```
Match length
% identity
                  78
                  (AJ001293) major intrinsic protein PIPB [Craterostigma
NCBI Description
                  plantagineum]
                  207931
Seq. No.
                  LIB3120-030-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2970051
BLAST score
                  456
E value
                  2.0e-45
Match length
                  117
% identity
                  74
NCBI Description
                 (AB012110) ARG10 [Vigna radiata]
                  207932
Seq. No.
                  LIB3120-030-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  g1001355
NCBI GI
BLAST score
                  144
E value
                  6.0e-09
Match length
                  84
% identity
                  38
NCBI Description
                 (D64006) auxin-induced protein [Synechocystis sp.]
                  207933
Seq. No.
                  LIB3120-030-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455158
BLAST score
                  559
E value
                  1.0e-57
Match length
                  133
% identity
                  78
NCBI Description
                 (AL021687) kinase-like protein [Arabidopsis thaliana]
                  207934
Seq. No.
Seq. ID
                  LIB3120-030-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1439609
BLAST score
                  596
E value
                  6.0e-62
Match length
                  143
% identity
NCBI Description
                  (U62778) delta-tonoplast intrinsic protein [Gossypium
                  hirsutum]
                  207935
Seq. No.
                  LIB3120-030-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266936
BLAST score
                  162
                  3.0e-11
E value
Match length
                  84
```

28612

50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi\_282960\_pir\_\_A42840 ribosomal protein L27 - common tobacco >gi\_170306 (M98473) ribosomal protein L27

```
[Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]
```

 Seq. No.
 207936

 Seq. ID
 LIB3120-030-Q1-K1-E2

 Method
 BLASTX

 NCBI GI
 g3914940

 BLAST score
 504

 E value
 3.0e-51

Match length 120 % identity 81

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)

>gi\_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

[Spinacia oleracea]

Seq. No. 207937

Seq. ID LIB3120-030-Q1-K1-E5

Method BLASTX
NCBI GI g505482
BLAST score 162
E value 1.0e-11
Match length 72
% identity 53

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 207938

Seq. ID LIB3120-030-Q1-K1-F1

Method BLASTX
NCBI GI g3023752
BLAST score 342
E value 4.0e-32
Match length 117
% identity 61

NCBI Description FERREDOXIN I PRECURSOR >gi\_1418982\_emb\_CAA99756\_ (Z75520)

ferredoxin-I [Lycopersicon esculentum]

Seq. No. 207939

Seq. ID LIB3120-030-Q1-K1-F4

Method BLASTX
NCBI GI 94468984
BLAST score 264
E value 3.0e-23
Match length 98
% identity 51

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 207940

Seq. ID LIB3120-030-Q1-K1-F6

Method BLASTX
NCBI GI g3252807
BLAST score 153
E value 9.0e-15
Match length 81
% identity 53

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]



```
Seq. No. 207941
```

Seq. ID LIB3120-030-Q1-K1-F7

Method BLASTX
NCBI GI g1352821
BLAST score 269
E value 1.0e-41
Match length 103
% identity 82

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207942

Seq. ID LIB3120-030-Q1-K1-G1

Method BLASTX
NCBI GI g1352821
BLAST score 613
E value 6.0e-64
Match length 120
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207943

Seq. ID LIB3120-030-Q1-K1-G4

Method BLASTX
NCBI GI g289920
BLAST score 584
E value 1.0e-60
Match length 111
% identity 96

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 207944 ·

Seq. ID LIB3120-030-Q1-K1-H1

Method BLASTX
NCBI GI g1703380
BLAST score 635
E value 2.0e-66
Match length 121
% identity 98

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)

ADP-ribosylation factor [Oryza sativa]

Seq. No. 207945

Seq. ID LIB3120-030-Q1-K1-H11

Method BLASTX
NCBI GI g2351580
BLAST score 145
E value 3.0e-09

· 黄芩



Match length 37 % identity

NCBI Description (U82433) thymidine diphospho-glucose 4-6-dehydratase

homolog [Prunus armeniaca]

Seq. No. 207946

LIB3120-030-Q1-K1-H2 Seq. ID

Method BLASTX NCBI GI g1352821 BLAST score 538 2.0e-55 E value 103 Match length 94 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207947

Seq. ID LIB3120-030-Q1-K1-H3

Method BLASTX NCBI GI g1352821 BLAST score 622 6.0e-65 E value 129 Match length 88 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

207948 Seq. No.

Seq. ID LIB3120-030-Q1-K1-H5

BLASTN Method NCBI GI q450504 BLAST score 34 9.0e-10 E value 66 Match length % identity

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate

carboxylase, small subunit

207949 Seq. No.

LIB3120-030-Q1-K1-H7 Seq. ID

Method BLASTX NCBI GI q1352821 600 BLAST score 2.0e-62 E value 129 Match length 86 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]



Seq. No. 207950

Seq. ID LIB3120-030-Q1-K1-H9

Method BLASTX
NCBI GI g115492
BLAST score 515
E value 2.0e-52
Match length 101
% identity 50

NCBI Description CALMODULIN-RELATED PROTEIN >gi\_169205 (M80831)

calmodulin-related protein [Petunia hybrida]

Seq. No. 207951

Seq. ID LIB3120-031-Q1-K1-A12

Method BLASTX
NCBI GI g1352817
BLAST score 402
E value 1.0e-39
Match length 86
% identity 90

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi\_532258 (L26078) ribulose

1,5-bisphosphate carboxylase [Viscum album]

Seq. No. 207952

Seq. ID LIB3120-031-Q1-K1-A2

Method BLASTX
NCBI GI g1352821
BLAST score 678
E value 2.0e-71
Match length 124
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Tibatobe biophophace daibon/rase

Seq. No. 207953

Seq. ID LIB3120-031-Q1-K1-A3

Method BLASTX
NCBI GI g1352821
BLAST score 188
E value 2.0e-14
Match length 61
% identity 66

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_(X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207954

Seq. ID LIB3120-031-Q1-K1-A4

Method BLASTX
NCBI GI g2982259
BLAST score 484



E value Match length 99 92 % identity (AF051212) probable 60s ribosomal protein L13a [Picea NCBI Description mariana] Seq. No. 207955 Seq. ID LIB3120-031-Q1-K1-A5 Method BLASTX q4063760 NCBI GI BLAST score 243 E value 1.0e-20 Match length 81 53 % identity NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana] 207956 Seq. No. LIB3120-031-Q1-K1-A6 Seq. ID Method BLASTX g289920 NCBI GI BLAST score 655 E value 6.0e-69 124 Match length % identity 98 (L07119) chlorophyll A/B binding protein [Gossypium NCBI Description hirsutum] 207957 Seq. No. Seq. ID LIB3120-031-Q1-K1-A8 Method BLASTX g1169422 NCBI GI 510 BLAST score 7.0e-54 E value Match length 124 % identity DIHYDROFOLATE REDUCTASE 1 / THYMIDYLATE SYNTHASE 1 NCBI Description (DHFR-TS) >gi 289193 (L08593) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana] 207958 Seq. No. LIB3120-031-Q1-K1-B1 Seq. ID Method BLASTX g1439609 NCBI GI BLAST score 628 1.0e-65 E value 126 Match length % identity 56 (U62778) delta-tonoplast intrinsic protein [Gossypium NCBI Description hirsutum] 207959 Seq. No. Seq. ID LIB3120-031-Q1-K1-B10 BLASTX Method g1620898 NCBI GI

28617

615

151

4.0e-64

BLAST score

E value Match length

NCBI Description

tabacum]



```
% identity
                  (D87957) protein involved in sexual development [Homo
NCBI Description
                  sapiens]
                  207960
Seq. No.
                  LIB3120-031-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g2499497
NCBI GI
                  332
BLAST score
E value
                  4.0e-31
                  93
Match length
                  72
% identity
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >qi 1161600 emb CAA88841 (Z48977) phosphoglycerate kinase
                   [Nicotiana tabacum]
                  207961
Seq. No.
                  LIB3120-031-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739387
BLAST score
                  195
E value
                  7.0e-15
Match length
                  95
% identity
                   45
                  (AC002505) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  207962
Seq. No.
Seq. ID
                  LIB3120-031-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                   g4406530
BLAST score
                   418
                   5.0e-41
E value
Match length
                   117
                   74
% identity
                   (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                   207963
Seq. No.
                   LIB3120-031-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g2765081
NCBI GI
BLAST score
                   428
                   2.0e-42
E value
                   118
Match length
                   72
% identity
                  (Y10557) g5bf [Arabidopsis thaliana]
NCBI Description
                   207964
Seq. No.
                   LIB3120-031-Q1-K1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4337001
                   377
BLAST score
                   3.0e-36
E value
                   75
Match length
                   83
% identity
```

(AF118129) Tsi1-interacting protein TSIP1 [Nicotiana



```
207965
Seq. No.
                  LIB3120-031-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  g4406530
NCBI GI
                  592
BLAST score
E value
                  2.0e-61
Match length
                  151
% identity
                  77
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  207966
Seq. No.
Seq. ID
                  LIB3120-031-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g136057
BLAST score
                  617
                  2.0e-64
E value
Match length
                  137
% identity
                  85
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi 556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
Seq. No.
                  207967
Seq. ID
                  LIB3120-031-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q113624
BLAST score
                  437
                  2.0e-43
E value
Match length
                  108
% identity
                  81
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                  >gi 22620 emb CAA46649 (X65742) fructose-bisphosphate
                  aldolase [Spinacia oleracea]
                  207968
Seq. No.
Seq. ID
                  LIB3120-031-Q1-K1-C5
                  BLASTX
Method
NCBI GI
                  q1168410
BLAST score
                  520
                   4.0e-53
E value
                  131
Match length
                  80
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                  >gi 2118267 pir S58167 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea >gi 927505 emb CAA61947 (X89829)
                   fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.
                  207969
Seq. ID
                  LIB3120-031-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  g3914604
BLAST score
                  239
```

4.0e-31 E value Match length 128 % identity 53

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR



(RUBISCO SMALL SUBUNIT) >gi\_217946\_dbj\_BAA03103\_ (D14001) riburose-1,5-bisphosphate carboxylase/oxygenase small subunit precursor [Lactuca sativa]

207970 Seq. No. LIB3120-031-Q1-K1-C9 Seq. ID Method BLASTX NCBI GI g421826 BLAST score 419 E value 3.0e-41 Match length 89 % identity 82

chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description

>gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No.

207971 Seq. ID

LIB3120-031-Q1-K1-D10 Method BLASTX NCBI GI q4512659

BLAST score 601 E value 1.0e-62 Match length 125 % identity 87

(AC006931) putative protein kinase [Arabidopsis thaliana] NCBI Description >qi 4544465 gb AAD22372.1 AC006580 4 (AC006580) putative

protein kinase [Arabidopsis thaliana]

Seq. No. 207972

LIB3120-031-Q1-K1-D11 Seq. ID

Method BLASTX NCBI GI g3643607 BLAST score 449 1.0e-44 E value Match length 94 % identity 89

(AC005395) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

207973

LIB3120-031-Q1-K1-D12 Seq. ID

BLASTX Method g1352821 NCBI GI 359 BLAST score 2.0e-34 E value 72 Match length 97 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC  $\overline{4.1.1.39}$ ) small chain precursor - upland cotton >gi\_450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

207974

Seq. ID LIB3120-031-Q1-K1-D2

Method BLASTX NCBI GI g1352821 BLAST score 557



E value 2.0e-57
Match length 105
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 207975

Seq. ID LIB3120-031-Q1-K1-D4

Method BLASTX
NCBI GI g2129740
BLAST score 444
E value 2.0e-44
Match length 94
% identity 87

NCBI Description small nuclear ribonucleoprotein - Arabidopsis thaliana

>gi\_2129756\_pir\_\_S71411 U1 snRNP 70K protein - Arabidopsis

thaliana >gi\_1255711 (M93439) small nuclear

ribonucleoprotein [Arabidopsis thaliana] >gi\_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No. 207976

Seq. ID LIB3120-031-Q1-K1-D5

Method BLASTN
NCBI GI g18511
BLAST score 231
E value 1.0e-127
Match length 319
% identity 93

NCBI Description G.hirsutum light regulated unknown reading frame DNA

Seq. No. 207977

Seq. ID LIB3120-031-Q1-K1-D7

Method BLASTX
NCBI GI g1354515
BLAST score 391
E value 7.0e-38
Match length 157
% identity 54

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 207978

Seq. ID LIB3120-031-Q1-K1-D8

Method BLASTN
NCBI GI g516563
BLAST score 76
E value 1.0e-34
Match length 130
% identity 89

NCBI Description Solanum tuberosum L. chloroplast ribosomal protein S16

(rps16) precursor mRNA, complete cds

Seq. No. 207979

Seq. ID LIB3120-031-Q1-K1-E1



Method BLASTX
NCBI GI g132168
BLAST score 568
E value 1.0e-58
Match length 131
% identity 77

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi\_81488\_pir\_\_A31082 ribulose-bisphosphate carboxylase activase precursor -spinach >gi\_170129 (J03610) rubisco activase precursor

[Spinacia oleracea]

Seq. No. 207980

Seq. ID LIB3120-031-Q1-K1-E11

Method BLASTX
NCBI GI g1354515
BLAST score 238
E value 5.0e-20
Match length 122
% identity 48

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 207981

Seq. ID LIB3120-031-Q1-K1-E4

Method BLASTX
NCBI GI g131194
BLAST score 213
E value 8.0e-27
Match length 91
% identity 71

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR

(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi\_72686\_pir\_\_F1SP5

photosystem I chain V precursor - spinach

>gi\_21299\_emb\_CAA31524 (X13134) PSI subunit V preprotein
(AA -69 to 98) [Spinacia oleracea] >gi\_226167\_prf\_\_1413236B

photosystem I reaction center V [Spinacia oleracea]

Seq. No. 207982

Seq. ID LIB3120-031-Q1-K1-E6

Method BLASTN
NCBI GI g2687435
BLAST score 79
E value 1.0e-36
Match length 266
% identity 85

NCBI Description Hamamelis virginiana large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 207983

Seq. ID LIB3120-031-Q1-K1-E7

Method BLASTX
NCBI GI g3169180
BLAST score 188
E value 3.0e-14
Match length 43

% identity 77

28622

14



NCBI Description (AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana] 207984 Seq. No. LIB3120-031-Q1-K1-F1 Seq. ID BLASTX Method NCBI GI q4406530 412 BLAST score 2.0e-40 E value Match length 116 74 % identity (AF126870) rubisco activase [Vigna radiata] NCBI Description 207985 Seq. No. Seq. ID LIB3120-031-Q1-K1-F11 Method BLASTX q135442 NCBI GI BLAST score 405 1.0e-39 E value Match length 94 83 % identity TUBULIN BETA-1 CHAIN >gi\_71590\_pir\_\_UBMUBM tubulin beta-1 NCBI Description chain - Arabidopsis thaliana >gi 166922 (M20405) beta-1 tubulin [Arabidopsis thaliana] Seq. No. 207986 Seq. ID LIB3120-031-Q1-K1-F2 Method BLASTX NCBI GI q2736288 255 BLAST score 3.0e-33 E value 95 Match length 79 % identity (AF031080) isopentenyl diphosphate isomerase II NCBI Description [Camptotheca acuminata] Seq. No. 207987 Seq. ID LIB3120-031-Q1-K1-F3 Method BLASTX NCBI GI g131397 BLAST score 215 2.0e-17 E value Match length 115 45 % identity OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD NCBI Description SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480 pir S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach

>gi 755802 emb CAA29056 (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi 225597 prf 1307179B luminal protein 16kD

[Spinacia oleracea]

207988 Seq. No.

Seq. ID LIB3120-031-Q1-K1-F4

BLASTX Method NCBI GI g119937



```
BLAST score
 E value
                    2.0e-17
 Match length
                    70
 % identity
                    67
 NCBI Description
                    FERREDOXIN I PRECURSOR >gi_65741_pir__FESP1 ferredoxin
                    [2Fe-2S] I precursor - spinach > \overline{g}i 170109 (M35660)
                    ferredoxin I precursor [Spinacia oleracea]
                    >gi_227453_prf__1704156A ferredoxin I [Spinacia oleracea]
 Seq. No.
                    207989
 Seq. ID
                    LIB3120-031-Q1-K1-F5
Method
                    BLASTX
NCBI GI
                    g2493046
BLAST score
                    302
E value
                    1.0e-27
Match length
                    91
 % identity
                    67
NCBI Description
                   ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                    >gi_82297_pir_ A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato
                    >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                    delta subunit [Ipomoea batatas]
Seq. No.
                    207990
Seq. ID
                   LIB3120-031-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g3320462
BLAST score
                    162
E value
                   3.0e-11
Match length
                   65
% identity
                   48
NCBI Description (AF062467) polygalacturonase precursor [Cucumis melo]
Seq. No.
                   207991
Seq. ID
                   LIB3120-031-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2765081
BLAST score
                   462
E value
                   3.0e-46
Match length
                   127
% identity
                   75
NCBI Description
                  (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                   207992
Seq. ID
                   LIB3120-031-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g1872544
BLAST score
                   200
E value
                   8.0e-19
Match length
                   106
% identity
                   51
NCBI Description
                   (U89014) early light-induced protein; ELIP [Arabidopsis
                   thaliana]
```

Seq. No. 207993

Seq. ID LIB3120-031-Q1-K1-G11

Method BLASTX

```
q4468813
NCBI GI
                  179
BLAST score
                  1.0e-13
E value
                  43
Match length
                  77
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                  207994
Seq. No.
                  LIB3120-031-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g2738949
NCBI GI
                  453
BLAST score
                  2.0e-45
E value
                  94
Match length
                  91
% identity
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                  ananassa]
                  207995
Seq. No.
                  LIB3120-031-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g217909
NCBI GI
BLAST score
                  484
                  9.0e-49
E value
                  138
Match length
% identity
                  73
                  (D14044) glycolate oxidase [Cucurbita sp.]
NCBI Description
                  207996
Seq. No.
                  LIB3120-031-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                  q2554675
NCBI GI
                  170
BLAST score
                  1.0e-12
E value
Match length
                  44
                  80
% identity
                  Three-Dimensional Structure Of Glycolate Oxidase With Bound
NCBI Description
                  Active-Site Inhibitors >gi_2624594_pdb_1AL7
                  Three-Dimensional Structures Of Glycolate Oxidase With
                  Bound Active-Site Inhibitors
                  207997
Seq. No.
                  LIB3120-031-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g228403
NCBI GI
                   383
BLAST score
                   3.0e-37
E value
Match length
                   82
% identity
NCBI Description glycolate oxidase [Lens culinaris]
```

Seq. No. 207998

Seq. ID LIB3120-031-Q1-K1-H11

Method BLASTX
NCBI GI g266936
BLAST score 147
E value 7.0e-10



```
Match length
% identity
                  62
                  50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27)
NCBI Description
                  >gi 282960 pir A42840 ribosomal protein L27 - common
                  tobacco >gi 170306 (M98473) ribosomal protein L27
                  [Nicotiana Tabacum] >gi_170326 (M75731) ribosomal protein
                  L27 [Nicotiana tabacum]
                  207999
Seq. No.
                  LIB3120-031-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1006704
BLAST score
                  191
                  5.0e-15
E value
                  49
Match length
                  76
% identity
                  (Z49749) light-harvesting chlorophyll a/b binding protein
NCBI Description
                  of photosystem II [Pseudotsuga menziesii]
                  208000
Seq. No.
                  LIB3120-031-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                  g461498
NCBI GI
BLAST score
                  175
                  3.0e-13
E value
Match length
                  69
                  51
% identity
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi 320619 pir S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi 296204_emb_CAA49199_ (X69421)
                  alanine aminotransferase [Panicum miliaceum]
Seq. No.
                  208001
                  LIB3120-031-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1181599
BLAST score
                  236
                   4.0e-20
E value
Match length
                  82
                   60
% identity
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
Seq. No.
                   208002
                  LIB3120-031-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1168411
BLAST score
                   181
                   6.0e-27
E value
Match length
                   117
                   68
% identity
```

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No.

208003

Seq. ID

LIB3120-032-Q1-K1-A1

Method NCBI GI BLASTX g115471



BLAST score 483 E value 1.0e-48 Match length 151 % identity 64

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

DEHYDRATASE) >gi\_100078\_pir\_\_S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi\_20673\_emb\_CAA36792\_(X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No. 208004

Seq. ID LIB3120-032-Q1-K1-A2

Method BLASTN
NCBI GI g19784
BLAST score 53
E value 5.0e-21
Match length 136
% identity 89

NCBI Description N.tabacum atpC mRNA for gamma subunit of ATP synthase

Seq. No. 208005

Seq. ID LIB3120-032-Q1-K1-A3

Method BLASTX
NCBI GI g625547
BLAST score 542
E value 1.0e-55
Match length 137
% identity 72

NCBI Description chlorophyll a/b-binding protein type I - common tobacco

>gi\_493723\_emb\_CAA45523\_ (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

Seq. No. 208006

Seq. ID LIB3120-032-Q1-K1-A5

Method BLASTX
NCBI GI g4512653
BLAST score 716
E value 5.0e-76
Match length 154
% identity 88

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 208007

Seq. ID LIB3120-032-Q1-K1-A6

Method BLASTX
NCBI GI g3367596
BLAST score 156
E value 3.0e-10
Match length 76
% identity 43

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 208008

Seq. ID LIB3120-032-Q1-K1-A7

Method BLASTX NCBI GI g2832644 BLAST score 222

```
E value 5.0e-18
Match length 72
% identity 64
NCBI Description (AL021710) teosinte branched1 - like protein [Arabidopsis thaliana]
Seq. No. 208009
```

 Seq. ID
 LIB3120-032-Q1-K1-A8

 Method
 BLASTX

 NCBI GI
 g3914603

 BLAST score
 756

 E value
 1.0e-80

 Match length
 151

 % identity
 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

 Seq. No.
 208010

 Seq. ID
 LIB3120-032-Q1-K1-B2

 Method
 BLASTX

 NCBI GI
 g2564237

 BLAST score
 531

E value 3.0e-54 Match length 117 % identity 80

NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 208011

Seq. ID LIB3120-032-Q1-K1-B5

Method BLASTX
NCBI GI g4218123
BLAST score 193
E value 6.0e-17
Match length 125
% identity 46

NCBI Description (AL035353) photosystem I subunit PSI-E-like protein

[Arabidopsis thaliana]

Seq. No. 208012

Seq. ID LIB3120-032-Q1-K1-B7

Method BLASTX
NCBI GI g20729
BLAST score 518
E value 9.0e-53
Match length 135
% identity 78

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 208013

Seq. ID LIB3120-032-Q1-K1-B8

Method BLASTX
NCBI GI g1421730
BLAST score 473
E value 2.0e-59
Match length 154



```
% identity 72
NCBI Description (U43082) RF2 [Zea mays]
Seq. No. 208014
Seq. ID LIB3120-032-Q1-K1-C1
Method BLASTX
```

NCBI GI g3068713
BLAST score 591
E value 3.0e-61
Match length 133
% identity 86

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 208015

Seq. ID LIB3120-032-Q1-K1-C2

Method BLASTX
NCBI GI g1352821
BLAST score 542
E value 1.0e-55
Match length 105
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208016

Seq. ID LIB3120-032-Q1-K1-C3

Method BLASTN
NCBI GI g2599346
BLAST score 95
E value 6.0e-46
Match length 119
% identity 95

NCBI Description Fragaria x ananassa tRNA-Leu (trnL) gene, chloroplast gene

for chloroplast RNA, partial sequence

Seq. No. 208017

Seq. ID LIB3120-032-Q1-K1-C4

Method BLASTX
NCBI GI g3980238
BLAST score 179
E value 5.0e-13
Match length 56
% identity 59

NCBI Description (Z21677) ribosomal protein L18 [Thermotoga maritima]

Seq. No. 208018

Seq. ID LIB3120-032-Q1-K1-D1

Method BLASTX
NCBI GI 9480737
BLAST score 352
E value 3.0e-33
Match length 89
% identity 79

NCBI Description triose phosphate/3-phosphoglycerate/phosphate translocator

Š



78

% identity

- common tobacco >gi\_629694\_pir\_\_S42583 phosphate
translocator - common tobacco >gi\_403023\_emb\_CAA52979\_
(X75088) phosphate translocator [Nicotiana tabacum]

208019 Seq. No. LIB3120-032-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI q20729 350 BLAST score 4.0e-33 E value Match length 102 70 % identity NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum] Seq. No. 208020 LIB3120-032-Q1-K1-D3 Seq. ID Method BLASTX NCBI GI q3107905 BLAST score 248 E value 3.0e-21 Match length 116 16 % identity (D85101) leaf protein [Ipomoea nil] NCBI Description Seq. No. 208021 LIB3120-032-Q1-K1-D4 Seq. ID Method BLASTX q2498291 NCBI GI BLAST score 253 8.0e-22 E value 126 Match length % identity DIHYDRODIPICOLINATE REDUCTASE >gi 1651716 dbj BAA16644 NCBI Description (D90899) dihydrodipicolinate reductase [Synechocystis sp.] Seq. No. 208022 Seq. ID LIB3120-032-Q1-K1-D5 Method BLASTX NCBI GI q3294491 BLAST score 192 E value 2.0e-14 Match length 118 % identity 37 NCBI Description (AF016421) Similar to nitrophenylphosphatase; coded for by C. elegans cDNA yk312h2.5; coded for by C. elegans cDNA yk267e8.5; coded for by C. elegans cDNA yk312h2.3 [Caenorhabditis elegans] 208023 Seq. No. Seq. ID LIB3120-032-Q1-K1-E1 Method BLASTX q4538963 NCBI GI 306 BLAST score 4.0e-28 E value Match length 75

28630

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

Time.

NCBI GI

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g18487



## [Arabidopsis thaliana]

```
208024
  Seq. No.
                    LIB3120-032-Q1-K1-E3
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4220524
  BLAST score
                    174
  E value
                    6.0e-18
                    107
  Match length
                    48
  % identity
  NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                    208025
  Seq. No.
                    LIB3120-032-Q1-K1-E4
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2462749
BLAST score
                    181
                    3.0e-13
  E value
  Match length
                    56
                    55
  % identity
  NCBI Description (AC002292) Putative Serine/Threonine protein kinase
                    [Arabidopsis thaliana]
                    208026
  Seq. No.
  Seq. ID
                    LIB3120-032-Q1-K1-F1
  Method
                    BLASTX
                    g99600
  NCBI GI
  BLAST score
                    414
  E value
                    1.0e-40
  Match length
                    98
                    84
  % identity
  NCBI Description chlorophyll a/b-binding protein - upland cotton
                    208027
  Seq. No.
                    LIB3120-032-Q1-K1-F3
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g1168411
                    325
  BLAST score
  E value
                    1.0e-37
  Match length
                    113
  % identity
                    79
  NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                    208028
  Seq. No.
  Seq. ID
                    LIB3120-032-Q1-K1-F5
  Method
                    BLASTX
  NCBI GI
                    q1168411
  BLAST score
                    559
  E value
                    1.0e-57
  Match length
                    146
  % identity
                    80
  NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                    208029
  Seq. No.
  Seq. ID
                    LIB3120-032-Q1-K1-F8
                    BLASTN
  Method
```

```
BLAST score
                   1.0e-21
E value
Match length
                  131
                  95
% identity
NCBI Description G. hirsutum mRNA for cotton catalase subunit
Seq. No.
                   208030
                  LIB3120-032-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g285317
BLAST score
                   229
E value
                   1.0e-27
Match length
                   115
                   65
% identity
NCBI Description dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea
                   208031
Seq. No.
Seq. ID
                   LIB3120-032-Q1-K1-G2
Method
                   BLASTN
NCBI GI
                   q289919
BLAST score
                   166
                   1.0e-88
E value
Match length
                   199
% identity
                   98
                  Gossypium hirsutum chloroplast photosystem II chlorophyll
NCBI Description
                   A/B-binding protein gene, complete cds
                   208032
Seq. No.
Seq. ID
                   LIB3120-032-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g131385
BLAST score
                   498
E value
                   2.0e-50
```

Match length 130

% identity 81

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

208033 Seq. No.

LIB3120-032-Q1-K1-G6 Seq. ID

Method BLASTX g553107 NCBI GI BLAST score 448 1.0e-50 E value 152 Match length % identity 71

(L04967) triosephosphate isomerase [Oryza sativa] NCBI Description

208034 Seq. No.

LIB3120-032-Q1-K1-H2 Seq. ID

Method BLASTX NCBI GI g118564 BLAST score 663 9.0e-70E value Match length 152 82 % identity



GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE NCBI Description REDUCTASE) (HPR) (GDH) >gi\_65955\_pir\_\_DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi 18275 emb CAA32764 (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus] 208035 Seq. No. Seq. ID LIB3120-032-Q1-K1-H4 Method BLASTX NCBI GI q421826 BLAST score 402 3.0e-39 E value 82 Match length % identity 83 NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis thaliana] 208036 Seq. No. Seq. ID LIB3120-032-Q1-K1-H6 Method BLASTX NCBI GI q3047405 249 BLAST score 3.0e-21E value Match length 140 % identity 33 (AF058333) tyrosine phosphorylated protein A [Escherichia NCBI Description coli] Seq. No. 208037 LIB3120-033-P1-K1-A1 Seq. ID Method BLASTN NCBI GI g3522932 BLAST score 40 E value 3.0e-13 96 Match length % identity 85 Arabidopsis thaliana chromosome II BAC F14M4 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 208038 Seq. No. LIB3120-033-P1-K1-A2 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 668

E value 2.0e-70 Match length 132 92 % identity

Seq. No.

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

208039



Seq. ID LIB3120-033-P1-K1-A3

Method BLASTX g1352821 NCBI GI BLAST score 433 7.0e-43E value Match length 85 % identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208040

Seq. ID LIB3120-033-P1-K1-A8

Method BLASTX NCBI GI g1352821 BLAST score 96 2.0e-09 E value 67 Match length % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

208041 Seq. No.

Seq. ID LIB3120-033-P1-K1-B1

Method BLASTX NCBI GI g1170567 BLAST score 482 E value 2.0e-53 Match length 145 % identity 74

NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi 1085960 pir S52648 INO1 protein - Citrus paradisi >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]

Seq. No. 208042

Seq. ID LIB3120-033-P1-K1-B2

Method BLASTX g1352821 NCBI GI BLAST score 649 4.0e-68 E value 122 Match length % identity 99

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208043

Seq. ID LIB3120-033-P1-K1-B3

BLASTX Method NCBI GI g1352821



BLAST score E value 2.0e-16 Match length 65 69 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

208044 Seq. No.

Seq. ID LIB3120-033-P1-K1-B5

Method BLASTX q1045614 NCBI GI BLAST score 157 1.0e-20 E value 104 Match length 56 % identity

(U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis] NCBI Description

208045 Seq. No.

LIB3120-033-P1-K1-B6 Seq. ID

Method BLASTX NCBI GI q1352821 BLAST score 269 7.0e-24 E value Match length 81 72 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208046

Seq. ID LIB3120-033-P1-K1-B8

Method BLASTX NCBI GI g1352821 BLAST score 267 E value 1.0e-23 Match length 69 80 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

208047 Seq. No.

Seq. ID LIB3120-033-P1-K1-C1

BLASTX Method NCBI GI q462195 BLAST score 395 2.0e-38 E value Match length 84 92 % identity

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi\_100682\_pir\_\_S21636 GOS2 protein - rice
>gi\_20238 emb\_CAA36190\_ (X51910) GOS2 [Oryza sativa]
>gi\_3789950 (AF094774) translation initiation factor [Oryza

satīva]

Seq. No. 208048

Seq. ID LIB3120-033-P1-K1-C2

Method BLASTX
NCBI GI g1352821
BLAST score 650
E value 3.0e-68
Match length 122
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208049

Seq. ID LIB3120-033-P1-K1-C3

Method BLASTX
NCBI GI g1352821
BLAST score 325
E value 2.0e-30
Match length 70
% identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208050

Seq. ID LIB3120-033-P1-K1-C4

Method BLASTX
NCBI GI g1352821
BLAST score 596
E value 5.0e-62
Match length 121
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208051

Seq. ID LIB3120-033-P1-K1-C5

Method BLASTX
NCBI GI g462195
BLAST score 123
E value 1.0e-10
Match length 61
% identity 70

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi 100682\_pir\_\_S21636 GOS2 protein - rice



>gi\_20238\_emb\_CAA36190\_ (X51910) GOŞ2 [Oryza sativa]
>gi\_3789950 (AF094774) translation initiation factor [Oryza sativa]

 Seq. No.
 208052

 Seq. ID
 LIB3120-033-P1-K1-C6

 Method
 BLASTX

NCBI GI g1352821 BLAST score 196 E value 3.0e-15 Match length 67 % identity 64

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208053

Seq. ID LIB3120-033-P1-K1-C8

Method BLASTX
NCBI GI g1352821
BLAST score 467
E value 6.0e-47
Match length 102
% identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208054

Seq. ID LIB3120-033-P1-K1-D2

Method BLASTX
NCBI GI g1352821
BLAST score 614
E value 5.0e-64
Match length 114
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208055

Seq. ID LIB3120-033-P1-K1-D3

Method BLASTX
NCBI GI g115581
BLAST score 416
E value 1.0e-65
Match length 141
% identity 83

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE)

>gi\_68031\_pir\_\_QYIX2 phosphoenolpyruvate carboxylase (EC
4.1.1.31) 2 - common ice plant >gi\_4469271\_emb\_CAA32728\_



(X14588) phosphoenolpyruvate carboxylase [Mesembryanthemum crystallinum]

Seq. No. 208056

Seq. ID LIB3120-033-P1-K1-D5

Method BLASTX
NCBI GI g100763
BLAST score 203
E value 1.0e-17
Match length 86
% identity 57

NCBI Description phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sorghum

Seq. No. 208057

Seq. ID LIB3120-033-P1-K1-D6

Method BLASTX
NCBI GI g1352821
BLAST score 465
E value 1.0e-46
Match length 114
% identity 80

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208058

Seq. ID LIB3120-033-P1-K1-D7

Method BLASTX
NCBI GI g115583
BLAST score 289
E value 2.0e-34
Match length 110
% identity 69

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) (CP28)

>gi 100758\_pir\_\_S18240 phosphoenolpyruvate carboxylase (EC

4.1.1.31) - sorghum >gi\_22593\_emb\_CAA42549\_ (X59925) phosphoenolpyruvate carboxylase [Sorghum bicolor]

Seq. No. 208059

Seq. ID LIB3120-033-P1-K1-D8

Method BLASTX
NCBI GI g231610
BLAST score 404
E value 2.0e-39
Match length 144
% identity 62

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi\_67880\_pir\_\_PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi\_19785\_emb\_CAA45152\_ (X63606) ATP synthase

Children .

(gamma subunit) [Nicotiana tabacum]

Seq. No. 208060

Seq. ID LIB3120-033-P1-K1-E1

Method BLASTN



```
NCBI GI g289919
BLAST score 53
E value 5.0e-21
Match length 129
% identity 86
NCBI Description Gossypi
A/B-bind
```

NCBI Description Gossypium hirsutum chloroplast photosystem II chlorophyll A/B-binding protein gene, complete cds

Seq. No. 208061

Seq. ID LIB3120-033-P1-K1-E2

Method BLASTX
NCBI GI g231610
BLAST score 545
E value 6.0e-56
Match length 143
% identity 76

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi\_67880\_pir\_\_PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi\_19785\_emb\_CAA45152\_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 208062

Seq. ID LIB3120-033-P1-K1-E4

Method BLASTX
NCBI GI g115473
BLAST score 335
E value 2.0e-31
Match length 99
% identity 63

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

DEHYDRATASE) >gi\_170219 (M94135) chloroplast carbonic anhydrase [Nicotiana tabacum] >gi\_445610\_prf\_\_1909357A

carbonic anhydrase [Nicotiana tabacum]

Seq. No. 208063

Seg. ID LIB3120-033-P1-K1-E6

Method BLASTX
NCBI GI g231610
BLAST score 476
E value 6.0e-48
Match length 128
% identity 77

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi\_67880\_pir\_\_PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi\_19785\_emb\_CAA45152\_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 208064

Seq. ID LIB3120-033-P1-K1-F2

Method BLASTX
NCBI GI g2454182
BLAST score 473
E value 1.0e-47
Match length 113
% identity 77



(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No. 208065

NCBI Description

Seq. ID LIB3120-033-P1-K1-F8

Method BLASTX
NCBI GI g1781348
BLAST score 260
E value 5.0e-23
Match length 74
% identity 69

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No. 208066

Seq. ID LIB3120-033-P1-K1-G2

Method BLASTX
NCBI GI g1781348
BLAST score 528
E value 5.0e-54
Match length 105
% identity 95

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No. 208067

Seq. ID LIB3120-033-P1-K1-G4

Method BLASTX
NCBI GI g3914940
BLAST score 367
E value 2.0e-40
Match length 141
% identity 67

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi\_2529376 (L76556) sedoheptulose-1,7-bisphosphatase

[Spinacia oleracea]

Seq. No. 208068

Seq. ID LIB3120-033-P1-K1-H3

Method BLASTX
NCBI GI g289920
BLAST score 541
E value 1.0e-55
Match length 107
% identity 93

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 208069

Seq. ID LIB3120-033-P1-K1-H4

Method BLASTX
NCBI GI g1352821
BLAST score 495
E value 4.0e-50
Match length 108
% identity 86



NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208070

Seq. ID LIB3120-033-P1-K1-H5

Method BLASTX
NCBI GI g1354515
BLAST score 138
E value 1.0e-08
Match length 65
% identity 52

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 208071

Seq. ID LIB3120-033-P1-K1-H8

Method BLASTX
NCBI GI g2529342
BLAST score 323
E value 3.0e-30
Match length 89
% identity 72

NCBI Description (L76554) transketolase [Spinacia oleracea]

Seq. No. 208072

Seq. ID LIB3120-034-Q1-K1-A1

Method BLASTX
NCBI GI g3386621
BLAST score 336
E value 8.0e-32
Match length 72

% identity 92

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 208073

Seq. ID LIB3120-034-Q1-K1-A2

Method BLASTX
NCBI GI g4206194
BLAST score 153
E value 2.0e-10
Match length 52
% identity 54

NCBI Description (AF071527) GH3-like protein [Arabidopsis thaliana]

>gi 4262168 gb\_AAD14468\_ (AC005275) putative GH3-like

protein [Arabidopsis thaliana]

Seq. No. 208074

Seq. ID LIB3120-034-Q1-K1-A4

Method BLASTX
NCBI GI g2754849
BLAST score 544
E value 5.0e-56
Match length 112
% identity 92



(AF039000) putative serine-glyoxylate aminotransferase NCBI Description [Fritillaria agrestis] 208075 Seq. No. LIB3120-034-Q1-K1-A5 Seq. ID Method BLASTX NCBI GI g20729 199 BLAST score 6.0e-16 E value Match length 67 64 % identity (X15190) precursor (AA -68 to 337) [Pisum sativum] NCBI Description Seq. No. 208076 LIB3120-034-Q1-K1-A6 Seq. ID Method BLASTX g1076534 NCBI GI 277 BLAST score 1.0e-24 E value 78 Match length 65 % identity monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden NCBI Description pea >gi\_497120 (U06461) monodehydroascorbate reductase [Pisum sativum] Seq. No. 208077 LIB3120-034-Q1-K1-A8 Seq. ID Method BLASTX g2501578 NCBI GI BLAST score 336 E value 9.0e-32 73 Match length 93 % identity NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi\_2129913\_pir\_\_S60047 ethylene-responsive protein 1 - Para rubber tree >gi 1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis] 208078 Seq. No. Seq. ID LIB3120-034-Q1-K1-B1 BLASTX Method NCBI GI q3687652 BLAST score 421 8.0e-42 E value Match length 86 94 % identity (AF047352) rubisco activase precursor [Datisca glomerata] NCBI Description Seq. No. 208079 Seq. ID LIB3120-034-Q1-K1-B11 Method BLASTX NCBI GI q2275202 BLAST score 214

28642

NCBI Description (AC002337) acyl-CoA synthetase isolog [Arabidopsis

3.0e-17

94

70

E value Match length

% identity



## thaliana]

 Seq. No.
 208080

 Seq. ID
 LIB3120-034-Q1-K1-B12

 Method
 BLASTX

 NCBI GI
 g1352821

NCBI GI g1352821 BLAST score 550 E value 1.0e-56 Match length 106 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208081

Seq. ID LIB3120-034-Q1-K1-B6

Method BLASTX
NCBI GI g289920
BLAST score 363
E value 6.0e-35
Match length 84
% identity 85

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 208082

Seq. ID LIB3120-034-Q1-K1-B7

Method BLASTN
NCBI GI g4455189
BLAST score 34
E value 1.0e-09
Match length 110
% identity 83

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSAII project)

Seq. No. 208083

Seq. ID LIB3120-034-Q1-K1-B8

Method BLASTX
NCBI GI g1076316
BLAST score 253
E value 9.0e-22
Match length 85
% identity 53

NCBI Description drought-induced protein Di19 - Arabidopsis thaliana

>gi 469110\_emb\_CAA55321\_ (X78584) Di19 [Arabidopsis

thaliana]

Seq. No. 208084

Seq. ID LIB3120-034-Q1-K1-C10

Method BLASTX
NCBI GI g543867
BLAST score 379
E value 1.0e-36
Match length 101



% identity 78 NCBI Description ATP SYN

ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_1076684\_pir\_\_A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi\_303626\_dbj\_BAA03526\_ (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

Seq. No. 208085

Seq. ID LIB3120-034-Q1-K1-C11

Method BLASTX
NCBI GI g399082
BLAST score 166
E value 1.0e-11
Match length 89
% identity 43

NCBI Description ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR

>gi\_322713\_pir\_\_S28171 H+-transporting ATP synthase (EC
3.6.1.34) delta chain, chloroplast - garden pea >gi\_169045

(M94558) ATP synthase delta subunit [Pisum sativum]

Seq. No. 208086

Seq. ID LIB3120-034-Q1-K1-C2

Method BLASTX
NCBI GI g1354515
BLAST score 178
E value 4.0e-13
Match length 101
% identity 46

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 208087

Seq. ID LIB3120-034-Q1-K1-C4

Method BLASTX
NCBI GI g505482
BLAST score 413
E value 1.0e-40
Match length 109
% identity 81

NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of

photosystem II [Nicotiana tabacum]

Seq. No. 208088

Seq. ID LIB3120-034-Q1-K1-C8

Method BLASTX
NCBI GI g140310
BLAST score 158
E value 1.0e-10
Match length 35
% identity 89

NCBI Description PHOTOSYSTEM II REACTION CENTRE T PROTEIN

>gi 82528 pir JQ0254 hypothetical 4K protein (psbH-petB

intergenic region) - rice chloroplast

>gi\_12014\_emb\_CAA33974\_ (X15901) ORF35 [Oryza sativa]
>gi\_2143324\_emb\_CAA73766\_ (Y13328) PSII subunit [Populus
deltoides] >gi\_226636\_prf\_\_1603356BK ORF 35 [Oryza sativa]

```
208089
Seq. No.
                  LIB3120-034-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g1199772
NCBI GI
                  287
BLAST score
E value
                  8.0e-26
Match length
                  108
% identity
                  60
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                  >qi 1199774 dbj BAA11855 (D83227) extensin like protein
                   [Populus nigra]
Seq. No.
                  208090
Seq. ID
                  LIB3120-034-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3617741
BLAST score
                  537
E value
                   4.0e-55
Match length
                  126
% identity
                  (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  208091
Seq. ID
                  LIB3120-034-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q3808101
BLAST score
                   515
E value
                  2.0e-52
Match length
                  129
% identity
                  79
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
                   208092
Seq. No.
Seq. ID
                  LIB3120-034-Q1-K1-D3
Method
                  BLASTX
                  g4049346
NCBI GI
BLAST score
                   250
E value
                  2.0e-21
                  102
Match length
                   48
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   208093
Seq. ID
                  LIB3120-034-Q1-K1-D4
Method
                  BLASTN
NCBI GI
                   g11957
```

Method BLASTN
NCBI GI g11957
BLAST score 36
E value 8.0e-11
Match length 68
% identity 88

NCBI Description Rice complete chloroplast genome

Seq. No. 208094

Seq. ID LIB3120-034-Q1-K1-D5

Method BLASTX NCBI GI g4127688



69

77

Match length

% identity

```
BLAST score
E value
                  2.0e-20
                  71
Match length
                  62
% identity
                  (AJ006065) isochorismate synthase [Catharanthus roseus]
NCBI Description
                  208095
Seq. No.
                  LIB3120-034-Q1-K1-D6
Seq. ID
                  BLASTN
Method
                  q3108320
NCBI GI
BLAST score
                  81
E value
                  1.0e-37
Match length
                  153
% identity
                  88
NCBI Description Gossypium barbadense clone pXP2-38 repetitive DNA sequence
                   208096
Seq. No.
Seq. ID
                  LIB3120-034-Q1-K1-D7
Method
                  BLASTX
                   q1354515
NCBI GI
BLAST score
                   229
                   5.0e-19
E value
Match length
                   116
% identity
                   50
                   (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                   tremuloides]
Seq. No.
                   208097
Seq. ID
                  LIB3120-034-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   576
                   1.0e-59
E value
Match length
                   109
                   97
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   208098
                   LIB3120-034-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2956717
BLAST score
                   247
E value
                   5.0e-21
Match length
                   116
% identity
                   53
NCBI Description (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
                   208099
Seq. No.
                   LIB3120-034-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   q3914473
NCBI GI
BLAST score
                   289
E value
                   5.0e-26
```

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT 28646

NCBI Description

```
V) (PSI-L) >gi_479684_pir__S35151 photosystem I chain XI - spinach >gi_396275_emb_CAA45775_ (X64445) subunit XI of photosystem I reaction center [Spinacia oleracea]
```

```
Seq. No.
                  LIB3120-034-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2961384
BLAST score
                   419
                   3.0e-41
E value
Match length
                  116
                   66
% identity
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
                   208101
Seq. No.
Seq. ID
                  LIB3120-034-Q1-K1-E11
Method
                  BLASTX
                   q1168411
NCBI GI
                   553
BLAST score
                   6.0e-57
E value
                   133
Match length
                   84
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
Seq. No.
                   208102
                   LIB3120-034-01-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244749
BLAST score
                   385
                   2.0e-37
E value
                   80
Match length
                   90
% identity
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   208103
                   LIB3120-034-Q1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122673
BLAST score
                   305
E value
                  4.0e-28
Match length
                   86
% identity
                   71
                   60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   208104
                   LIB3120-034-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   q462264
NCBI GI
                   309
BLAST score
                   2.0e-28
E value
                   119
Match length
                   54
% identity
```

28647

GTP-BINDING PROTEIN HFLX >gi 1361024 pir S56398 GTPase

homolog protein hflX - Escherichia coli >gi\_436156 (U00005) putative GTPase required for high frequency lysogenization



by bacteriophage lambda [Escherichia coli] >gi\_537014 (U14003) putative GTPase required for high frequency lysogenization by bacteriophage lambda; TTG start codon [Escherichia coli] >gi\_1790615 (AE000489) GTP - binding subunit of protease specific for phage lambda cII repressor [Escherichia coli]

 Seq. No.
 208105

 Seq. ID
 LIB3120-034-Q1-K1-E6

 Method
 BLASTX

 NCBI GI
 g400890

 BLAST score
 310

BLAST score 310 E value 2.0e-28 Match length 139 % identity 42

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi\_282837\_pir\_\_S26953 photosystem II 22K protein precursor
- spinach >gi\_21307\_emb\_CAA48557\_(X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi\_260917\_bbs\_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 208106

Seq. ID LIB3120-034-Q1-K1-E7

Method BLASTX
NCBI GI g1788928
BLAST score 307
E value 4.0e-28
Match length 137
% identity 46

NCBI Description (AE000344) quinolinate synthetase, B protein [Escherichia

coli]

Seq. No. 208107

Seq. ID LIB3120-034-Q1-K1-E9

Method BLASTX
NCBI GI g1781348
BLAST score 639
E value 4.0e-67
Match length 130
% identity 94

NCBI Description (Y10380) homologous to plastidic aldolases [Solanum

tuberosum]

Seq. No. 208108

Seq. ID LIB3120-034-Q1-K1-F10

Method BLASTX
NCBI GI g4309738
BLAST score 240
E value 3.0e-20
Match length 78
% identity 63

NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 208109

Seq. ID LIB3120-034-Q1-K1-F11

Method BLASTX

```
NCBI GI
                   g3075391
BLAST score
                  379
                  2.0e-36
E value
                  140
Match length
                  53
% identity
NCBI Description
                  (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                  208110
Seq. ID
                  LIB3120-034-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g115473
BLAST score
                  242
                  2.0e-20
E value
                  77
Match length
```

% identity 58

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

DEHYDRATASE) >gi\_170219 (M94135) chloroplast carbonic anhydrase [Nicotiana tabacum] >gi 445610 prf 1909357A

carbonic anhydrase [Nicotiana tabacum]

Seq. No. 208111

Seq. ID LIB3120-034-Q1-K1-F5

Method BLASTX
NCBI GI g132675
BLAST score 420
E value 2.0e-41
Match length 94
% identity 94

NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi 71222 pir R5NT14

ribosomal protein L14 - common tobacco chloroplast >gi\_11864\_emb\_CAA77379\_ (Z00044) ribosomal protein L14 [Nicotiana tabacum] >gi\_225233\_prf\_\_1211235BQ ribosomal

protein L14 [Nicotiana tabacum]

Seq. No. 208112

Seq. ID LIB3120-034-Q1-K1-F6

Method BLASTX
NCBI GI g2832661
BLAST score 338
E value 8.0e-32
Match length 118
% identity 57

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 208113

Seq. ID LIB3120-034-Q1-K1-F7

Method BLASTX
NCBI GI g2062167
BLAST score 462
E value 3.0e-46
Match length 99
% identity 87

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 208114



```
Seq. ID
                  LIB3120-034-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q1709825
BLAST score
                  295
                  1.0e-27
E value
Match length
                  125
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  208115
Seq. ID
                  LIB3120-034-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q2244811
BLAST score
                  266
E value
                  3.0e-23
Match length
                  111
% identity
                  58
                  (Z97336) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  208116
Seq. No.
Seq. ID
                  LIB3120-034-Q1-K1-G1
Method
                  BLASTX
                  g2454182
NCBI GI
BLAST score
                  267
E value
                  6.0e-33
Match length
                  85
                  89
% identity
NCBI Description
                  (U80185) pyruvate dehydrogenase El alpha subunit
                   [Arabidopsis thaliana]
Seq. No.
                  208117
Seq. ID
                  LIB3120-034-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2191197
BLAST score
                  254
                  8.0e-22
E value
Match length
                  100
% identity
                  75
                   (AF007271) contains similarity to Synechococcus PCC7942
NCBI Description
                  chromosomal region used as basis of neutral siteII
                  recombinational cloning vector (PID:g1174192) [Arabidopsis
                  thaliana]
Seq. No.
                  208118
Seq. ID
                  LIB3120-034-Q1-K1-G11
Method
                  BLASTX
```

NCBI GI g3914603 BLAST score 623 4.0e-65 E value Match length 131 89 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE NCBI Description PRECURSOR (RUBISCO ACTIVASE) >gi\_1778414 (U74321)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

```
208119
Seq. No.
                  LIB3120-034-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421826
BLAST score
                  215
E value
                  2.0e-17
Match length
                  84
% identity
                  52
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
                  208120
Seq. No.
                  LIB3120-034-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g4127688
NCBI GI
                   135
BLAST score
                   3.0e-15
E value
                  70
Match length
% identity
                   63
                  (AJ006065) isochorismate synthase [Catharanthus roseus]
NCBI Description
                   208121
Seq. No.
                  LIB3120-034-Q1-K1-G3
Seq. ID
Method
                   BLASTX
                   g2894598
NCBI GI
BLAST score
                   169
                   4.0e-12
E value
                   37
Match length
                   81
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   208122
Seq. No.
                   LIB3120-034-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1350680
BLAST score
                   433
                   7.0e-43
E value
                   105
Match length
% identity
                   79
```

60S RIBOSOMAL PROTEIN L1 NCBI Description

208123 Seq. No.

LIB3120-034-Q1-K1-G5 Seq. ID

Method BLASTX NCBI GI q3063709 BLAST score 164 E value 2.0e-11 Match length 77 43 % identity

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 208124

LIB3120-034-Q1-K1-G7 Seq. ID

Method BLASTX NCBI GI g231688 BLAST score 637



E value 6.0e-67
Match length 117
% identity 98
NCBI Description CATALAS

NCBI Description CATALASE ISOZYME 2 >gi\_99599\_pir\_\_S17493 catalase (EC 1.11.1.6) - upland cotton >gi\_18488\_emb\_CAA39998\_ (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No. 208125

Seq. ID LIB3120-034-Q1-K1-G9

Method BLASTX
NCBI GI g1771778
BLAST score 655
E value 8.0e-69
Match length 148
% identity 87

NCBI Description (X99320) 23 kDa oxygen evolving protein of photosystem II

[Solanum tuberosum]

Seq. No. 208126

Seq. ID LIB3120-034-Q1-K1-H1

Method BLASTX
NCBI GI g3288821
BLAST score 348
E value 3.0e-38
Match length 103
% identity 79

NCBI Description (AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]

Seq. No. 208127

Seq. ID LIB3120-034-Q1-K1-H10

Method BLASTX
NCBI GI g2864617
BLAST score 226
E value 1.0e-18
Match length 117
% identity 44

NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like

protein [Arabidopsis thaliana]

Seq. No. 208128

Seq. ID LIB3120-034-Q1-K1-H11

Method BLASTX
NCBI GI g3766248
BLAST score 205
E value 4.0e-16
Match length 117
% identity 43

NCBI Description (Y18227) blue copper binding-like protein [Arabidopsis

thaliana]

Seq. No. 208129

Seq. ID LIB3120-034-Q1-K1-H12

Method BLASTX
NCBI GI g1172664
BLAST score 452
E value 3.0e-45



Match length % identity 80

PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

> >gi\_419791\_pir\_\_S31165 photosystem I chain III precursor -Flaveria trinervia >gi\_298482\_bbs\_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria

trinervia, Peptide, 232 aa] >gi\_168173 (M83119) photosystem

I subunit III [Flaveria trinervia]

Seq. No. 208130

Seq. ID LIB3120-034-Q1-K1-H4

Method BLASTX q2511594 NCBI GI 509 BLAST score E value 8.0e-52 Match length 105 92 % identity

(Y13694) multicatalytic endopeptidase complex, proteasome NCBI Description

precursor, beta subunit [Arabidopsis thaliana]

>gi\_2827525\_emb\_CAA16533\_ (AL021633) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit

[Arabidopsis thaliana] >gi\_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

208131 Seq. No.

LIB3120-034-Q1-K1-H6 Seq. ID

Method BLASTX NCBI GI q1172664 421 BLAST score 5.0e-48 E value 112 Match length % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR NCBI Description

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi\_419791\_pir\_\_S31165 photosystem I chain III precursor Flaveria trinervia >gi\_298482 bbs\_127083 photosystem I
reaction center subunit III, PSI-RC PsaF [Flaveria

trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem

I subunit III [Flaveria trinervia]

208132 Seq. No.

Seq. ID LIB3120-034-Q1-K1-H9

Method BLASTN NCBI GI g2924257 BLAST score 49 E value 1.0e-18 Match length 61 % identity 95

NCBI Description Tobacco chloroplast genome DNA

208133 Seq. No.

Seq. ID LIB3120-036-Q1-K1-A1

Method BLASTX g3759184 NCBI GI BLAST score 160 E value 7.0e-11



Match length % identity

(AB018441) phi-1 [Nicotiana tabacum] NCBI Description

Seq. No.

208134

Seq. ID

LIB3120-036-Q1-K1-A10

Method NCBI GI BLASTN q289919

BLAST score E value

99

Match length

7.0e-49 127

% identity

94

NCBI Description Gossypium hirsutum chloroplast photosystem II chlorophyll

A/B-binding protein gene, complete cds

Seq. No.

208135

Seq. ID

LIB3120-036-Q1-K1-A11

Method NCBI GI BLAST score BLASTX q625547 600

E value Match length 2.0e-62 147

79

% identity NCBI Description

chlorophyll a/b-binding protein type I - common tobacco

>gi\_493723\_emb\_CAA45523\_ (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

Seq. No.

208136

Seq. ID

LIB3120-036-Q1-K1-A12

Method NCBI GI BLAST score E value

BLASTX g100616 469 4.0e-47

> 125 75

Match length % identity

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi\_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >qi 167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No.

208137

Seq. ID

LIB3120-036-Q1-K1-A3

Method NCBI GI BLASTX q1352821

BLAST score

627

E value

1.0e-65

Match length

120

% identity

96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.



Seq. ID LIB3120-036-Q1-K1-A6

Method BLASTX
NCBI GI g1352821
BLAST score 658
E value 3.0e-69
Match length 128
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505 emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208139

Seq. ID LIB3120-036-Q1-K1-A8

Method BLASTX
NCBI GI g1085922
BLAST score 142
E value 7.0e-09
Match length 86
% identity 43

NCBI Description hypothetical protein 224 - evening primrose mitochondrion

>gi\_459533\_emb\_CAA54968\_ (X78038) orf224; homology to ribosomal protein S1 of E. coli [Oenothera berteriana]

Seq. No. 208140

Seq. ID LIB3120-036-Q1-K1-B11

Method BLASTX
NCBI GI g2129825
BLAST score 346
E value 1.0e-32
Match length 82
% identity 85

NCBI Description dynamin-like protein phragmoplastin 12 - soybean

>gi\_1217994 (U25547) SDL [Glycine max]

Seq. No. 208141

Seq. ID LIB3120-036-Q1-K1-B12

Method BLASTX
NCBI GI g3158476
BLAST score 624
E value 3.0e-65
Match length 139
% identity 85

NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 208142

Seq. ID LIB3120-036-Q1-K1-B2

Method BLASTX
NCBI GI g3776574
BLAST score 231
E value 4.0e-19
Match length 92
% identity 62

NCBI Description (AC005388) Similar to T11J7.13 gi 2880051 putative protein

kinase from Arabidopsis thaliana BAC gb AC002340.

[Arabidopsis thaliana]

```
208143
Seq. No.
Seq. ID
                   LIB3120-036-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   575
                   2.0e-59
E value
Match length
                   108
% identity
                    98
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                    (RUBISCO SMALL SUBUNIT) >gi 279581 pir_RKCNSU
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >qi 450505 emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   208144
Seq. ID
                   LIB3120-036-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   g1168470
BLAST score
                    653
E value
                    1.0e-68
Match length
                    148
% identity
                   PROTEIN KINASE APK1A >gi_282877_pir__ S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) -
NCBI Description
                   Arabidopsis thaliana >gi 217829 dbj BAA02092 (D12522)
                   protein tyrosine-serine-threonine kinase [Arabidopsis
                    thaliana]
Seq. No. Seq. ID
                    208145
                   LIB3120-036-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                    g3924594
```

Method BLASTX
NCBI GI g3924594
BLAST score 452
E value 4.0e-45
Match length 110
% identity 30

NCBI Description (AF069442) putative ribonucleoprotein [Arabidopsis

thaliana] >gi 4262139 gb AAD14439 (AC005275) putative

ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 208146

Seq. ID LIB3120-036-Q1-K1-B6

Method BLASTX
NCBI GI g1709651
BLAST score 401
E value 4.0e-39
Match length 128
% identity 62

NCBI Description PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209

plastocyanin a precursor - black poplar

>gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 208147

Seq. ID LIB3120-036-Q1-K1-B7

Method BLASTX

NCBI GI

E value

BLAST score

Match length

g1352821

2.0e-61

591

114

```
q167367
NCBI GI
BLAST score
                  502
                  5.0e-51
E value
                  129
Match length
                  76
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  208148
Seq. No.
                  LIB3120-036-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g407353
BLAST score
                  465
E value
                  1.0e-46
Match length
                  136
                  70
% identity
NCBI Description (D21054) PSI-H precursor [Nicotiana sylvestris]
                  208149
Seq. No.
                  LIB3120-036-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g508304
NCBI GI
BLAST score
                  312
                  9.0e-29
E value
Match length
                  78
% identity
                  73
                  (L22305) corC [Medicago sativa]
NCBI Description
                  208150
Seq. No.
                  LIB3120-036-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g2493694
NCBI GI
                  246
BLAST score
                  6.0e-21
E value
                  98
Match length
% identity
                  53
                  PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII
NCBI Description
                  6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II
                  protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein
                  of photosystem II [Spinacia oleracea]
Seq. No.
                  208151
                  LIB3120-036-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g3822036
NCBI GI
BLAST score
                  258
                  3.0e-22
E value
                  128
Match length
% identity
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
Seq. No.
                  208152
                  LIB3120-036-Q1-K1-C2
Seq. ID
Method
                  BLASTX
```



% identity 97
NCBI Description RIBUL(RUBT)

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208153

Seq. ID LIB3120-036-Q1-K1-C3

Method BLASTX
NCBI GI g1170897
BLAST score 584
E value 2.0e-60
Match length 129
% identity 88

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi\_1076276 pir S52039 NAD-malate dehydrogenase - cucumber

>gi\_695311 (L31 $\overline{90}$ 0) glyoxysomal malate dehydrogenase

[Cucumis sativus]

Seq. No. 208154

Seq. ID LIB3120-036-Q1-K1-C4

Method BLASTX
NCBI GI g3850621
BLAST score 719
E value 2.0e-76
Match length 139
% identity 92

NCBI Description (Y15382) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 208155

Seq. ID LIB3120-036-Q1-K1-C6

Method BLASTX
NCBI GI g82167
BLAST score 710
E value 3.0e-75
Match length 145
% identity 95

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A, chloroplast - common

tobacco (fragment)

Seq. No. 208156

Seq. ID LIB3120-036-Q1-K1-C7

Method BLASTX
NCBI GI g289920
BLAST score 780
E value 2.0e-83
Match length 147
% identity 99

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 208157

Seq. ID LIB3120-036-Q1-K1-C8

Method BLASTX



```
NCBI GI
                  q1084336
BLAST score
                  343
                  3.0e - 32
E value
Match length
                  84
% identity
                  76
                  chlorophyll a/b-binding protein type II - Arabidopsis
NCBI Description
                  thaliana >gi 541565 (U03395) PSI type II chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  208158
Seq. ID
                  LIB3120-036-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2342685
BLAST score
                  299
E value
                  4.0e-27
Match length
                  134
% identity
                  45
                  (AC000106) Contains similarity to Rhodococcus amidase
NCBI Description
                  (gb D16207). ESTs gb T20504, gb H36650, gb N97423, gb H36595
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  208159
                  LIB3120-036-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  g3046815
NCBI GI
BLAST score
                  181
E value
                  2.0e-13
Match length
                  74
                  49
% identity
NCBI Description
                  (AL021687) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  208160
                  LIB3120-036-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583108
BLAST score
                  338
                  1.0e-31
E value
Match length
                  139
% identity
                  53
NCBI Description
                  (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                  208161
Seq. ID
                  LIB3120-036-Q1-K1-D2
                  BLASTX
                  q100616
                  477
                  5.0e-48
                  118
```

Method NCBI GI BLAST score E value Match length % identity 76

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi 167093 (M55448) ribulose 1,5-bisphosphate

carboxylase activase [Hordeum vulgare] >gi\_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

208162 Seq. No.

Seq. ID LIB3120-036-Q1-K1-D3



Method BLASTX
NCBI GI g1352821
BLAST score 506
E value 2.0e-51
Match length 106
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208163

Seq. ID LIB3120-036-Q1-K1-D6

Method BLASTX
NCBI GI g122085
BLAST score 577
E value 8.0e-60
Match length 124
% identity 95

NCBI Description

HISTONE H3 >gi\_81641 pir S06250 histone H3 - Arabidopsis thaliana >gi\_82482 pir\_ S04099 histone H3 (variant H3R-21) - rice >gi\_1362194 pir\_ S57626 histone H3 - maize >gi\_20251 emb\_CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253 emb\_CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi\_168506 (M35388) histone H3 [Zea mays] >gi\_169655 (M77493) histone H3 [Petroselinum crispum] >gi\_1696 $\overline{5}$ 7 (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3
[Petroselinum crispum] >gi\_387565 (M17130) histone H3
[Arabidopsis thaliana] >gi\_387567 (M17131) histone H3
[Arabidopsis thaliana] >gi\_886738 emb\_CAA59111 (X84377) histone 3 [Zea mays]  $>gi_1\overline{0}40764$  (M35 $\overline{3}87$ ) histone H3 [Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3  $\label{local_condition} \begin{tabular}{ll} homolog [Brassica napus] > & ji_1531754_emb_CAA57811_ (X82414) \\ \end{tabular}$ Histone H3 [Asparagus officinalis] >gi\_1667592 (U77296) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb\_M17131 and gb\_M35387 from A. thaliana. ESTs gb\_H76511 gb\_ $\overline{\text{H}}$ 76255, gb\_AA7 $\overline{1}$ 2452, gb\_N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea] >gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 208164

Seq. ID LIB3120-036-Q1-K1-E1

Method BLASTX
NCBI GI g1352821
BLAST score 466
E value 8.0e-47
Match length 90
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581 pir\_ RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

Seq. No.

Seq. ID

208170

LIB3120-036-Q1-K1-F1





## ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
208165
Seq. No.
                  LIB3120-036-Q1-K1-E12
Seq. ID
Method
                  BLASTX
                  g100454
NCBI GI
BLAST score
                  602
                  1.0e-62
E value
                  144
Match length
% identity
                  84
                  photosystem II oxygen-evolving complex protein 1 - potato
NCBI Description
                  >gi 809113 emb CAA35601 (X17578) 33kDa precursor protein
                  of oxygen-evolving complex [Solanum tuberosum]
Seq. No.
                  208166
                  LIB3120-036-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g4335772
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
Match length
                  88
                  44
% identity
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                  208167
Seq. No.
                  LIB3120-036-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1181599
BLAST score
                  460
                  5.0e-46
E value
Match length
                  135
% identity
                  73
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
                  208168
Seq. No.
                  LIB3120-036-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3650030
BLAST score
                  340
                  6.0e-32
E value
Match length
                  129
% identity
                  59
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]
                  208169
Seq. No.
                  LIB3120-036-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832644
BLAST score
                  219
E value
                  7.0e-18
Match length
                  113
% identity
                  53
                   (AL021710) teosinte branched1 - like protein [Arabidopsis
NCBI Description
                  thaliana]
```



Method BLASTX NCBI GI q132714 BLAST score 454 E value 3.0e-45 115 Match length 79 % identity

CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 (RIBOSOMAL PROTEIN NCBI Description

CS-L24) >gi\_71248\_pir\_\_R5SP16 ribosomal protein L16 - spinach chloroplast >gi\_12311\_emb\_CAA31716\_ (X13336)

ribosomal protein L16 [Spinacia oleracea]

Seq. No. 208171

Seq. ID LIB3120-036-Q1-K1-F10

Method BLASTX NCBI GI a1353352 289 BLAST score 4.0e-26 E value Match length 119 % identity 47

(U31975) alanine aminotransferase [Chlamydomonas NCBI Description

reinhardtii]

Seq. No. 208172

Seq. ID LIB3120-036-Q1-K1-F2

Method BLASTX a1709358 NCBI GI BLAST score 434 6.0e-43 E value Match length 135 % identity 61

NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE NCBI Description

PHOSPHOHYDROLASE) (NTPASE) >gi\_629638\_pir\_\_S48859

nucleoside triphosphatase - garden pea

>gi\_2129890\_pir\_\_S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea >gi\_563612\_emb\_CAA83655\_ (Z32743) nucleoside triphosphatase

[Pisum satīvum] >gi\_4519173 dbj\_BAA75506.1 (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No. 208173

Seq. ID LIB3120-036-Q1-K1-F3

Method BLASTX NCBI GI g2832660 BLAST score 255 5.0e-22 E value Match length 124 % identity

NCBI Description (AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No. 208174

LIB3120-036-Q1-K1-F4 Seq. ID

BLASTX Method g125578 NCBI GI BLAST score 397 1.0e-38 E value Match length 104 71 % identity



PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)

(PRK) >gi 167266 (M73707) phosphoribulokinase

[Mesembryanthemum crystallinum]

Seq. No. 208175

NCBI Description

Seq. ID LIB3120-036-Q1-K1-F5

Method BLASTX
NCBI GI g4204274
BLAST score 237
E value 2.0e-20
Match length 51
% identity 86

NCBI Description (AC004146) ribulose bisphosphate carboxylase, small subunit

[Arabidopsis thaliana]

Seq. No. 208176

Seq. ID LIB3120-036-Q1-K1-F6

Method BLASTX
NCBI GI g1172664
BLAST score 609
E value 2.0e-63
Match length 126
% identity 90

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi\_419791\_pir\_\_S31165 photosystem I chain III precursor Flaveria trinervia >gi\_298482\_bbs\_127083 photosystem I
reaction center subunit III, PSI-RC PsaF [Flaveria

trinervia, Peptide, 232 aa] >gi\_168173 (M83119) photosystem

I subunit III [Flaveria trinervia]

Seq. No. 208177

Seq. ID LIB3120-036-Q1-K1-F7

Method BLASTX
NCBI GI g282833
BLAST score 216
E value 2.0e-17
Match length 54
% identity 83

NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)

Seq. No. 208178

Seq. ID LIB3120-036-Q1-K1-F8

Method BLASTX
NCBI GI g19157
BLAST score 488
E value 3.0e-49
Match length 133
% identity 74

NCBI Description (Z11999) 33kDa precursor protein of oxygen-evolving complex

[Lycopersicon esculentum] >gi\_738944\_prf\_\_2001459A 02 evolving protein complex:SUBUNIT=33kD [Lycopersicon

esculentum]

Seq. No. 208179

Seq. ID LIB3120-036-Q1-K1-G1

Method BLASTX



NCBI GI g1363484 BLAST score 263 E value 6.0e-23 Match length 74 % identity 65

NCBI Description IAA13 protein - Arabidopsis thaliana >gi\_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi\_2459414 (AC002332) auxin

inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No. 208180

Seq. ID LIB3120-036-Q1-K1-G10

Method BLASTX
NCBI GI g3461821
BLAST score 158
E value 1.0e-10
Match length 133
% identity 32

NCBI Description (AC004138) putative nucleoside triphosphatase [Arabidopsis

thaliana]

Seq. No. 208181

Seq. ID LIB3120-036-Q1-K1-G12

Method BLASTX
NCBI GI g2262143
BLAST score 492
E value 8.0e-50
Match length 133
% identity 71

NCBI Description (AC002330) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 208182

Seq. ID LIB3120-036-Q1-K1-G2

Method BLASTX
NCBI GI g445116
BLAST score 191
E value 4.0e-15
Match length 46
% identity 76

NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]

Seq. No. 208183

Seq. ID LIB3120-036-Q1-K1-G5

Method BLASTX
NCBI GI g129915
BLAST score 191
E value 4.0e-15
Match length 56
% identity 64

NCBI Description PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR

>gi\_66912\_pir\_\_TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
precursor, chloroplast - wheat >gi\_21833\_emb\_CAA33303\_
(X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum

aestivum] >gi\_3293043\_emb\_CAA51931\_ (X73528)
phosphoglycerate kinase [Triticum aestivum]

Seq. No. 208184



LIB3120-036-Q1-K1-G7 Seq. ID

Method BLASTX NCBI GI a1352821 BLAST score 614 4.0e-64 E value Match length 126 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase  $(EC \overline{4.1.1.39})$  small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208185

Seq. ID LIB3120-036-Q1-K1-G8

Method BLASTX NCBI GI g417103 BLAST score 362 E value 2.0e-34 Match length 122 % identity 64

HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 208186

Seq. ID LIB3120-036-Q1-K1-H1

Method BLASTX NCBI GI g1652467 BLAST score 219 1.0e-17 E value Match length 65 % identity

NCBI Description (D90905) hypothetical protein [Synechocystis sp.]

Seq. No. 208187

Seq. ID LIB3120-036-Q1-K1-H10

Method BLASTX NCBI GI g1431629 BLAST score 338 E value 8.0e-32



Match length 87 % identity 70

NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No. 208188

Seq. ID LIB3120-036-Q1-K1-H11

Method BLASTX
NCBI GI g1652467
BLAST score 207
E value 2.0e-16
Match length 65
% identity 60

NCBI Description (D90905) hypothetical protein [Synechocystis sp.]

Seq. No. 208189

Seq. ID LIB3120-036-Q1-K1-H12

Method BLASTX
NCBI GI g2191128
BLAST score 169
E value 7.0e-12
Match length 115
% identity 51

NCBI Description (AF007269) belongs to the L5P family of ribosomal proteins

[Arabidopsis thaliana]

Seq. No. 208190

Seq. ID LIB3120-036-Q1-K1-H2

Method BLASTX
NCBI GI g2864602
BLAST score 322
E value 8.0e-30
Match length 144
% identity 58

NCBI Description (Y12071) thylakoid lumen rotamase [Spinacia oleracea]

Seq. No. 208191

Seq. ID LIB3120-036-Q1-K1-H4

Method BLASTX
NCBI GI g2062167
BLAST score 476
E value 7.0e-48
Match length 138
% identity 63

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 208192

Seq. ID LIB3120-036-Q1-K1-H5

Method BLASTX
NCBI GI g1352821
BLAST score 649
E value 4.0e-68
Match length 133
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain



precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

208193 Seq. No. LIB3120-036-Q1-K1-H6 Seq. ID Method BLASTX NCBI GI g3024020 BLAST score 335 2.0e-31 E value Match length 79 82 % identity NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi\_2225881\_dbj\_BAA20877\_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum] 208194 Seq. No. LIB3120-036-Q1-K1-H8 Seq. ID Method BLASTX g1351279 NCBI GI BLAST score 494 E value 6.0e-50 132 Match length 73 % identity NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi\_602590\_emb\_CAA58230\_ (X83227) triosephosphate isomerase [Petunia x hybrida] 208195 Seq. No. LIB3120-037-P1-K1-A2 Seq. ID Method BLASTX q1352821 NCBI GI 665 BLAST score 5.0e-70 E value Match length 127 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 208196 LIB3120-037-P1-K1-A3 Seq. ID Method BLASTX NCBI GI q480450 BLAST score 153 E value 4.0e-10 Match length 103 % identity 42 ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis NCBI Description thaliana >gi\_402552\_emb\_CAA49506\_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No. 208197

Seq. ID LIB3120-037-P1-K1-A4

Method BLASTX NCBI GI g4406530



```
BLAST score
                  8.0e-27
E value
Match length
                  85
                  72
% identity
                  (AF126870) rubisco activase [Vigna radiata]
NCBI Description
                  208198
Seq. No.
                  LIB3120-037-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885884
BLAST score
                  203
                  3.0e-16
E value
                  59
Match length
                  64
% identity
NCBI Description
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                  208199
Seq. No.
                  LIB3120-037-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3834310
BLAST score
                  690
E value
                  6.0e-73
Match length
                  137
                  98
% identity
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                  gb D83004 from Homo sapiens. ESTs gb T88233, gb Z24464,
                  gb N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  208200
                  LIB3120-037-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g20733
NCBI GI
BLAST score
                  283
E value
                  2.0e-25
Match length
                  70
                  74
% identity
NCBI Description
                   (X15188) precursor C-terminal fragment (AA -80 to 367)
                   [Pisum sativum]
Seq. No.
                  208201
Seq. ID
                  LIB3120-037-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g4454461
BLAST score
                  153
E value
                  5.0e-10
Match length
                  109
                  38
% identity
NCBI Description
                   (AC006234) putative cell wall protein precursor
                   [Arabidopsis thaliana]
```

Seq. No. 208202

Seq. ID LIB3120-037-P1-K1-C2

Method BLASTX g2190012 NCBI GI BLAST score 244 E value 1.0e-20

28668

C. er



Match length % identity 62

NCBI Description (AB004242) din1 [Raphanus sativus]

Seq. No.

208203

Seq. ID

LIB3120-037-P1-K1-C3

Method NCBI GI BLASTX q3355476

BLAST score

364

E value Match length 8.0e-35

% identity

103 63

NCBI Description

(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.

208204

Seq. ID

LIB3120-037-P1-K1-C4

Method BLASTX NCBI GI q131397 BLAST score E value

218 8.0e-18

Match length % identity

110 48

NCBI Description

OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_81480\_pir\_\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No.

208205

Seq. ID

LIB3120-037-P1-K1-D2

Method BLASTX NCBI GI q2662341 BLAST score . 728 E value 2.0e-77 Match length 143 % identity 97

NCBI Description

(D63580) EF-1 alpha [Oryza sativa]

>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza satīva] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No.

208206

Seq. ID

LIB3120-037-P1-K1-D3

Method BLASTX NCBI GI q1352821 BLAST score 311 7.0e-29 E value Match length 68 88

% identity NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
208207
Seq. No.
Seq. ID
                  LIB3120-037-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3769673
BLAST score
                  444
                  4.0e-44
E value
Match length
                  139
% identity
                  57
                  (AF095285) Tic20 [Pisum sativum]
NCBI Description
                  208208
Seq. No.
                  LIB3120-037-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249417
BLAST score
                  210
                  1.0e-16
E value
Match length
                  64
                  58
% identity
NCBI Description
                  (AC006072) hypothetical protein [Arabidopsis thaliana]
                  208209
Seq. No.
                  LIB3120-037-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2920666
BLAST score
                  282
E value
                  2.0e-25
Match length
                  82
% identity
                  66
                  (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                  [Glycine max]
                  208210
Seq. No.
Seq. ID
                  LIB3120-037-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4127456
BLAST score
                  340
E value
                  6.0e-32
Match length
                  127
% identity
                  60
NCBI Description
                 (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                  208211
Seq. ID
                  LIB3120-037-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g399082
BLAST score
                  153
E value
                  5.0e-10
Match length
                  101
% identity
                  45
NCBI Description
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
                  >gi_322713_pir__S28171 H+-transporting ATP synthase (EC
                  3.6.1.34) delta chain, chloroplast - garden pea >gi_169045
```

Seq. No. 208212

Seq. ID LIB3120-037-P1-K1-G6

(M94558) ATP synthase delta subunit [Pisum sativum]



```
Method BLASTX
NCBI GI g4098129
BLAST score 735
E value 3.0e-78
Match length 140
% identity 97
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No. 208213
```

Seq. ID LIB3120-037-P1-K1-H1 Method BLASTX

Method BLASTX
NCBI GI g1345698
BLAST score 400
E value 3.0e-39
Match length 84
% identity 89

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

a/b-binding protein - upland cotton

>gi 452314 emb CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 208214

Seq. ID LIB3120-037-P1-K1-H12

Method BLASTX
NCBI GI g3036882
BLAST score 220
E value 6.0e-18
Match length 82
% identity 54

NCBI Description (AL022374) putative DNA hydrolase [Streptomyces coelicolor]

Seq. No. 208215

Seq. ID LIB3120-037-P1-K1-H2

Method BLASTX
NCBI GI g2662341
BLAST score 594
E value 7.0e-62
Match length 114
% identity 97

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 208216

Seq. ID LIB3120-037-P1-K1-H3

Method BLASTN
NCBI GI g728715
BLAST score 45
E value 4.0e-16
Match length 101
% identity 86

NCBI Description S.oleracea mRNA for 6.1 kDa polypeptide of photosystem II

Seq. No. 208217

Seq. ID LIB3120-037-P1-K1-H4

BLAST score

E value

176 3.0e-13



```
Method
                  BLASTN
NCBI GI
                  g289919
BLAST score
                  37
                  8.0e-12
E value
Match length
                  117
                  83
% identity
                  Gossypium hirsutum chloroplast photosystem II chlorophyll
NCBI Description
                  A/B-binding protein gene, complete cds
                  208218
Seq. No.
                  LIB3120-038-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  q167367
NCBI GI
BLAST score
                  425
E value
                  3.0e-42
Match length
                  94
                  91
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  208219
Seq. No.
                  LIB3120-038-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  g3033513
NCBI GI
BLAST score
                  294
                  2.0e-26
E value
Match length
                  111
% identity
                  56
                  (AF041068) rubisco activase [Phaseolus vulgaris]
NCBI Description
                  208220
Seq. No.
                  LIB3120-038-P1-K1-C2
Seq. ID
                  BLASTN
Method
                  q3702734
NCBI GI
BLAST score
                  33
E value
                  5.0e-09
Match length
                  69
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNB8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  208221
                  LIB3120-038-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023752
BLAST score
                  287
                  7.0e-26
E value
Match length
                  90
                   67
% identity
                  FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
NCBI Description
                   ferredoxin-I [Lycopersicon esculentum]
                  208222
Seq. No.
Seq. ID
                  LIB3120-038-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q115471
```



Match length 49 % identity CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE NCBI Description DEHYDRATASE) >gi 100078\_pir\_\_S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi\_20673\_emb\_CAA36792 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum] 208223 Seq. No. LIB3120-039-P1-K1-A2 Seq. ID BLASTX Method g2980785 NCBI GI 148 BLAST score 8.0e-10 E value Match length 52 % identity 54 (AL022198) SERINE CARBOXYPEPTIDASE II - like protein NCBI Description [Arabidopsis thaliana] 208224 Seq. No. LIB3120-039-P1-K1-A4 Seq. ID Method BLASTX g3417451 NCBI GI BLAST score 327 9.0e-31 E value Match length 88 % identity 72 (AB013728) light-harvesting chlorophyll a/b-binding protein NCBI Description of photosystem II [Cryptomeria japonica] 208225 Seq. No. LIB3120-039-P1-K1-A6 Seq. ID BLASTX Method NCBI GI q3417451 BLAST score 518 5.0e-53 E value Match length 107 91 % identity (AB013728) light-harvesting chlorophyll a/b-binding protein NCBI Description of photosystem II [Cryptomeria japonica] 208226 Seq. No. LIB3120-039-P1-K1-B3 Seq. ID Method BLASTX NCBI GI q1658197 BLAST score 408 E value 5.0e-40 Match length 98 77 % identity (U74630) calreticulin [Ricinus communis] >gi\_1763297 NCBI Description (U74631) calreticulin [Ricinus communis]

208227 Seq. No.

LIB3120-039-P1-K1-B4 Seq. ID

BLASTX Method NCBI GI g4538963 BLAST score 142 E value 3.0e-09



Match length 43 % identity 72

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana]

Seq. No. 208228

Seq. ID LIB3120-039-P1-K1-B5

Method BLASTX
NCBI GI g4406530
BLAST score 191
E value 4.0e-15
Match length 46
% identity 83

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 208229

Seq. ID LIB3120-039-P1-K1-B8

Method BLASTX
NCBI GI g1174592
BLAST score 289
E value 5.0e-33
Match length 93
% identity 82

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin

- garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 208230

Seq. ID LIB3120-039-P1-K1-C1

Method BLASTX
NCBI GI g585452
BLAST score 200
E value 6.0e-16
Match length 82
% identity 49

NCBI Description MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM

PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi\_1076666\_pir\_\_A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi\_438131\_emb\_CAA80547\_ (Z23002) precursor of the 59kDa subunit of the mitochondrial

NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No. 208231

Seq. ID LIB3120-039-P1-K1-C3

Method BLASTX
NCBI GI g1084358
BLAST score 300
E value 2.0e-27
Match length 92
% identity 63

NCBI Description ATP synthase - soybean

Seq. No. 208232

Seq. ID LIB3120-039-P1-K1-C6

Method BLASTX NCBI GI g1839022



BLAST score E value 8.0e-18 Match length 48 77 % identity

NCBI Description (Y11121) amino acid carrier [Ricinus communis]

Seq. No.

208233

Seq. ID

LIB3120-039-P1-K1-D2

Method BLASTX NCBI GI q2851455 BLAST score 281 E value 3.0e-25 Match length 61 % identity

DYNAMIN-LIKE PROTEIN >gi\_2267213 (L36939) dynamin-like GTP NCBI Description

binding protein [Arabidopsis thaliana]

Seq. No.

208234

Seq. ID

LIB3120-039-P1-K1-D3

Method BLASTX NCBI GI q1352821 BLAST score 478 E value 4.0e-48 Match length 97 % identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

208235

Seq. ID LIB3120-039-P1-K1-D4

BLASTX q4406530 270

BLAST score 7.0e-24 E value Match length 78 % identity 73

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No.

208236

Seq. ID

Method

NCBI GI

LIB3120-039-P1-K1-D5

Method BLASTX NCBI GI g1352821 BLAST score 254 E value 4.0e-22 Match length 71 % identity 73

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

208237

Seq. ID

LIB3120-039-P1-K1-E2



```
Method
                  BLASTX
NCBI GI
                  q121353
BLAST score
                  376
E value
                  4.0e-43
                  99
Match length
                  84
% identity
NCBI Description
                  GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA)
                  (GLUTAMATE-AMMONIA LIGASE) >gi 68596 pir AJFBQD
                  glutamate--ammonia ligase (EC 6.3.1.2) delta precursor,
                  chloroplast - kidney bean >gi 21005 emb CAA31234 (X12738)
                  GS precursor protein [Phaseolus vulgaris]
Seq. No.
                  208238
Seq. ID
                  LIB3120-039-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2809247
BLAST score
                  173
E value
                  2.0e-12
Match length
                  88
% identity
                  5
NCBI Description
                  (AC002560) F21B7.16 [Arabidopsis thaliana]
                  208239
Seq. No.
                  LIB3120-039-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169586
BLAST score
                  235
                  3.0e-20
E value
Match length
                  53
% identity
                  81
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  (CY-F1) >gi 542079 pir S41287 fructose-bisphosphatase (EC
                  3.1.3.11) - potato >gi 440591 emb CAA54265 (X76946)
                  fructose-1,6-bisphosphatase [Solanum tuberosum]
Seq. No.
                  208240
Seq. ID
                  LIB3120-039-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1169586
BLAST score
                  296
E value
                  1.0e-30
Match length
                  79
                  84
% identity
NCBI Description
                  FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
```

(CY-F1) >gi\_542079\_pir\_S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi\_440591\_emb\_CAA54265\_ (X76946)

fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No. 208241

Seq. ID LIB3120-039-P1-K1-F6

Method BLASTX NCBI GI g1771778 BLAST score 160 E value 5.0e-18 Match length 66

% identity NCBI Description (X99320) 23 kDa oxygen evolving protein of photosystem II [Solanum tuberosum] 208242 Seq. No. LIB3120-039-P1-K1-F8 Seq. ID Method BLASTX g2275219 NCBI GI BLAST score 330 3.0e-31 E value Match length 68 90 % identity NCBI Description (AC002337) unknown protein [Arabidopsis thaliana] 208243 Seq. No. LIB3120-039-P1-K1-G8 Seq. ID Method BLASTN NCBI GI g18058 78 BLAST score E value 2.0e-36 Match length 98 95 % identity NCBI Description Citrus limon cistron for 26S ribosomal RNA 208244 Seq. No. Seq. ID LIB3120-039-P1-K1-H1 Method BLASTX g505482 NCBI GI BLAST score 400 E value 4.0e-39 Match length 108 % identity 78 (X64349) 33 kDa polypeptide of water-oxidizing complex of NCBI Description photosystem II [Nicotiana tabacum] Seq. No. 208245 Seq. ID LIB3120-039-P1-K1-H2 Method BLASTX NCBI GI q3868758 BLAST score 168 E value 2.0e-12 Match length 48 % identity 67 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa] Seq. No. 208246 Seq. ID LIB3120-039-P1-K1-H3 Method BLASTX NCBI GI q1781348 BLAST score 478

E value 2.0e-48 Match length 100 % identity 92

(Y10380) homologous to plastidic aldolases [Solanum NCBI Description

tuberosum]

Seq. No. 208247



```
Seq. ID
                   LIB3120-039-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g547911
BLAST score
                   176
E value
                   1.0e-12
Match length
                   123
% identity
                   34
NCBI Description
                   MO25 PROTEIN >gi_2143483_pir__I57997 hypothetical
                   calcium-binding protein - mouse >gi_262934_bbs_121784
                   (S51858) putative Ca2+ binding protein [mice, embryos,
                   Peptide, 341 aa] [Mus sp.]
Seq. No.
                   208248
Seq. ID
                   LIB3120-039-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g4567268
BLAST score
                   397
E value
                   5.0e-39
Match length
                   87
% identity
                   92
NCBI Description
                   (AC006841) putative fructose biphosphate aldolase
                   [Arabidopsis thaliana]
Seq. No.
                   208249
Seq. ID
                   LIB3120-039-P1-K1-H8
Method
                   BLASTN
NCBI GI
                   g2687432
BLAST score
                   60
E value
                   1.0e-25
Match length
                   104
% identity
                   90
NCBI Description
                  Plumbago auriculata large subunit 26S ribosomal RNA gene,
                   partial sequence
Seq. No.
                   208250
Seq. ID
                  LIB3120-043-P1-K1-A1
Method
                  BLASTN
NCBI GI
                   g450504
BLAST score
                   46
E value
                   4.0e-17
Match length
                   149
% identity
                   82
NCBI Description
                  G.hirsutum rbcS gene for ribulose-1,5-bisphosphate
                  carboxylase, small subunit
Seq. No.
                  208251
Seq. ID
                  LIB3120-043-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  540
E value
                  1.0e-55
Match length
                  106
% identity
NCBI Description
                 (D63581) EF-1 alpha [Oryza sativa]
```

Seq. No. 208252

Seq. ID LIB3120-043-P1-K1-A12



```
Method
                  BLASTX
NCBI GI
                  g2832628
BLAST score
                  238
E value
                  4.0e-20
Match length
                  95
                  54
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  208253
Seq. No.
                  LIB3120-043-P1-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18058
BLAST score
                  224
                  1.0e-123
E value
Match length
                  263
% identity
                  97
                 Citrus limon cistron for 26S ribosomal RNA
NCBI Description
Seq. No.
                  208254
                  LIB3120-043-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  227
E value
                  3.0e-19
Match length
                  43
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  208255
                  LIB3120-043-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129698
BLAST score
                  169
                  2.0e-12
E value
Match length
                  46
% identity
                  67
                  protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                  >qi 1054633 emb CAA63387 (X92728) protein kinase
                  [Arabidopsis thaliana]
                  208256
Seq. No.
                  LIB3120-043-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241926
BLAST score
                  38
E value
                  5.0e-12
```

Match length 82 % identity 87

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSG15, complete sequence [Arabidopsis thaliana]

Seq. No. 208257

Seq. ID LIB3120-043-P1-K1-B1



```
Method BLASTN
NCBI GI g3089318
BLAST score 75
```

E value 3.0e-34 Match length 173 % identity 93

NCBI Description Rhododendron camtschaticum chloroplast matK gene for

ribosomal maturase, complete cds

Seq. No. 208258

Seq. ID LIB3120-043-P1-K1-B11

Method BLASTX
NCBI GI g629541
BLAST score 290
E value 2.0e-26
Match length 78
% identity 76

NCBI Description plasma membrane intrinsic protein 1c - Arabidopsis thaliana

>gi 472875 emb CAA53476 (X75882) plasma membrane intrinsic

protein 1c [Arabidopsis thaliana]

Seq. No. 208259

Seq. ID LIB3120-043-P1-K1-B12

Method BLASTX
NCBI GI g1458245
BLAST score 149
E value 1.0e-09
Match length 109
% identity 29

NCBI Description (U64834) coded for by C. elegans cDNA cm17a1; coded for by

C. elegans cDNA cm7g1; coded for by C. elegans cDNA

CEMSE26F; similar to methyltransferases [Caenorhabditis

elegans]

Seq. No. 208260

Seq. ID LIB3120-043-P1-K1-B3

Method BLASTX
NCBI GI g2131751
BLAST score 208
E value 1.0e-16
Match length 69
% identity 57

NCBI Description hypothetical protein YLR019w - yeast (Saccharomyces

cerevisiae) >gi\_1360322\_emb\_CAA97541\_ (Z73191) ORF YLR019w

[Saccharomyces cerevisiae]

Seq. No. 208261

Seq. ID LIB3120-043-P1-K1-B7

Method BLASTN
NCBI GI 9450504
BLAST score 33
E value 2.0e-09
Match length 69
% identity 87

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate

carboxylase, small subunit

```
Seq. No.
Seq. ID
                  LIB3120-043-P1-K1-B8
                  BLASTX
```

Method NCBI GI g445613 BLAST score 200 E value 7.0e-16Match length 67 % identity 63

NCBI Description ribosomal protein L7 [Solanum tuberosum]

208263 Seq. No.

Seq. ID LIB3120-043-P1-K1-C12

Method BLASTX g231688 NCBI GI BLAST score 554 E value 3.0e-57 Match length 105 100 % identity

NCBI Description CATALASE ISOZYME 2 >gi 99599 pir S17493 catalase (EC 1.11.1.6) - upland cotton >gi 18488 emb CAA39998 (X56675)

subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No. 208264

Seq. ID LIB3120-043-P1-K1-C2

Method BLASTX NCBI GI g4417203 BLAST score 286 E value 4.0e-26 Match length 58 % identity 93

NCBI Description (AB006386) maturase [Tilia kiusiana]

Seq. No. 208265

Seq. ID LIB3120-043-P1-K1-C3

Method BLASTX NCBI GI g2696804 BLAST score 345 6.0e-33 E value Match length 81 % identity 81

NCBI Description (AB009665) water channel protein [Oryza sativa]

Seq. No. 208266

Seq. ID LIB3120-043-P1-K1-C4

Method BLASTX NCBI GI q289920 BLAST score 174 E value 4.0e-13 Match length 37 95 % identity

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 208267

Seq. ID LIB3120-043-P1-K1-C6

Method BLASTN NCBI GI g4210572



```
BLAST score
E value
                  7.0e-22
Match length
                  78
% identity
                  92
                  Tilia kiusiana chloroplast matK gene for maturase, partial
NCBI Description
Seq. No.
                  208268
                  LIB3120-043-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4314396
BLAST score
                  197
E value
                  2.0e-15
Match length
                  74
% identity
                  51
                  (AC006232) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  208269
Seq. No.
                  LIB3120-043-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g445116
BLAST score
                  254
E value
                  6.0e-22
Match length
                  88
                  56
% identity
NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]
                  208270
Seq. No.
                  LIB3120-043-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131397
BLAST score
                  161
E value
                  1.0e-11
Match length
                  56
% identity
                  61
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi 81480 pir S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi 225597 prf 1307179B luminal protein 16kD
                  [Spinacia oleracea]
Seq. No.
                  208271
                  LIB3120-043-P1-K1-D12
Seq. ID
Method
                  BLASTX
```

g2795809 NCBI GI BLAST score 566 E value 1.0e-58 Match length 116 % identity 89

NCBI Description (AC003674) putative expansin [Arabidopsis thaliana]

Seq. No. 208272

Seq. ID LIB3120-043-P1-K1-D5



```
BLASTX
Method
NCBI GI
                  g1352821
BLAST score
                  271
                  4.0e-24
E value
Match length
                  59
                  88
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  208273
Seq. No.
                  LIB3120-043-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  g289920
NCBI GI
BLAST score
                  358
                  1.0e-34
E value
Match length
                  69
                  99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  208274
Seq. No.
                  LIB3120-043-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  q3913651
NCBI GI
BLAST score
                  141
E value
                  5.0e-09
                  42
Match length
                  71
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                  208275
                  LIB3120-043-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g289920
NCBI GI
BLAST score
                  538
E value
                  3.0e-55
                  104
Match length
                  97
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  208276
Seq. No.
                  LIB3120-043-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g285286
BLAST score
                  350
E value
                  3.0e-33
Match length
                  116
% identity
                  55
```

Seq. No. 208277

NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia

BLAST score

355

```
Seq. ID
                    LIB3120-043-P1-K1-E11
 Method
                    BLASTX
 NCBI GI
                    g1354515
 BLAST score
                    152
 E value
                    3.0e-10
 Match length
                    93
 % identity
                    44
 NCBI Description
                   (U55837) carbonic anhydrase [Populus tremula x Populus
                    tremuloides]
 Seq. No.
                   208278
 Seq. ID
                   LIB3120-043-P1-K1-E12
 Method
                   BLASTX
 NCBI GI
                   q285286
 BLAST score
                   282
 E value
                   2.0e-25
Match length
                   80
 % identity
                   57
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
Seq. No.
                   208279
Seq. ID
                   LIB3120-043-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q2149021
BLAST score
                   265
E value
                   9.0e-24
Match length
                   54
% identity
                   94
NCBI Description
                   (U72290) ADPG pyrophosphorylase large subunit [Arabidopsis
                   thaliana]
Seq. No.
                   208280
Seq. ID
                   LIB3120-043-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g4008159
BLAST score
                   265
E value
                   9.0e-24
Match length
                   53
% identity
                   92
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                   208281
Seq. ID
                   LIB3120-043-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g4490293
BLAST score
                   203
E value
                   2.0e-16
Match length
                   46
% identity
                   (AL035678) WD-repeat protein-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  208282
Seq. ID
                  LIB3120-043-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g631978
```



E value 7.0e-34 Match length 108 % identity 62

NCBI Description cytochrome P-450 oxidase - Mentha piperita

>gi\_493475\_emb\_CAA83941\_ (Z33875) cytochrome P-450 oxidase

[Mentha x piperita]

Seq. No. 208283

Seq. ID LIB3120-043-P1-K1-F3

Method BLASTX
NCBI GI g1708422
BLAST score 148
E value 5.0e-10
Match length 52
% identity 62

NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi 1030068 emb CAA63056

(X92075) NAD(P)H oxidoreductase, isoflavone reductase

homologue [Solanum tuberosum]

Seq. No. 208284

Seq. ID LIB3120-043-P1-K1-F6

Method BLASTX
NCBI GI g1170714
BLAST score 323
E value 2.0e-30
Match length 74
% identity 84

NCBI Description SHAGGY RELATED PROTEIN KINASE ASK-GAMMA

>gi\_541850\_pir\_\_S41597 protein kinase ASK-gamma (EC
2.7.1.-) - Arabidopsis thaliana >gi\_456509\_emb\_CAA53180\_
(X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
[Arabidopsis thaliana] >gi\_2059329\_emb\_CAA73247\_ (Y12710)

shaggy-like kinase gamma [Arabidopsis thaliana]

Seq. No. 208285

Seq. ID LIB3120-043-P1-K1-F9

Method BLASTX
NCBI GI g3336903
BLAST score 348
E value 4.0e-33
Match length 91
% identity 76

NCBI Description (Y10809) bZIP DNA-binding protein [Petroselinum crispum]

Seq. No. 208286

Seq. ID LIB3120-043-P1-K1-G10

Method BLASTX
NCBI GI g4406768
BLAST score 334
E value 2.0e-31
Match length 120
% identity 51

NCBI Description (AC006836) putative flavonol sulfotransferase [Arabidopsis

thaliana]

Seq. No. 208287

Seq. ID LIB3120-043-P1-K1-G11



```
Method
                  BLASTX
NCBI GI
                  g231610
BLAST score
                  237
E value
                  6.0e-20
Match length
                  104
% identity
                  53
NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                  >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi_19785 emb CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
                  208288
Seq. No.
Seq. ID
                  LIB3120-043-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g4454014
BLAST score
                  150
E value
                  8.0e-10
Match length
                  74
% identity
                  42
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
                  208289
Seq. No.
                  LIB3120-043-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3560529
BLAST score
                  181
E value
                  7.0e-14
Match length
                  43
% identity
                  84
NCBI Description
                  (AF039598) light harvesting chlorophyll A/B binding protein
                  [Prunus persica]
                  208290
Seq. No.
                  LIB3120-043-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131167
BLAST score
                  198
E value
                  1.0e-15
Match length
                  87
% identity
                  48
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_100292_pir__S18348 photosystem I chain II precursor -
                  wood tobacco >gi 19748_emb_CAA42623_ (X60008) PSI-D2
                  [Nicotiana sylvestris]
Seq. No.
                  208291
Seq. ID
                  LIB3120-043-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1652892
BLAST score
                  246
```

E value 4.0e-21 Match length 89 % identity 26

NCBI Description (D90909) ABC transporter [Synechocystis sp.]



```
Seq. No.
                  208292
Seq. ID
                  LIB3120-043-P1-K1-G7
Method
                  BLASTX
                  g231610
NCBI GI
BLAST score
                  225
E value
                  1.0e-18
Match length
                  92
% identity
                  57
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi_19785_emb_CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
Seq. No.
                  208293
Seq. ID
                  LIB3120-043-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g4530585
BLAST score
                  350
E value
                  3.0e-33
Match length
                  84
                  74
% identity
NCBI Description
                  (AF130978) B12D protein [Ipomoea batatas]
Seq. No.
                  208294
Seq. ID
                  LIB3120-043-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  342
E value
                  3.0e-32
Match length
                  118
% identity
                  57
NCBI Description
                  (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
                  208295
Seq. No.
Seq. ID
                  LIB3120-043-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4544402
BLAST score
                  238
                  2.0e-20
E value
Match length
                  77
% identity
                  12
NCBI Description
                  (AC007047) putative leucine rich repeat protein
                  [Arabidopsis thaliana]
Seq. No.
                  208296
Seq. ID
                  LIB3120-043-P1-K1-H12
Method
                  BLASTX
```

NCBI GI g479406 BLAST score 573 E value 2.0e-59 Match length 112 % identity

NCBI Description chlorophyll a/b-binding protein - garden pea

>gi\_20671\_emb\_CAA49149 (X69215) chlorophyll a/b-binding

protein [Pisum sativum]



```
208297
Seq. No.
Seq. ID
                  LIB3120-043-P1-K1-H2
Method
                  BLASTX
                  g1173638
NCBI GI
                  208
BLAST score
                  5.0e-17
E value
Match length
                  59
% identity
                  64
                  (U35779) 1-aminocyclopropane-1-carboxylate synthase
NCBI Description
                  [Triticum aestivum]
                  208298
Seq. No.
                  LIB3120-043-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3319882
BLAST score
                  276
                  7.0e-25
E value
Match length
                  67
% identity
                  81
NCBI Description
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
                  208299
Seq. No.
Seq. ID
                  LIB3120-043-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  5.0e-11
E value
Match length
                  41
% identity
                  63
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  208300
Seq. No.
Seq. ID
                  LIB3120-044-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g68200
                  158
BLAST score
                  3.0e-11
E value
Match length
                  50
                  70
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
NCBI Description
                  chloroplast - spinach >gi 22633 emb CAA47293 (X66814)
                  fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.
                  208301
                  LIB3120-044-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345698
BLAST score
                  217
E value
                  4.0e-18
Match length
                  57
                  77
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
```

28688

a/b-binding protein - upland cotton

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

>gi\_452314\_emb\_CAA38025\_ (X54090) chlorophyll ab binding

- 166°

E value

6.0e-38



## protein [Gossypium hirsutum]

```
Seq. No.
                  208302
Seq. ID
                  LIB3120-044-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3914605
BLAST score
                  100
                  5.0e-10
E value
Match length
                  43
% identity
                  74
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                  PRECURSOR (RUBISCO ACTIVASE) >gi 541930 pir S39551
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                  apple tree >gi 415852 emb CAA79857 (Z21794)
                  ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                  [Malus domestica]
Seq. No.
                  208303
Seq. ID
                  LIB3120-044-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1084372
BLAST score
                  309
E value
                  6.0e-29
Match length
                  65
% identity
                  95
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC
                  1.2.1.9) - garden pea
Seq. No.
                  208304
                  LIB3120-044-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885344
BLAST score
                  163
                  3.0e-11
E value
Match length
                  92
                  34
% identity
NCBI Description
                  (AC005623) unknown protein [Arabidopsis thaliana]
                  >qi 4557057 gb AAD22497.1 AC007154 1 (AC007154) unknown
                  protein [Arabidopsis thaliana]
                  208305
Seq. No.
                  LIB3120-044-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g289919
BLAST score
                  55
E value
                  2.0e-22
Match length
                  83
                  92
% identity
                  Gossypium hirsutum chloroplast photosystem II chlorophyll
NCBI Description
                  A/B-binding protein gene, complete cds
Seq. No.
                  208306
                  LIB3120-044-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  q2970641
NCBI GI
BLAST score
                  387
```



Match length % identity 92 (AF052194) xyloglucan endotransglycosylase precursor NCBI Description [Actinidia deliciosa] 208307 Seq. No. LIB3120-044-P1-K1-B12 Seq. ID BLASTX Method NCBI GI g445116 605 BLAST score 4.0e-63 E value 124 Match length % identity 91 light-harvesting complex IIa protein; [Hordeum vulgare] NCBI Description Seq. No. 208308 LIB3120-044-P1-K1-B4 Seq. ID Method BLASTX q3445210 NCBI GI BLAST score 184 5.0e-14 E value Match length 74 45 % identity (AC004786) putative flavonol 3-o-glucosyltransferase NCBI Description [Arabidopsis thaliana] Seq. No. 208309 LIB3120-044-P1-K1-B5 Seq. ID Method BLASTX NCBI GI g4309737 BLAST score 173 6.0e-13 E value Match length 40 % identity 85 NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana] 208310 Seq. No. LIB3120-044-P1-K1-B8 Seq. ID Method BLASTX NCBI GI g1130682 BLAST score 310 E value 5.0e-29 Match length 66 91 % identity NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum] 208311 Seq. No. LIB3120-044-P1-K1-C1 Seq. ID Method BLASTN NCBI GI q289919 BLAST score 120

E value 3.0e-61 Match length 156 % identity

Gossypium hirsutum chloroplast photosystem II chlorophyll NCBI Description

A/B-binding protein gene, complete cds

Match length

NCBI Description

% identity

234



```
Seq. No.
                  208312
                  LIB3120-044-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q99485
BLAST score
                  359
                  3.0e-34
E value
                  80
Match length
                  82
% identity
NCBI Description
                  chlorophyll a/b-binding protein (clone pINEab 21) - Scotch
                  pine >gi_20788_emb_CAA41404_ (X58514) Type 1 chlorophyll a
                  /b-binding protein [Pinus sylvestris]
                  208313
Seq. No.
                  LIB3120-044-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266579
BLAST score
                  205
                  1.0e-16
E value
Match length
                  49
% identity
                  69
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 169713 (L02306)
NCBI Description
                  metallothionein [Ricinus communis]
                  208314
Seq. No.
Seq. ID
                  LIB3120-044-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g625547
BLAST score
                  397
                  9.0e-39
E value
                  110
Match length
% identity
                  73
                  chlorophyll a/b-binding protein type I - common tobacco
NCBI Description
                  >gi 493723 emb CAA45523 (X64198) photosystem I
                  light-harvesting chlorophyll a/b-binding protein [Nicotiana
                  tabacum]
                  208315
Seq. No.
Seq. ID
                  LIB3120-044-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  33
E value
                  3.0e-09
Match length
                  69
% identity
                  87
NCBI Description Rice complete chloroplast genome
Seq. No.
                  208316
Seq. ID
                  LIB3120-044-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g450504
BLAST score
                  110
E value
                  4.0e-55
```

28691

carboxylase, small subunit

G.hirsutum rbcS gene for ribulose-1,5-bisphosphate



```
Seq. No.
                  208317
Seq. ID
                  LIB3120-044-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1170028
BLAST score
                  357
E value
                  3.0e-34
Match length
                  76
% identity
                  84
NCBI Description
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA
                  1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1)
                  >gi_454357 (U03773)
                  glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis
                  thaliana]
Seq. No.
                  208318
                  LIB3120-044-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115834
BLAST score
                  264
E value
                  1.0e-23
Match length
                  54
                  91
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10B PRECURSOR
                   (CAB-10B) (LHCP) >gi_100202 pir S11878 chlorophyll
                  a/b-binding protein Cab10B - tomato >gi 170400 (M32606)
                  chlorophyll b-binding protein [Lycopersicon esculentum]
Seq. No.
                  208319
                  LIB3120-044-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  g3169719
NCBI GI
BLAST score
                  139
                  8.0e-09
E value
Match length
                  43
% identity
                  60
NCBI Description
                  (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]
Seq. No.
                  208320
                  LIB3120-044-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  172
E value
                  1.0e-12
Match length
                  81
% identity
                  56
NCBI Description
                  (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                  [Arabidopsis thaliana]
Seq. No.
                  208321
Seq. ID
                  LIB3120-044-P1-K1-E2
Method
                  BLASTN
```

NCBI GI g3821780 BLAST score 32 E value 9.0e-09 Match length 43 63 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
Seq. No.
                  208322
Seq. ID
                  LIB3120-044-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q1170567
BLAST score
                  238
E value
                  1.0e-20
Match length
                  52
% identity
                  83
NCBI Description
                 MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
                  >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi
                  >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                  208323
Seq. ID
                  LIB3120-044-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3738261
BLAST score
                  441
E value
                  5.0e-44
Match length
                  99
% identity
                  91
NCBI Description
                  (AB018412) chloroplast phosphoglycerate kinase [Populus
                  nigra]
Seq. No.
                  208324
Seq. ID
                  LIB3120-044-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  267
E value
                  5.0e-24
Match length
                  48
% identity
                  96
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  208325
Seq. ID
                  LIB3120-044-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1928981
BLAST score
                  304
E value
                  3.0e-28
Match length
                  65
% identity
                  92
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  208326
Seq. ID
                  LIB3120-044-P1-K1-G12
```

Method BLASTX NCBI GI g487006 BLAST score 571 E value 4.0e-59 Match length 116 % identity 92



NCBI Description protoporphyrin IX magnesium chelatase - garden snapdragon >gi\_312129\_emb\_CAA51664\_ (X73144) protoporphyrin IX:Mg

Chelatase [Antirrhinum majus]

Seq. No. 208327

Seq. ID LIB3120-044-P1-K1-G2

Method BLASTX
NCBI GI g3128195
BLAST score 178
E value 2.0e-18
Match length 55
% identity 88

NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase

[Arabidopsis thaliana] >gi\_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis

thaliana]

Seq. No. 208328

Seq. ID LIB3120-044-P1-K1-G4

Method BLASTX
NCBI GI g1352821
BLAST score 274
E value 2.0e-24
Match length 78
% identity 74

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208329

Seq. ID LIB3120-044-P1-K1-G5

Method BLASTN
NCBI GI g450504
BLAST score 39
E value 3.0e-13
Match length 87
% identity 86

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate

carboxylase, small subunit

Seq. No. 208330

Seq. ID LIB3120-044-P1-K1-G6

Method BLASTX
NCBI GI g3128195
BLAST score 290
E value 5.0e-26
Match length 65
% identity 86

NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase

[Arabidopsis thaliana] >gi\_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis

thaliana]

Seq. No. 208331

Seq. ID LIB3120-044-P1-K1-H11



Method BLASTX
NCBI GI g1352821
BLAST score 397
E value 9.0e-39
Match length 80
% identity 93
NCBI Description RIBULOSE (RUBISCO ribulose

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208332

Seq. ID LIB3120-044-P1-K1-H12

Method BLASTX
NCBI GI g3643090
BLAST score 410
E value 3.0e-40
Match length 108
% identity 70

NCBI Description (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 208333

Seq. ID LIB3120-044-P1-K1-H2

Method BLASTN
NCBI GI g450504
BLAST score 144
E value 2.0e-75
Match length 176
% identity 95

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate

carboxylase, small subunit

Seq. No. 208334

Seq. ID LIB3120-045-P1-K1-A5

Method BLASTN
NCBI GI g450504
BLAST score 67
E value 1.0e-29
Match length 162
% identity 84

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate

carboxylase, small subunit

Seq. No. 208335

Seq. ID LIB3120-045-P1-K1-A6

Method BLASTX
NCBI GI g3348077
BLAST score 238
E value 1.0e-22
Match length 74
% identity 74

NCBI Description (AF078080) isochorismate synthase [Arabidopsis thaliana]

Seq. No. 208336

Seq. ID LIB3120-045-P1-K1-B3

NCBI GI

BLAST score



```
BLASTX
 Method
 NCBI GI
                   g289920
 BLAST score
                   566
 E value
                   1.0e-58
 Match length
                   111
 % identity
                   96
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
Seq. No.
                   208337
Seq. ID
                   LIB3120-045-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g2384956
BLAST score
                   155
E value
                   3.0e-10
Match length
                   119
% identity
                   34
                   (AF022985) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   208338
Seq. ID
                   LIB3120-045-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2440044
BLAST score
                   166
E value
                   6.0e-12
Match length
                   45
% identity
                   69
NCBI Description
                   (AJ001293) major intrinsic protein PIPB [Craterostigma
                   plantagineum]
Seq. No.
                   208339
Seq. ID
                   LIB3120-045-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g289920
BLAST score
                   595
E value
                   6.0e-62
Match length
                   114
% identity
                   96
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                   208340
Seq. ID
                  LIB3120-045-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g286001
BLAST score
                  155
E value
                  2.0e-10
Match length
                  75
% identity
                  41
NCBI Description (D13630) KIAA0005 [Homo sapiens]
Seq. No.
                  208341
Seq. ID
                  LIB3120-045-P1-K1-D5
Method
                  BLASTN
```

28696

q4519191

```
1.0e-20
E value
Match length
                  96
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9P8, complete sequence
                  208342
Seq. No.
                  LIB3120-045-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2970654
BLAST score
                  181
E value
                   6.0e-14
                   63
Match length
% identity
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
NCBI Description
                  unguiculata]
Seq. No.
                  208343
Seq. ID
                  LIB3120-045-P1-K1-E8
                  BLASTN
Method
NCBI GI
                   q20490
BLAST score
                   32
                   1.0e-08
E value
                   40
Match length
                   95
% identity
                  Petunia rbcS gene (ssu8) for ribulose 1,5-bisphosphate
NCBI Description
                   carboxylase small subunit
                   208344
Seq. No.
Seq. ID
                   LIB3120-045-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   q929812
BLAST score
                   39
                   8.0e-13
E value
Match length
                   91
                   86
% identity
NCBI Description P.nigra mRNA for plastocyanin a
                   208345
Seq. No.
                   LIB3120-045-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1064883
BLAST score
                   210
                   5.0e-17
E value
Match length
                   58
% identity
                   43
NCBI Description (X92976) ZAP1 [Arabidopsis thaliana]
```

208346 Seq. No.

LIB3120-045-P1-K1-H7 Seq. ID

BLASTX Method g541950 NCBI GI BLAST score 138 7.0e-09 E value 40 Match length 72 % identity

NCBI Description SPCP1 protein - soybean >gi\_310576 (L12257) nodulin-26



## [Glycine max]

 Seq. No.
 208347

 Seq. ID
 LIB3120-046-P1-K1-A11

 Method
 BLASTX

 NCBI GI
 g1345698

BLAST score 397
E value 5.0e-39
Match length 81
% identity 91

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

a/b-binding protein - upland cotton

>gi\_452314\_emb\_CAA38025\_ (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 208348

Seq. ID LIB3120-046-P1-K1-A12

Method BLASTX
NCBI GI g1345698
BLAST score 146
E value 8.0e-10
Match length 61
% identity 57

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

a/b-binding protein - upland cotton

>gi\_452314\_emb\_CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 208349

Seq. ID LIB3120-046-P1-K1-A4

Method BLASTN
NCBI GI g166915
BLAST score 43
E value 3.0e-15
Match length 79
% identity 89

NCBI Description Arabidopsis thaliana alpha-4 tubulin (TUA4) gene, complete

cds

Seq. No. 208350

Seq. ID LIB3120-046-P1-K1-A7

Method BLASTX
NCBI GI g3913640
BLAST score 158
E value 4.0e-11
Match length 40
% identity 78

NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)

>gi\_3041775\_dbj\_BAA25422\_ (AB007193)
fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 208351

Seq. ID LIB3120-046-P1-K1-B12

Method BLASTN



```
NCBI GI
                   q3108261
BLAST score
                   79
E value
                  1.0e-36
Match length
                  183
% identity
                  86
NCBI Description Gossypium barbadense clone pXP063 repetitive DNA sequence
Seq. No.
                  208352
                  LIB3120-046-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115792
BLAST score
                  161
E value
                  1.0e-11
Match length
                  41
% identity
                  83
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I 21
NCBI Description
                  PRECURSOR (CAB-21) (LHCP) >gi_72742_pir__CDNT21 chlorophyll
                  a/b-binding protein precursor (cab-21) - common tobacco
                  >gi_19823_emb_CAA36957 (X52743) Cab21 protein precursor
                   [Nicotiana tabacum]
Seq. No.
                  208353
Seq. ID
                  LIB3120-046-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3252854
BLAST score
                  325
E value
                  2.0e-30
Match length
                  70
% identity
                  90
                  (AF020424) glutamate decarboxylase isozyme 2 [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  208354
Seq. ID
                  LIB3120-046-P1-K1-B7
Method
                  BLASTX
                  q2462756
NCBI GI
BLAST score
                  163
E value
                  8.0e-12
Match length
                  42
% identity
                  76
NCBI Description
                  (AC002292) putative receptor kinase [Arabidopsis thaliana]
Seq. No.
                  208355
Seq. ID
                  LIB3120-046-P1-K1-C1
Method
                  BLASTX
                  g289920
NCBI GI
BLAST score
                  321
E value
                  4.0e-30
Match length
                  73
% identity
                  88
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
```

Seq. No. 208356

Seq. ID LIB3120-046-P1-K1-C12

Method BLASTX NCBI GI g21839

```
BLAST score
E value
                  8.0e-47
Match length
                  91
% identity
                  93
NCBI Description
                  (X57952) phosphoribulokinase [Triticum aestivum]
Seq. No.
                  208357
Seq. ID
                  LIB3120-046-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1076678
BLAST score
                  221
E value
                  3.0e-21
Match length
                  58
% identity
                  89
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                  208358
Seq. ID
                  LIB3120-046-P1-K1-C4
```

Method BLASTN

NCBI GI g2258103 BLAST score 44 1.0e-15 E value Match length 48 % identity 98

NCBI Description Arabidopsis thaliana chloroplast genes for trnC and rpoB,

partial cds

Seq. No. 208359

Seq. ID LIB3120-046-P1-K1-C9

Method BLASTX g4263710 NCBI GI BLAST score 281 E value 7.0e-26 Match length 76 % identity 53

NCBI Description (AC006223) putative pur-alpha transcriptional activator

protein [Arabidopsis thaliana]

Seq. No. 208360

Seq. ID LIB3120-046-P1-K1-D1

Method BLASTN NCBI GI g2924651 BLAST score 43 E value 3.0e-15 Match length 83 % identity 88

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 208361

Seq. ID LIB3120-046-P1-K1-D12

Method BLASTX NCBI GI g66179 BLAST score 359 E value 2.0e-34 Match length 96 % identity 71



NCBI Description NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - common tobacco chloroplast >gi\_225255\_prf\_\_1211235CP NADH

dehydrogenase 4-like ORF 509B [Nicotiana tabacum]

Seq. No. 208362

Seq. ID LIB3120-046-P1-K1-D4

Method BLASTX
NCBI GI g1352821
BLAST score 362
E value 5.0e-43
Match length 89
% identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208363

Seq. ID LIB3120-046-P1-K1-D5

Method BLASTX
NCBI GI g1352821
BLAST score 335
E value 1.0e-31
Match length 67
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208364

Seq. ID LIB3120-046-P1-K1-D6

Method BLASTX
NCBI GI g2191152
BLAST score 355
E value 4.0e-34
Match length 81
% identity 81

NCBI Description (AF007269) A IG002N01.31 gene product [Arabidopsis

thaliana]

Seq. No. 208365

Seq. ID LIB3120-046-P1-K1-E1

Method BLASTX
NCBI GI g4218120
BLAST score 150
E value 3.0e-10
Match length 44
% identity 64

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 208366

Seq. ID LIB3120-046-P1-K1-E10

Method BLASTX



```
g4455192
NCBI GI
BLAST score
                  230
                  2.0e-19
E value
Match length
                  72
% identity
                  61
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  208367
Seq. No.
                  LIB3120-046-P1-K1-E4
Seq. ID
Method
                  BLASTX
                  q4091806
NCBI GI
BLAST score
                  162
                  1.0e-11
E value
Match length
                  46
% identity
                  72
NCBI Description
                  (AF052585) CONSTANS-like protein 2 [Malus domestica]
Seq. No.
                  208368
                  LIB3120-046-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q282833
BLAST score
                  179
                  1.0e-13
E value
Match length
                  42
% identity
                  88
NCBI Description phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
Seq. No.
                  208369
Seq. ID
                  LIB3120-046-P1-K1-E8
                  BLASTX
Method
                  q289920
NCBI GI
BLAST score
                  269
                  3.0e-24
E value
                  53
Match length
                  96
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  208370
                  LIB3120-046-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2494280
BLAST score
                  250
                  5.0e-22
E value
Match length
                  76
% identity
                  62
                  ELONGATION FACTOR TS (EF-TS) >gi 1653231 dbj BAA18146_
NCBI Description
                   (D90912) elongation factor TS [Synechocystis sp.]
Seq. No.
                  208371
Seq. ID
                  LIB3120-046-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3738261
```

NCBI GI g3738261
BLAST score 124
E value 1.0e-10
Match length 84
% identity 54



(AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 208372

NCBI Description

Seq. ID LIB3120-046-P1-K1-F2

Method BLASTX
NCBI GI 94091804
BLAST score 208
E value 4.0e-17
Match length 57
% identity 72

NCBI Description (AF052584) CONSTANS-like protein 1 [Malus domestica]

Seq. No. 208373

Seq. ID LIB3120-046-P1-K1-F4

Method BLASTX
NCBI GI g2245066
BLAST score 311
E value 7.0e-29
Match length 83
% identity 65

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 208374

Seq. ID LIB3120-046-P1-K1-F6

Method BLASTX
NCBI GI g1352821
BLAST score 303
E value 6.0e-28
Match length 65
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208375

Seq. ID LIB3120-046-P1-K1-F7

Method BLASTX
NCBI GI g20729
BLAST score 141
E value 3.0e-09
Match length 48
% identity 62

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No. 208376

Seq. ID LIB3120-046-P1-K1-F8

Method BLASTX
NCBI GI g1345698
BLAST score 333
E value 2.0e-31
Match length 72
% identity 89

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll



a/b-binding protein - upland cotton >qi 452314 emb CAA38025 (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No. 208377

Seq. ID LIB3120-046-P1-K1-F9

Method BLASTX NCBI GI g1352821 BLAST score 251 6.0e-22 E value Match length 50 98 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505\_emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208378

Seq. ID LIB3120-046-P1-K1-G1

Method BLASTX NCBI GI g289920 BLAST score 344 7.0e-33 E value Match length 68 94 % identity

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

Seq. No. 208379

LIB3120-046-P1-K1-G10 Seq. ID

BLASTX Method NCBI GI g3608179 BLAST score 361 E value 1.0e-34 Match length 94

% identity

NCBI Description (AB008188) cyclin D [Pisum sativum]

208380 Seq. No.

Seq. ID LIB3120-046-P1-K1-G11

Method BLASTX NCBI GI q625547 BLAST score 350 E value 3.0e-33 Match length 99 % identity 71

NCBI Description chlorophyll a/b-binding protein type I - common tobacco

>gi 493723 emb CAA45523 (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

Seq. No. 208381

LIB3120-046-P1-K1-G12 Seq. ID

Method BLASTX NCBI GI g2318137 BLAST score 333



E value 1.0e-31
Match length 74
% identity 89

NCBI Description (AF014052) Mg protoporphyrin IX chelatase [Nicotiana

tabacum]

Seq. No. 208382

Seq. ID LIB3120-046-P1-K1-G2

Method BLASTX
NCBI GI g131397
BLAST score 184
E value 3.0e-14
Match length 56
% identity 70

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD

SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480 pir\_S00008 photosystem II oxygen-evolving

complex protein 3 precursor - spinach

>gi\_755802\_emb\_CAA29056\_ (X05512) 16 kDa protein of the
photosynthetic oxygen- evolving protein (OEC) [Spinacia
oleracea] >gi\_225597\_prf\_\_1307179B luminal protein 16kD

[Spinacia oleracea]

Seq. No. 208383

Seq. ID LIB3120-046-P1-K1-G5

Method BLASTX
NCBI GI g1352821
BLAST score 391
E value 3.0e-38
Match length 79
% identity 90

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208384

Seq. ID LIB3120-046-P1-K1-G6

Method BLASTX
NCBI GI g3080439
BLAST score 176
E value 3.0e-13
Match length 69
% identity 58

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 208385

Seq. ID LIB3120-046-P1-K1-G7

Method BLASTN
NCBI GI g450504
BLAST score 144
E value 1.0e-75
Match length 148
% identity 99

NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate

carboxylase, small subunit



Seq. No. 208386 LIB3120-046-P1-K1-G8 Seq. ID Method BLASTN NCBI GI g289919 BLAST score 113 3.0e-57 E value Match length 117 % identity 99 Gossypium hirsutum chloroplast photosystem II chlorophyll NCBI Description A/B-binding protein gene, complete cds 208387 Seq. No. LIB3120-046-P1-K1-G9 Seq. ID Method BLASTX NCBI GI g231610 BLAST score 315 E value 3.0e-29 Match length 109 % identity NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >qi 67880 pir PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum] Seq. No. 208388 Seq. ID LIB3120-046-P1-K1-H1 Method BLASTX NCBI GI g1929027 BLAST score 189 7.0e-15 E value Match length 39 95 % identity NCBI Description (Y11038) BV-70/5 [Beta vulgaris] 208389 Seq. No. LIB3120-046-P1-K1-H12 Seq. ID Method BLASTX g3643090 NCBI GI BLAST score 486 4.0e-49 E value Match length 128 70 % identity (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum NCBI Description crystallinum] 208390 Seq. No. LIB3120-046-P1-K1-H3 Seq. ID Method BLASTX NCBI GI q2499710 BLAST score 185

2.0e-14 E value Match length 43 79 % identity

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

28706

·12' :+.



>gi\_1438075 (L33686) phospholipase D [Ricinus communis]

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208391
Seq. No.
                  LIB3120-046-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  g3868758
NCBI GI
BLAST score
                  203
                   7.0e-16
E value
                   53
Match length
                   70
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                   208392
Seq. No.
Seq. ID
                   LIB3120-046-P1-K1-H9
                   BLASTX
Method
                   g4218120
NCBI GI
                   150
BLAST score
                   6.0e-10
E value
                   89
Match length
                   46
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   208393
Seq. No.
                   LIB3120-048-P1-K1-A2
Seq. ID
                   BLASTX
Method
                   g1208497
NCBI GI
                   236
BLAST score
                   3.0e-20
E value
                   64
Match length
                   56
% identity
NCBI Description (D38125) EREBP-4 [Nicotiana tabacum]
                   208394
Seq. No.
Seq. ID
                   LIB3120-048-P1-K1-A3
                   BLASTX
Method
NCBI GI
                   g20729
BLAST score
                   333
E value
                   2.0e-31
                   99
Match length
                   70
% identity
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   208395
Seq. No.
                   LIB3120-048-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   g1352821
NCBI GI
                   204
BLAST score
E value
                   2.0e-16
                   52
Match length
                   73
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                   ribulose-bisphosphate carboxylase \overline{(EC 4.1.1.39)} small chain
```

28707

precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]



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Seq. No.
                   208396
                  LIB3120-048-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1006835
BLAST score
                   311
E value
                   6.0e-29
Match length
                   67
                  82
% identity
                  (U35111) rubisco activase precursor [Nicotiana tabacum]
NCBI Description
Seq. No.
                   208397
                   LIB3120-048-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2407801
BLAST score
                   51
E value
                   7.0e-20
Match length
                   179
% identity
                   83
NCBI Description Arabidopsis thaliana mRNA for histone H2B
Seq. No.
                   208398
Seq. ID
                   LIB3120-048-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q1718097
BLAST score
                   284
E value
                   2.0e-25
Match length
                   89
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                   lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar
                   ATPase subunit DVA41 [Dictyostelium discoideum]
                   208399
Seq. No.
                   LIB3120-048-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3253137
BLAST score
                   377
E value
                   1.0e-36
Match length
                   91
% identity
                   75
                  (U24194) cyclin [Lupinus luteus]
NCBI Description
                   208400
Seq. No.
                   LIB3120-048-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   397
E value
                   7.0e-39
Match length
                   78
```

% identity 99

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi 279581 pir \_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

BLAST score

E value Match length 203 2.0e-16

70



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208401
Seq. No.
                  LIB3120-048-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171997
BLAST score
                  146
                  8.0e-10
E value
Match length
                   56
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi_633597_emb_CAA55075
NCBI Description
                   (X78269) phenylalanine ammonia-Tyase [Nicotiana tabacum]
                   208402
Seq. No.
                   LIB3120-048-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q121353
BLAST score
                   240
E value
                   3.0e-28
                   72
Match length
                   89
% identity
                  GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA)
NCBI Description
                   (GLUTAMATE-AMMONIA LIGASE) > gi 68596 pir AJFBQD
                   glutamate--ammonia ligase (EC \overline{6}.3.1.\overline{2}) delta precursor,
                   chloroplast - kidney bean >gi_21005_emb_CAA31234 (X12738)
                   GS precursor protein [Phaseolus vulgaris]
Seq. No.
                   208403
Seq. ID
                   LIB3120-048-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q2499535
BLAST score
                   205
E value
                   3.0e-16
Match length
                   79
% identity
                   59
                   2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681
NCBI Description
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                   oleracea]
                   208404
Seq. No.
                   LIB3120-048-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q479406
                   450
BLAST score
                   5.0e-45
E value
                   93
Match length
                   86
% identity
                   chlorophyll a/b-binding protein - garden pea
NCBI Description
                   >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                   protein [Pisum sativum]
                   208405
Seq. No.
Seq. ID
                   LIB3120-048-P1-K1-E3
                   BLASTX
Method
                   g1170203
NCBI GI
```

·\_\*,



Seq. ID LIB3120-048-P1-K1-E4 Method BLASTX

NCBI GI g1354515
BLAST score 195
E value 2.0e-15
Match length 70
% identity 63

NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus

tremuloides]

Seq. No. 208407

Seq. ID LIB3120-048-P1-K1-E5

Method BLASTX
NCBI GI g4185139
BLAST score 159
E value 5.0e-11
Match length 73
% identity 48

NCBI Description (AC005724) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No. 208408

Seq. ID LIB3120-048-P1-K1-F1

Method BLASTX
NCBI GI g1352821
BLAST score 347
E value 5.0e-33
Match length 68
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208409

Seq. ID LIB3120-048-P1-K1-F2

Method BLASTX
NCBI GI g1168411
BLAST score 491
E value 8.0e-50
Match length 117
% identity 85

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

Seq. No. 208410

Seq. ID LIB3120-048-P1-K1-F5

Method BLASTX
NCBI GI g1352821
BLAST score 330
E value 6.0e-31
Match length 80



```
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                  208411
Seq. No.
                  LIB3120-048-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1354515
                  176
BLAST score
                  2.0e-13
E value
                  55
Match length
% identity
                 (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  208412
Seq. No.
                  LIB3120-048-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  a2129753
                  412
BLAST score
                  1.0e-40
E value
                  94
Match length
                  89
% identity
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                  [Arabidopsis thaliana]
                  208413
Seq. No.
Seq. ID
                  LIB3120-048-P1-K1-H4
Method
                  BLASTX
                  q2244732
NCBI GI
BLAST score
                  380
                  9.0e-37
E value
Match length
                  84
% identity
                  86
                 (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
NCBI Description
                  208414
Seq. No.
                  LIB3120-053-P1-K1-A1
Seq. ID
Method
                  BLASTX
                  q267122
NCBI GI
                  151
BLAST score
                  2.0e-10
E value
                  42
Match length
% identity
                  THIOREDOXIN H-TYPE (TRX-H) >gi_478400_pir__JQ2242
NCBI Description
                   thioredoxin h - Arabidopsis thaliana
                   >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis
                   thaliana] >gi 1388080 (U35827) thioredoxin h [Arabidopsis
```

thaliana]

208415 Seq. No.

LIB3120-053-P1-K1-A10 Seq. ID

BLASTX Method

Seq. No.

208420



```
g3876384
NCBI GI
                  100
BLAST score
                  8.0e-11
E value
Match length
                  69
                  52
% identity
                  (Z78419) predicted using Genefinder; Similarity to Xenopus
NCBI Description
                  cap binding protein (TR:G984260) [Caenorhabditis elegans]
                  208416
Seq. No.
                  LIB3120-053-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  g1705651
NCBI GI
                  179
BLAST score
                  3.0e-13
E value
Match length
                  54
% identity
                  61
                  20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT)
NCBI Description
                  (CBP20) >gi 984139_emb_CAA58962_ (X84157) subunit of the
                  dimeric cap binding complex CBC [Homo sapiens]
                  >qi 1582342 prf 2118330A cap-binding protein [Homo
                  sapiens]
                  208417
Seq. No.
                  LIB3120-053-P1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g82263
BLAST score
                  144
                  2.0e-09
E value
Match length
                  76
                  57
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)3II) - potato
                  208418
Seq. No.
                  LIB3120-053-P1-K1-A4
Seq. ID
                  BLASTX
Method
                  g3914473
NCBI GI
BLAST score
                   403
                  1.0e-39
E value
                  88
Match length
                   89
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_479684_pir__S35151 photosystem I chain XI -
                   spinach >gi 396275 emb CAA45775 (X64445) subunit XI of
                  photosystem I reaction center [Spinacia oleracea]
                   208419
Seq. No.
                  LIB3120-053-P1-K1-A5
Seq. ID
Method
                   BLASTX
                   g228403
NCBI GI
BLAST score
                   403
E value
                   2.0e-39
                   91
Match length
                   85
% identity
                  glycolate oxidase [Lens culinaris]
NCBI Description
```



```
LIB3120-053-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3687652
BLAST score
                  267
                  5.0e-24
E value
Match length
                  59
% identity
NCBI Description
                  (AF047352) rubisco activase precursor [Datisca glomerata]
                  208421
Seq. No.
                  LIB3120-053-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  292
                  7.0e-27
E value
                  62
Match length
% identity
                  87
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                  ribulose-bisphosphate carboxylase (EC \overline{4.1.1.39}) small chain
                  precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   208422
Seq. No.
                  LIB3120-053-P1-K1-B12
Seq. ID
                  BLASTN
Method
NCBI GI
                   g18487
BLAST score
                   57
                   1.0e-23
E value
                   81
Match length
% identity
                   93
NCBI Description G. hirsutum mRNA for cotton catalase subunit
                   208423
Seq. No.
                   LIB3120-053-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   q289920
NCBI GI
BLAST score
                   596
                   5.0e-62
E value
                   116
Match length
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   208424
                   LIB3120-053-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g267069
                   297
BLAST score
                   2.0e-27
E value
Match length
                   53
% identity
                   98
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
```

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916



```
Seq. No.
                   208425
Seq. ID
                   LIB3120-053-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g4193388
BLAST score
                   269
E value
                   8.0e-28
Match length
                   79
% identity
                   84
NCBI Description
                   (AF091455) translationally controlled tumor protein (Hevea
                   brasiliensis]
Seq. No.
                   208426
Seq. ID
                   LIB3120-053-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   a3643611
BLAST score
                   139
E value
                   6.0e-09
Match length
                   41
% identity
                   71
NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]
Seq. No.
                   208427
Seq. ID
                   LIB3120-053-P1-K1-C11
Method
                  BLASTX
NCBI GI
                   q100196
BLAST score
                  159
                   7.0e-23
E value
Match length
                  82
% identity
                  72
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
Seq. No.
                  208428
Seq. ID
                  LIB3120-053-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g121344
BLAST score
                  252
E value
                  9.0e-22
Match length
                  85
% identity
                  59
NCBI Description
                  GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR
                   (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)
                  >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC
                  6.3.1.2) delta precursor, chloroplast - garden pea
                  >gi_169059 (M20664) glutamine synthetase (chloroplast GS2)
                   (EC 6.3.1.2) [Pisum sativum]
Seq. No.
                  208429
Seq. ID
                  LIB3120-053-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  193
E value
                  4.0e-15
Match length
                  40
% identity
                  97
NCBI Description
```

28714

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

NCBI Description

communis]



precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
208430
Seq. No.
                  LIB3120-053-P1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4508082
                  164
BLAST score
                  1.0e-11
E value
                   34
Match length
                   91
% identity
                   (AC005882) Putative RNA polymerase II subunit Rpb10
NCBI Description
                   [Arabidopsis thaliana]
                   208431
Seq. No.
                   LIB3120-053-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   g3421134
NCBI GI
                   323
BLAST score
                   3.0e-30
E value
                   72
Match length
                   89
% identity
                  (AF045666) arginine decarboxylase [Theobroma cacao]
NCBI Description
                   208432
Seq. No.
Seq. ID
                   LIB3120-053-P1-K1-C8
                   BLASTX
Method
NCBI GI
                   g1076389
                   261
BLAST score
                   3.0e-23
E value
                   66
Match length
% identity
                   protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                   >qi 683502 emb CAA57528 (X82002) protein phosphatase 2A 65
                   kDa regulatory subunit [Arabidopsis thaliana]
                   208433
Seq. No.
Seq. ID
                   LIB3120-053-P1-K1-D2
                   BLASTX
Method
NCBI GI
                   q1363479
                   106
BLAST score
                   5.0e-12
E value
                   81
Match length
 % identity
                   photosystem I protein psaL - cucumber
NCBI Description
                   >gi 801740 dbj BAA09047_ (D50456) PsaL [Cucumis sativus]
                   208434
 Seq. No.
                   LIB3120-053-P1-K1-E1
 Seq. ID
                   BLASTX
 Method
                   g4101626
 NCBI GI
 BLAST score
                   180
                   8.0e-14
 E value
 Match length
                   59
 % identity
```

28715

(AF005096) desaturase/cytochrome b5 protein [Ricinus

NCBI Description



```
208435
Seq. No.
Seq. ID
                  LIB3120-053-P1-K1-E10
                  BLASTX
Method
NCBI GI
                  g2499542
BLAST score
                  269
                  5.0e-24
E value
                  81
Match length
% identity
                  IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP)
NCBI Description
                  >gi 1218042 (U48448) secreted purple acid phosphatase
                  precursor [Arabidopsis thaliana]
                  208436
Seq. No.
                  LIB3120-053-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  q3068713
NCBI GI
BLAST score
                  181
                  1.0e-13
E value
Match length
                  66
% identity
                   65
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   208437
Seq. No.
                  LIB3120-053-P1-K1-E7
Seq. ID
                  BLASTN
Method
NCBI GI
                   g450504
                   38
BLAST score
                   5.0e-12
E value
Match length
                   65
% identity
                   89
                  G.hirsutum rbcS gene for ribulose-1,5-bisphosphate
NCBI Description
                   carboxylase, small subunit
                   208438
Seq. No.
Seq. ID
                   LIB3120-053-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q419760
BLAST score
                   388
                   8.0e-38
E value
Match length
                   94
% identity
                   43
                   P-glycoprotein atpgp1 - Arabidopsis thaliana
NCBI Description
                   >qi 3849833 emb CAA43646 (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
                   208439
Seq. No.
                   LIB3120-053-P1-K1-F1
Seq. ID
Method
                   BLASTN
                   g450504
NCBI GI
BLAST score
                   46
                   6.0e-17
E value
Match length
                   65
% identity
                   92
```

carboxylase, small subunit

G.hirsutum rbcS gene for ribulose-1,5-bisphosphate



```
Seq. No.
Seq. ID
                  LIB3120-053-P1-K1-F3
                  BLASTX
Method
                  g1345698
NCBI GI
                  425
BLAST score
                  4.0e-42
E value
Match length
                  87
% identity
                  92
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR .
NCBI Description
                  (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll
                  a/b-binding protein - upland cotton
                  >gi 452314_emb CAA38025_ (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
                  208441
Seq. No.
                  LIB3120-053-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1351279
                  170
BLAST score
                  2.0e-12
E value
                  59
Match length
                  58
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase
                   [Petunia x hybrida]
                  208442
Seq. No.
                  LIB3120-053-P1-K1-F9
Seq. ID
                  BLASTN
Method
                   g289919
NCBI GI
                   60
BLAST score
                   7.0e-26
E value
                   72
Match length
                   96
% identity
                  Gossypium hirsutum chloroplast photosystem II chlorophyll
NCBI Description
                   A/B-binding protein gene, complete cds
                   208443
Seq. No.
                   LIB3120-053-P1-K1-G11
Seq. ID
                   BLASTX
Method
                   g1545805
NCBI GI
BLAST score
                   239
                   2.0e-20
E value
Match length
                   81
 % identity
NCBI Description (D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
                   208444
Seq. No.
                   LIB3120-053-P1-K1-G2
Seq. ID
```

Method BLASTX
NCBI GI g1352821
BLAST score 535
E value 8.0e-55
Match length 102
% identity 98

% identity 98 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

208445 Seq. No. LIB3120-053-P1-K1-G9 Seq. ID BLASTX Method q3334321 NCBI GI BLAST score 145 1.0e-09 E value 40 Match length 72 % identity GTP-BINDING PROTEIN SAR1A >gi\_2108345 (U55035) small NCBI Description GTP-binding protein Bsarla [Brassica rapa] 208446 Seq. No. LIB3120-053-P1-K1-H3 Seq. ID BLASTX Method q421826 NCBI GI 275 BLAST score E value 6.0e-25 Match length 63 % identity 79 chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description >qi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis thaliana] Seq. No. 208447 LIB3120-053-P1-K1-H4 Seq. ID Method BLASTX q399091 NCBI GI BLAST score 492

Method BLASTX
NCBI GI g399091
BLAST score 492
E value 6.0e-50
Match length 105
% identity 97
NCBI Description PYROPHOS

NCBI Description PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)

(H+-PPASE) >gi\_282878\_pir\_\_A38230 inorganic pyrophosphatase

(EC 3.6.1.1), H+-translocating pyrophosphate-energized -

Arabidopsis thaliana >gi\_166634 (M81892) vacuolar

H+-phosphatase [Arabidopsis thaliana]

Seq. No. 208448

Seq. ID LIB3120-053-P1-K1-H5

Method BLASTX
NCBI GI g3075488
BLAST score 123
E value 2.0e-10
Match length 83
% identity 52

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.

208449

Seq. ID LIB3120-053-P1-K1-H6

Method BLASTX
NCBI GI g1354515
BLAST score 279



```
8.0e-25
E value
                  113
Match length
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  208450
Seq. No.
Seq. ID
                  LIB3120-053-P1-K1-H8
                  BLASTX
Method
NCBI GI
                  q1354515
BLAST score
                  200
                  1.0e-15
E value
Match length
                  94
                  50
% identity
NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus
                  tremuloides]
                  208451
Seq. No.
                  LIB3120-054-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1345698
BLAST score
                  432
E value
                  9.0e-43
                  106
Match length
                  76
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
                  (CAB-151) (LHCP) >gi_99601 pir S20917 chlorophyll
                  a/b-binding protein - upland cotton
                  >gi 452314 emb CAA38025 (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
Seq. No.
                  208452
Seq. ID
                  LIB3120-054-P1-K1-A3
                  BLASTX
Method
                  g2245037
NCBI GI
                  170
BLAST score
                  8.0e-14
E value
Match length
                  69
% identity
NCBI Description (Z97342) nuclear antigen homolog [Arabidopsis thaliana]
                  208453
Seq. No.
Seq. ID
                  LIB3120-054-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q3549665
BLAST score
                  173
E value
                  2.0e-12
Match length
                  103
% identity
NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 208454

Seq. ID LIB3120-054-P1-K1-A6

Method BLASTX q4426565 NCBI GI BLAST score 163 3.0e-11 E value



```
Match length
 % identity
                   (AF031483) unknown [Rattus norvegicus]
 NCBI Description
                    208455
 Seq. No.
                   LIB3120-054-P1-K1-A7
 Seq. ID
                   BLASTX
 Method
                    q1352821
 NCBI GI
                    331
 BLAST score
                    4.0e-31
· E value
                    74
 Match length
 % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                    ribulose bisphosphate carboxylase [Gossypium hirsutum]
                    208456
 Seq. No.
 Seq. ID
                    LIB3120-054-P1-K1-A8
                    BLASTX
 Method
                    q2459430
 NCBI GI
 BLAST score
                    153
                    3.0e-10
 E value
                    43
 Match length
  % identity
                   (AC002332) putative CUC2 protein [Arabidopsis thaliana]
 NCBI Description
                    208457
  Seq. No.
  Seq. ID
                    LIB3120-054-P1-K1-B10
                    BLASTX
 Method
                    a1168408
  NCBI GI
  BLAST score
                    188
                    1.0e-14
  E value
                    58
  Match length
  % identity
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
  NCBI Description
                    >gi 2118268_pir S58168 fructose-bisphosphate aldolase (EC
                    4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)
                    fructose-1,6-bisphosphate aldolase [Pisum sativum]
                    208458
  Seq. No.
  Seq. ID
                    LIB3120-054-P1-K1-B2
  Method
                    BLASTX
  NCBI GI
                    q1931647
  BLAST score
                    627
                    1.0e-65
  E value
  Match length
                    129
```

% identity 89

(U95973) endomembrane protein EMP70 precusor isolog NCBI Description

[Arabidopsis thaliana]

Seq. No. 208459

LIB3120-054-P1-K1-B4 Seq. ID

BLASTX Method q2464912 NCBI GI 146 BLAST score



```
3.0e-09
E value
Match length
                  103
                   31
% identity
                   (Z99708) salt-inducible like protein [Arabidopsis thaliana]
NCBI Description
                  208460
Seq. No.
                  LIB3120-054-P1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1352821
                   229
BLAST score
E value
                   2.0e-19
                   70
Match length
                   61
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_279581 pir RKCNSU
                   ribulose-bisphosphate carboxylase \overline{(\text{EC }\overline{4.}1.1.39)} small chain
                   precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
                   208461
Seq. No.
                   LIB3120-054-P1-K1-B9
Seq. ID
                   BLASTX
Method
                   q231688
NCBI GI
                   301
BLAST score
                   9.0e-28
E value
                   59
Match length
                   95
% identity
                   CATALASE ISOZYME 2 >gi_99599_pir__S17493 catalase (EC
NCBI Description
                   1.11.1.6) - upland cotton >gi_18488_emb_CAA39998_ (X56675)
                   subunit 2 of cotton catalase [Gossypium hirsutum]
                   208462
Seq. No.
                   LIB3120-054-P1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q267069
BLAST score
                   497
                   2.0e-50
E value
Match length
                   91
                   99
 % identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   208463
 Seq. No.
                   LIB3120-054-P1-K1-C3
 Seq. ID
 Method
                   BLASTX
                   g1352821
 NCBI GI
                    418
 BLAST score
                    3.0e-41
 E value
                   88
 Match length
                    92
 % identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT) >gi 279581_pir __RKCNSU
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]



```
208464
Seq. No.
                  LIB3120-054-P1-K1-C6
Seq. ID
                  BLASTX
Method
                  g515692
NCBI GI
                  247
BLAST score
                  1.0e-21
E value
                  65
Match length
% identity
                  72
                  (U12286) beta-tubulin [Glycine max]
NCBI Description
                  208465
Seq. No.
                  LIB3120-054-P1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3851636
                  301
BLAST score
                   9.0e-28
E value
                   73
Match length
                   75
% identity
                   (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   208466
Seq. No.
                   LIB3120-054-P1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q131385
                   489
BLAST score
E value
                   2.0e-49
                   124
Match length
                   82
% identity
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN)
 Seq. No.
                   208467
                   LIB3120-054-P1-K1-D2
 Seq. ID
                   BLASTX
Method
                   g3482913
 NCBI GI
                   143
 BLAST score
                   2.0e-09
 E value
                   65
Match length
                   43
 % identity
                   (AC003970) Similar to MtN21, gi_2598575, Megicago
 NCBI Description
                   truncatula nodulation induced gene [Arabidopsis thaliana]
                   208468
 Seq. No.
                   LIB3120-054-P1-K1-D4
 Seq. ID
                   BLASTX
 Method
                   q3688182
 NCBI GI
                   219
 BLAST score
                   9.0e-18
 E value
                   134
 Match length
                    43
 % identity
 NCBI Description (AL031804) P-Protein - like protein [Arabidopsis thaliana]
```

28722

208469

LIB3120-054-P1-K1-D5

Seq. No.

Seq. ID

E value

Match length

% identity

1.0e-29 109

57



```
BLASTX
Method
                  q2454184
NCBI GI
                  125
BLAST score
                  3.0e-10
E value
                  43
Match length
                  67
% identity
                   (U80186) pyruvate dehydrogenase E1 beta subunit
NCBI Description
                   [Arabidopsis thaliana]
                  208470
Seq. No.
                  LIB3120-054-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  q267082
NCBI GI
                  750
BLAST score
                   6.0e-80
E value
                  144
Match length
                   98
% identity
                  TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
NCBI Description
                   chain - Arabidopsis thalīana >gī_166908 (M84705) beta-8
                   tubulin [Arabidopsis thaliana]
                   208471
Seq. No.
                   LIB3120-054-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131397
BLAST score
                   137
E value
                   1.0e-08
Match length
                   52
% identity
                   60
                   OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                   SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi_81480_pir__S00008 photosystem II oxygen-evolving
                   complex protein 3 precursor - spinach
                   >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                   photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                   [Spinacia oleracea]
                   208472
Seq. No.
                   LIB3120-054-P1-K1-E11
Seq. ID
                   BLASTX
Method
                   g289920
NCBI GI
BLAST score
                   262
                   3.0e-23
E value
Match length
                   77
                   73
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   208473
Seq. No.
                   LIB3120-054-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   q4454012
NCBI GI
BLAST score
                   318
```



NCBI Description (AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No. 208474

Seq. ID LIB3120-054-P1-K1-F3

Method BLASTX
NCBI GI g100616
BLAST score 184
E value 3.0e-14
Match length 39

% identity 87
NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi\_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi\_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 208475

Seq. ID LIB3120-054-P1-K1-F4

Method BLASTX
NCBI GI g132659
BLAST score 155
E value 2.0e-10
Match length 39
% identity 62

NCBI Description 50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)

>gi\_81483\_pir\_\_A32033 ribosomal protein L13 precursor,
chloroplast - spinach >gi\_170133 (J04461) ribosomal protein

L13 [Spinacia oleracea]

Seq. No. 208476

Seq. ID LIB3120-054-P1-K1-F5

Method BLASTX
NCBI GI g1352821
BLAST score 150
E value 4.0e-10
Match length 57
% identity 61

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208477

Seq. ID LIB3120-054-P1-K1-G11

Method BLASTX
NCBI GI g1709651
BLAST score 145
E value 2.0e-09
Match length 84
% identity 38

NCBI Description PLASTOCYANIN A PRECURSOR >gi\_2117431\_pir\_\_S58209

plastocyanin a precursor - black poplar

>gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus

nigra]

```
Seq. No.
Seq. ID
                  LIB3120-054-P1-K1-G3
                  BLASTN
Method
                  g18511
NCBI GI
                  335
BLAST score
                  0.0e + 00
E value
Match length
                  375
                   97
% identity
NCBI Description G.hirsutum light regulated unknown reading frame DNA
                   208479
Seq. No.
                  LIB3120-054-P1-K1-G4
Seq. ID
Method
                  BLASTX
                   q421826
NCBI GI
                   329
BLAST score
                   1.0e-30
E value
                   103
Match length
                   62
% identity
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                   >gi 298036 emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
                   208480
Seq. No.
                   LIB3120-054-P1-K1-G8
Seq. ID
                   BLASTX
Method
                   q100616
NCBI GI
                   235
BLAST score
                   3.0e-20
E value
                   64
Match length
                   67
% identity
                   ribulose-bisphosphate carboxylase activase B precursor -
NCBI Description
                   barley >gi 167093 (M55448) ribulose 1,5-bisphosphate
                   carboxylase activase [Hordeum vulgare] >gi_167095 (M55449)
                   ribulose 1,5-bisphosphate carboxylase activase [Hordeum
                   vulgare]
Seq. No.
                   208481
Seq. ID
                   LIB3120-054-P1-K1-H1
Method
                   BLASTX
                   q515616
NCBI GI
                   423
BLAST score
E value
                   3.0e-50
Match length
                   119
                   79
```

% identity

(X61608) LHC II Type III chlorophyll a /b binding protein NCBI Description

[Brassica napus]

208482 Seq. No.

LIB3120-054-P1-K1-H11 Seq. ID

BLASTX Method g3869088 NCBI GI BLAST score 384 2.0e-37 E value Match length 79 % identity 92

(AB019427) elongation factor-1 alpha [Nicotiana paniculata] NCBI Description

Seq. ID

Method

NCBI GI



```
208483
Seq. No.
Seq. ID
                  LIB3120-054-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g100196
BLAST score
                   645
                  1.0e-67
E value
                  142
Match length
% identity
                  84
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
                  208484
Seq. No.
Seq. ID
                  LIB3120-054-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g289919
BLAST score
                  105
E value
                  2.0e-52
Match length
                  129
                  95
% identity
NCBI Description
                  Gossypium hirsutum chloroplast photosystem II chlorophyll
                  A/B-binding protein gene, complete cds
                  208485
Seq. No.
Seq. ID
                  LIB3120-054-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  470
                  3.0e-47
E value
Match length
                  110
% identity
                  82
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  208486
Seq. ID
                  LIB3120-054-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3860250
BLAST score
                  160
                  1.0e-11
E value
Match length
                  66
% identity
                  64
NCBI Description
                   (AC005824) putative chloroplast prephenate dehydratase
                  [Arabidopsis thaliana]
                  208487
Seq. No.
Seq. ID
                  LIB3120-055-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3641340
BLAST score
                  205
E value
                  2.0e-16
Match length
                  93
% identity
                  45
                  (AF090329) cyclohexanone monooxygenase homolog [Pseudomonas
NCBI Description
                  fluorescens]
Seq. No.
                  208488
```

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LIB3120-056-Q1-K1-C4

BLASTX

g2909483



```
BLAST score 424
E value 7.0e-42
Match length 119
% identity 63
NCRI Description (AL0219
```

NCBI Description (AL021930) hypothetical protein Rv0294 [Mycobacterium tuberculosis]

Seq. No. 208489

Seq. ID LIB3120-060-Q1-K1-A1

Method BLASTX
NCBI GI g3334441
BLAST score 172
E value 3.0e-12
Match length 128
% identity 23

NCBI Description HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II >qi 2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 208490

BLAST score 643 E value 2.0e-67 Match length 140 % identity 89

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi\_481942\_pir\_\_S40212 glycine

hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei

>gi\_437995\_emb\_CAA81078\_ (Z25859) glycine
hydroxymethyltransferase [Flaveria pringlei]

Seq. No. 208491

Seq. ID LIB3120-060-Q1-K1-A12

Method BLASTX
NCBI GI g2494275
BLAST score 267
E value 2.0e-23
Match length 75
% identity 63

NCBI Description ELONGATION FACTOR P (EF-P) >gi\_1399829 (U59235) elongation

factor P [Synechococcus PCC7942]

Seq. No. 208492

Seq. ID LIB3120-060-Q1-K1-A2

Method BLASTX
NCBI GI g3738328
BLAST score 629
E value 8.0e-66
Match length 148
% identity 79

% identity 79
NCBI Description (AC005170) putative serine carboxypeptidase [Arabidopsis

thaliana]

Seq. No. 208493



```
LIB3120-060-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  q3287696
NCBI GI
BLAST score
                  547
E value
                  3.0e-56
Match length
                  121
% identity
                  (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
                  transferase gb D86180 from Pisum sativum. This ORF may be
                  part of a larger gene that lies in the overlapping region.
                  [Arabidopsis thaliana]
                  208494
Seq. No.
Seq. ID
                  LIB3120-060-Q1-K1-A4
                  BLASTX
Method
NCBI GI
                  g3913651
BLAST score
                  247
E value
                  2.0e-21
                  85
Match length
                   61
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi_2225993 emb_CAA74359 (Y14032)
                 ferredoxin--NADP(+) reductase [Nicotiana tabacum]
                   208495
Seq. No.
                  LIB3120-060-Q1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2459420
                   716
BLAST score
                   5.0e-76
E value
                   140
Match length
% identity
                   (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                   thaliana]
                   208496
Seq. No.
                   LIB3120-060-Q1-K1-A6
Seq. ID
Method
                   BLASTN
                   g12144
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
Match length
                   52
% identity
                   92
                   Pea chloroplast genes for F(O)-ATP synthase subunits a and
NCBI Description
                   c (partial)
                   208497
Seq. No.
Seq. ID
                   LIB3120-060-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g4567302
BLAST score
                   348
```

7.0e-33 E value Match length 142 % identity 59

(AC005956) unknown protein [Arabidopsis thaliana] NCBI Description

208498 Seq. No.



LIB3120-060-Q1-K1-A8 Seq. ID

BLASTX Method g100675 NCBI GI 703 BLAST score 2.0e-74 E value 144 Match length 92 % identity

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) NCBI Description

precursor - rice >gi 169759 (J04960) ADP-glucose

pyrophosphorylase 51kD subunit (EC 2.7.7.27) [Oryza sativa]

208499 Seq. No.

LIB3120-060-Q1-K1-B10 Seq. ID

BLASTX Method NCBI GI g4008441 239 BLAST score 4.0e-20 E value 87 Match length 56 % identity

(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 NCBI Description

comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

208500 Seq. No.

LIB3120-060-Q1-K1-B12 Seq. ID

BLASTX Method NCBI GI g1352821 756 BLAST score 1.0e-80 E value 147 Match length 94 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb\_CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208501

LIB3120-060-Q1-K1-B2 Seq. ID

Method BLASTX NCBI GI g3023436 BLAST score 515 2.0e-52 E value Match length 106 93 % identity

CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA NCBI Description

3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi\_857578 (U27116) caffeoyl-CoA 3-O-methyltransferase [Populus

tremuloides]

208502 Seq. No.

LIB3120-060-Q1-K1-B3 Seq. ID

Method BLASTX NCBI GI g1354515 BLAST score 229 E value 6.0e-19

Match length

NCBI Description

% identity

141 99



```
Match length
                  48
% identity
                  (U55837) carbonic anhydrase [Populus tremula x Populus
NCBI Description
                  tremuloides]
                  208503
Seq. No.
                  LIB3120-060-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                  g100200
NCBI GI
                  438
BLAST score
                  2.0e-43
E value
                  118
Match length
                  73
% identity
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
                  208504
Seq. No.
                  LIB3120-060-Q1-K1-B5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2062705
                  36
BLAST score
                  1.0e-10
E value
                  53
Match length
                  41
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  208505
Seq. No.
                  LIB3120-060-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  q2581785
NCBI GI
BLAST score
                  470
                  3.0e-47
E value
                  120
Match length
                  75
% identity
                  (U94999) class 2 non-symbiotic hemoglobin [Arabidopsis
NCBI Description
                  thaliana]
                  208506
Seq. No.
                  LIB3120-060-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3695061
                   304
BLAST score
                  8.0e-28
E value
Match length
                  94
                   63
% identity
                  (AF064788) rac GTPase activating protein 2 [Lotus
NCBI Description
                  japonicus]
                   208507
Seq. No.
Seq. ID
                  LIB3120-060-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                   q1352821
BLAST score
                   758
E value
                   6.0e-81
```

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RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581\_pir\_\_RKCNSU

NCBI Description



ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208508 LIB3120-060-Q1-K1-B9 Seq. ID Method BLASTX NCBI GI q4091806 BLAST score 391 E value 7.0e-38 Match length 99 70 % identity NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica] Seq. No. 208509 LIB3120-060-Q1-K1-C1 Seq. ID Method BLASTX NCBI GI g2129538 BLAST score 295 E value 8.0e-27 62 Match length 89 % identity NCBI Description AT103 protein - Arabidopsis thaliana >gi\_1033195 (U38232) AT103 [Arabidopsis thaliana] Seq. No. 208510 Seq. ID LIB3120-060-Q1-K1-C10 Method BLASTX NCBI GI g3947735 BLAST score 187 E value 5.0e-14Match length 72 % identity 56 NCBI Description (AJ009720) NL27 [Solanum tuberosum] 208511 Seq. No. Seq. ID LIB3120-060-Q1-K1-C12 Method BLASTX NCBI GI q1174162 BLAST score 593 E value 1.0e-61 Match length 119 % identity 88 NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi 3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana] Seq. No. 208512 Seq. ID LIB3120-060-Q1-K1-C2 Method BLASTX NCBI GI q1709825 370 BLAST score 2.0e-35 E value Match length 129 % identity 67

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PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]



```
Seq. No.
                  208513
Seq. ID
                  LIB3120-060-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  400
E value
                  6.0e-39
Match length
                  113
% identity
                  74
NCBI Description
                 (AF126870) rubisco activase [Vigna radiata]
                  208514
Seq. No.
                  LIB3120-060-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g119150
NCBI GI
BLAST score
                  619
E value
                  9.0e-65
Match length
                  120
% identity
                  96
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi 82081 pir S10507 translation elongation factor eEF-1
                  alpha chain - tomato > gi 19273 emb CAA32618 (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha
                  [Lycopersicon esculentum]
Seq. No.
                  208515
Seq. ID
                  LIB3120-060-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g121689
BLAST score
                  409
                  5.0e-40
E value
                  111
Match length
% identity
                  62
NCBI Description
                  GAST1 PROTEIN PRECURSOR >gi 100217 pir S22151 GAST1
                  protein - tomato >gi 19247 emb CAA44807 (X63093) gast1
                  [Lycopersicon esculentum]
Seq. No.
                  208516
Seq. ID
                  LIB3120-060-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  422
E value
                  1.0e-41
Match length
                  104
% identity
                  82
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208517

Seq. ID LIB3120-060-Q1-K1-D1

Method BLASTX NCBI GI g2827661 BLAST score 357

```
E value
Match length
% identity
                  59
                  (AL021637) hyuC-like protein [Arabidopsis thaliana]
NCBI Description
                  208518
Seq. No.
Seq. ID
                  LIB3120-060-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1814403
                  529
BLAST score
E value
                  4.0e-54
Match length
                  142
% identity
                  74
                  (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                  crystallinum]
                  208519
Seq. No.
Seq. ID
                  LIB3120-060-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2754816
BLAST score
                  145
E value
                  4.0e-09
Match length
                  141
% identity
                  33
                  (AF021346) non-race specific disease resistance protein
NCBI Description
                  [Arabidopsis thaliana]
                  208520
Seq. No.
Seq. ID
                  LIB3120-060-Q1-K1-D2
                  BLASTX
Method
                  q1657948
NCBI GI
BLAST score
                  639
                  6.0e-67
E value
Match length
                  148
% identity
                  82
NCBI Description
                  (U73466) MipC [Mesembryanthemum crystallinum]
```

Seq. No. 208521 Seq. ID LIB3120-060-Q1-K1-D3 Method BLASTX NCBI GI q3660471 BLAST score 523 E value 2.0e-53

Match length 124 % identity 77

(AJ001809) succinate dehydrogenase flavoprotein alpha NCBI Description

subunit [Arabidopsis thaliana]

Seq. No. 208522

Seq. ID LIB3120-060-Q1-K1-D5

Method BLASTX NCBI GI g487046 BLAST score 372 E value 1.0e-35 Match length 133 % identity 60

NCBI Description photosystem I chain II precursor - wood tobacco



208523

```
>gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
[Nicotiana sylvestris]
```

Seq. ID LIB3120-060-Q1-K1-D6
Method BLASTX
NCBI GI g2129910
BLAST score 429
E value 2.0e-42
Match length 133
% identity 59

NCBI Description cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - cider tree

>gi\_971397\_emb\_CAA53211\_ (X75480) cinnamyl-alcohol

dehydrogenase [Eucalyptus gunnii]

Seq. No. 208524

Seq. No.

Seq. ID LIB3120-060-Q1-K1-D9

Method BLASTX
NCBI GI g3269292
BLAST score 164
E value 3.0e-11
Match length 50
% identity 56

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 208525

Seq. ID LIB3120-060-Q1-K1-E11

Method BLASTX
NCBI GI g1709825
BLAST score 443
E value 5.0e-44
Match length 143
% identity 69

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi\_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No. 208526

Seq. ID LIB3120-060-Q1-K1-E12

Method BLASTX
NCBI GI g1001355
BLAST score 252
E value 1.0e-21
Match length 135
% identity 39

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 208527

Seq. ID LIB3120-060-Q1-K1-E4

Method BLASTX
NCBI GI g131385
BLAST score 606
E value 4.0e-63
Match length 144
% identity 85

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)



208528 Seq. No. LIB3120-060-Q1-K1-E7 Seq. ID Method BLASTX g3915699 NCBI GI BLAST score 602 1.0e-62 E value Match length 135 % identity 84 AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T NCBI Description PROTEIN) >gi\_541970\_pir\_\_S40260 T-protein - garden pea >gi\_1362061\_pir\_\_S56661\_glycine\_decarboxylase T protein precursor - garden pea >gi\_438217\_emb\_CAA81080\_ (Z25861) T-protein [Pisum sativum] >gi\_3021553\_emb\_CAA10976\_ (AJ222771) T protein [Pisum sativum] 208529 Seq. No. Seq. ID LIB3120-060-Q1-K1-F11 Method BLASTX NCBI GI q2864617 BLAST score 315 5.0e-29 E value 108 Match length % identity 60 (AL021811) H+-transporting ATP synthase chain9 - like NCBI Description protein [Arabidopsis thaliana] Seq. No. 208530 LIB3120-060-Q1-K1-F2 Seq. ID Method BLASTX NCBI GI g1352821 BLAST score 500 1.0e-50 E value 105 Match length 90 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] 208531 Seq. No. LIB3120-060-Q1-K1-F3 Seq. ID BLASTX Method g430947 NCBI GI BLAST score 318 1.0e-29 E value Match length 96 71 % identity (U01103) PSI type III chlorophyll a/b-binding protein NCBI Description [Arabidopsis thaliana]

Seq. No. 208532

Seq. ID LIB3120-060-Q1-K1-F6

Method BLASTX NCBI GI g115833 BLAST score 562



E value 6.0e-58
Match length 138
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR

(CAB-10A) (LHCP) >gi\_100195\_pir\_\_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi\_170394 (M32605)

a-binding protein [Lycopersicon esculentum]

Seq. No. 208533

Seq. ID LIB3120-060-Q1-K1-F7

Method BLASTX
NCBI GI g1352821
BLAST score 636
E value 1.0e-66
Match length 120
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208534

Seq. ID LIB3120-060-Q1-K1-G1

Method BLASTX
NCBI GI g625547
BLAST score 569
E value 9.0e-59
Match length 141
% identity 78

NCBI Description chlorophyll a/b-binding protein type I - common tobacco

>qi 493723 emb CAA45523 (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

Seq. No. 208535

Seq. ID LIB3120-060-Q1-K1-G10

Method BLASTX
NCBI GI g1352821
BLAST score 509
E value 3.0e-57
Match length 122
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 208536

Seq. ID LIB3120-060-Q1-K1-G12

Method BLASTX
NCBI GI g4033838
BLAST score 142
E value 9.0e-09
Match length 76
% identity 46



```
NCBI Description (Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No. 208537
Seq. ID LIB3120-060-Q1-K1-G3
```

Method BLASTX
NCBI GI g4249391
BLAST score 233
E value 1.0e-19
Match length 63
% identity 67

NCBI Description (AC005966) Similar to gi\_3249076 T13D8.16 beta glucosidase

from Arabidopsis thaliana BAC gb\_AC004473. [Arabidopsis

thaliana]

Seq. No. 208538

Seq. ID LIB3120-060-Q1-K1-G6

Method BLASTX
NCBI GI g2129538
BLAST score 421
E value 2.0e-41
Match length 87
% identity 91

NCBI Description AT103 protein - Arabidopsis thaliana >gi\_1033195 (U38232)

AT103 [Arabidopsis thaliana]

Seq. No. 208539

Seq. ID LIB3120-060-Q1-K1-G8

Method PLASTX
NCBI GI g2827002
BLAST score 261
E value 7.0e-23
Match length 100
% identity 61

NCBI Description (AF005993) HSP70 [Triticum aestivum]

Seq. No. 208540

Seq. ID LIB3120-060-Q1-K1-H1

Method BLASTX
NCBI GI g3914605
BLAST score 567
E value 1.0e-58
Match length 123
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE

PRECURSOR (RUBISCO ACTIVASE) >gi\_541930\_pir\_\_S39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi\_415852\_emb\_CAA79857 (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 208541

Seq. ID LIB3120-060-Q1-K1-H10

Method BLASTX
NCBI GI g452341
BLAST score 201
E value 8.0e-28
Match length 72



% identity NCBI Description (X68682) type II light-harvesting chlorophyll a /b-binding protein [Zea mays] 208542 Seq. No. LIB3120-060-Q1-K1-H3 Seq. ID Method BLASTX NCBI GI g2326947 BLAST score 124 8.0e-15 E value Match length 92 % identity 58 NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays] 208543 Seq. No. LIB3120-060-Q1-K1-H4 Seq. ID Method BLASTX NCBI GI g231688 BLAST score 544 E value 5.0e-56 Match length 108 % identity 95 CATALASE ISOZYME 2 >gi\_99599\_pir\_\_S17493 catalase (EC NCBI Description 1.11.1.6) - upland cotton >gi\_18488\_emb\_CAA39998\_subunit 2 of cotton catalase [Gossypium hirsutum] 208544 Seq. No. Seq. ID LIB3120-060-Q1-K1-H5 Method BLASTX NCBI GI g1351279 179 BLAST score 1.0e-13 E value Match length 63 % identity 68 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 602590 emb CAA58230 (X83227) triosephosphate isomerase [Petunia x hybrida] Seq. No. 208545 LIB3135-002-Q1-K1-A1 Seq. ID Method BLASTX NCBI GI g113029 BLAST score 569 E value 5.0e-59 Match length 107 % identity 99 ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) NCBI Description >gi\_68209\_pir\_\_WZCNIU isocitrate lyase (EC 4.1.3.1) upland cotton >gi\_18486\_emb\_CAA36381\_ (X52136) isocitrate lyase (AA 1-576) [Gossypium hirsutum]

Seq. No. 208546

Seq. ID LIB3135-002-Q1-K1-A10

Method BLASTX NCBI GI g1170747 BLAST score 455



E value 2.0e-45
Match length 105
% identity 85
NCBI Description LATE EM

n LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345 (M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 208547

Seq. ID LIB3135-002-Q1-K1-A2

Method BLASTX
NCBI GI g136640
BLAST score 422
E value 8.0e-42
Match length 79
% identity 97

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

Seq. No. 208548

Seq. ID LIB3135-002-Q1-K1-A6

Method BLASTX
NCBI GI g3885327
BLAST score 152
E value 5.0e-10
Match length 50
% identity 64

NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208549

Seq. ID LIB3135-002-Q1-K1-A9

Method BLASTX
NCBI GI g2980795
BLAST score 522
E value 3.0e-53
Match length 115
% identity 89

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 208550

Seq. ID LIB3135-002-Q1-K1-B1

Method BLASTX
NCBI GI g3080423
BLAST score 298
E value 4.0e-27
Match length 113
% identity 52

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 208551

Seq. ID LIB3135-002-Q1-K1-B11

Method BLASTX
NCBI GI g1709761
BLAST score 539
E value 2.0e-55
Match length 121



% identity PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE NCBI Description COMPLEX 27 KD SUBUNIT) > gi 1262146 emb CAA65660 (X96974) proteasome subunit [Spinacia oleracea] 208552 Seq. No. Seq. ID LIB3135-002-Q1-K1-B12 Method BLASTX q120668 NCBI GI 359 BLAST score E value 3.0e-34 Match length 75 % identity 91 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi\_82399\_pir\_\_A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi 167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi 225347\_prf\_ dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var. distichum] 208553 Seq. No. Seq. ID LIB3135-002-Q1-K1-B3 Method BLASTX q2252854 NCBI GI 173 BLAST score 2.0e-12 E value Match length 66 % identity 56 (AF013294) similar to auxin-induced protein [Arabidopsis NCBI Description thaliana] Seq. No. 208554 Seq. ID LIB3135-002-Q1-K1-B4 Method BLASTX g2244763 NCBI GI 277 BLAST score 6.0e-25 E value Match length 88 % identity 60 (Z97335) A6 anther-specific protein [Arabidopsis thaliana] NCBI Description 208555 Seq. No. Seq. ID LIB3135-002-Q1-K1-B7 Method BLASTX q1854386 NCBI GI BLAST score 504 3.0e-51 E value 121 Match length

79 % identity

(AB001375) similar to soluble NSF attachment protein [Vitis NCBI Description

vinifera]

208556 Seq. No.

Seq. ID LIB3135-002-Q1-K1-B8

Method BLASTX NCBI GI g2702281



```
BLAST score
E value
                  4.0e-25
                  67
Match length
                  73
% identity
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                  208557
Seq. No.
                  LIB3135-002-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131772
BLAST score
                  179
                  2.0e-13
E value
Match length
                  100
% identity
                  45
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  208558
Seq. No.
Seq. ID
                  LIB3135-002-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g129808
BLAST score
                  247
E value
                  4.0e-21
Match length
                  108
                  77
% identity
                  CATIONIC PEROXIDASE 2 PRECURSOR >gi_99873_pir_B38265
NCBI Description
                  peroxidase (EC 1.11.1.7) precursor, cationic (clone PNC2) -
                  peanut >gi_166475 (M37637) cationic peroxidase [Arachis
                  hypogaea]
                  208559
Seq. No.
Seq. ID
                  LIB3135-002-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1173218
BLAST score
                  605
                  5.0e-63
E value
Match length
                  121
% identity
                  97
                  40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >qi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  208560
Seq. ID
                  LIB3135-002-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1651828
BLAST score
                  328
E value
                  2.0e-30
Match length
                  108
% identity
                  60
                  (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]
NCBI Description
```

Seq. No. 208561

Seq. ID LIB3135-002-Q1-K1-C6

Method BLASTX



```
NCBI GI
                  q2982266
BLAST score
                  449
E value
                  1.0e-44
                  101
Match length
% identity
                  85
NCBI Description
                  (AF051216) probable fibrillarin [Picea mariana]
                  208562
Seq. No.
Seq. ID
                  LIB3135-002-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1931647
BLAST score
                  390
E value
                  4.0e-38
Match length
                  95
                  77
% identity
                  (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  208563
Seq. ID
                  LIB3135-002-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3413424
BLAST score
                  256
E value
                  5.0e-22
Match length
                  148
% identity
                  41
NCBI Description
                  (AJ006309) hypothetical protein [Arabidopsis thaliana]
                  208564
Seq. No.
Seq. ID
                  LIB3135-002-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2935450
BLAST score
                  445
                  3.0e-44
E value
Match length
                  91
% identity
                  99
NCBI Description (AF048824) histone H2B [Malus domestica]
Seq. No.
                  208565
Seq. ID
                  LIB3135-002-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2213626
BLAST score
                  341
E value
                  4.0e-32
Match length
                  126
                  49
% identity
NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana]
Seq. No.
                  208566
Seq. ID
                  LIB3135-002-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g322750
BLAST score
                  516
                  9.0e-53
E value
Match length
                  102
% identity
                  100
```

NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco



```
>gi_170217 (M74100) ubiquitin fusion protein [Nicotiana
sylvestris]
```

Seq. No. 208567

Seq. ID LIB3135-002-Q1-K1-D4

Method BLASTN
NCBI GI g2244788
BLAST score 48
E value 5.0e-18

Match length 80 % identity 90

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 208568

Seq. ID LIB3135-002-Q1-K1-D6

Method BLASTN
NCBI GI g2564048
BLAST score 35
E value 3.0e-10
Match length 236

% identity 61

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKD15, complete sequence [Arabidopsis thaliana]

Seq. No. 208569

Seq. ID LIB3135-002-Q1-K1-E1

Method BLASTX
NCBI GI g2827536
BLAST score 180
E value 1.0e-13
Match length 140
% identity 37

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208570

Seq. ID LIB3135-002-Q1-K1-E10

Method BLASTX
NCBI GI g2947060
BLAST score 706
E value 8.0e-75
Match length 149
% identity 90

NCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No. 208571

Seq. ID LIB3135-002-Q1-K1-E12

Method BLASTX 92935300 BLAST score 734 E value 4.0e-78 Match length 152 % identity 95

NCBI Description (AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase

2 [Gossypium hirsutum]

Seq. No. 208572

Seq. No. Seq. ID

Method



```
LIB3135-002-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3805845
                  541
BLAST score
E value
                  1.0e-55
                  124
Match length
                  81
% identity
                 (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                  208573
Seq. No.
                  LIB3135-002-Q1-K1-E5
Seq. ID
Method
                  BLASTN
                  q2829205
NCBI GI
                  159
BLAST score
                  4.0e-84
E value
                  382
Match length
                  17
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  208574
Seq. No.
Seq. ID
                  LIB3135-002-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2935298
BLAST score
                  411
                  1.0e-40
E value
                  89
Match length
                  91
% identity
                  (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                  1 [Gossypium hirsutum]
Seq. No.
                  208575
Seq. ID
                  LIB3135-002-Q1-K1-E7
                  BLASTX
Method
                  g1350720
NCBI GI
                  402
BLAST score
                  2.0e-39
E value
                  99
Match length
                  76
% identity
                  60S RIBOSOMAL PROTEIN L32
NCBI Description
                  208576
Seq. No.
Seq. ID
                  LIB3135-002-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g586339
BLAST score
                  346
                  1.0e-32
E value
Match length
                  111
                  57
% identity
                  PEROXISOMAL-COENZYME A SYNTHETASE >gi 626794 pir S46098
NCBI Description
                  probable AMP-binding protein - yeast (Saccharomyces
                  cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c
                  [Saccharomyces cerevisiae]
                  208577
```

28744

LIB3135-002-Q1-K1-F1

BLASTX

Match length

% identity

56

84



```
NCBI GI
                    g3413700
· BLAST score
                    337
                    9.0e-32
 E value
 Match length
                    125
                    58
 % identity
 NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]
                    208578
 Seq. No.
 Seq. ID
                    LIB3135-002-Q1-K1-F11
 Method
                    BLASTX
                    g629858
 NCBI GI
                    532
 BLAST score
                    2.0e-54
 E value
                    119
 Match length
 % identity
                    85
 NCBI Description protein kinase C inhibitor - maize
                    208579
 Seq. No.
 Seq. ID
                    LIB3135-002-Q1-K1-F3
                    BLASTX
 Method
 NCBI GI
                    g310570
 BLAST score
                    362
                    1.0e-34
 E value
 Match length
                    79
                    86
 % identity
                    (L20806) a Lea protein with hydrophobic domain, high pI
 NCBI Description
                    value (11.6); 15kD protein; putative [Glycine max]
                    208580
 Seq. No.
 Seq. ID
                    LIB3135-002-Q1-K1-F5
                    BLASTX
 Method
 NCBI GI
                    g3021357
 BLAST score
                    554
                    2.0e-62
 E value
                    143
 Match length
                    75
 % identity
                    (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
 NCBI Description
                    tetragonoloba]
 Seq. No.
                    208581
 Seq. ID
                    LIB3135-002-Q1-K1-F6
 Method
                    BLASTX
 NCBI GI
                    q3334665
                    152
 BLAST score
                    4.0e-10
 E value
                    89
 Match length
 % identity
                   (Y10492) putative cytochrome P450 [Glycine max]
 NCBI Description
                    208582
 Seq. No.
                    LIB3135-002-Q1-K1-F7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3236242
 BLAST score
                    229
 E value
                    6.0e-19
```

```
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 208583
Seq. ID LIB3135-002-Q1-K1-F8
Method BLASTX
```

NCBI GI g2911059 BLAST score 314 E value 5.0e-29 Match length 70 % identity 76

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

 Seq. No.
 208584

 Seq. ID
 LIB3135-002-Q1-K1-G1

 Method
 BLASTX

 NCBI GI
 g1350720

 BLAST score
 338

E value 6.0e-32 Match length 86 % identity 74

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 208585

Seq. ID LIB3135-002-Q1-K1-G11

Method BLASTN
NCBI GI g11802
BLAST score 291
E value 1.0e-163
Match length 315
% identity 98

NCBI Description Tobacco chloropast DNA homologous to ribosomal protein S12

gene

Seq. No. 208586

Seq. ID LIB3135-002-Q1-K1-G4

Method BLASTX
NCBI GI 94105798
BLAST score 475
E value 8.0e-48
Match length 136
% identity 53

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 208587

Seq. ID LIB3135-002-Q1-K1-H11

Method BLASTX
NCBI GI g3341695
BLAST score 461
E value 4.0e-46
Match length 120
% identity 71

NCBI Description (AC003672) putative thiamin pyrophosphokinase [Arabidopsis

thaliana]

Seq. No. 208588

Seq. ID LIB3135-002-Q1-K1-H5

```
BLASTX
Method
NCBI GI
                  g1743354
BLAST score
                  370
                  2.0e-35
E value
Match length
                  115
% identity
                  55
NCBI Description
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
                  208589
Seq. No.
                  LIB3135-002-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417148
BLAST score
                  257
                  2.0e-22
E value
Match length
                  108
% identity
                  46
                  PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
NCBI Description
                   (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                  soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.
                  208590
                  LIB3135-003-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136739
BLAST score
                  373
E value
                  9.0e-36
Match length
                  82
```

% identity 85
NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi\_67061\_pir\_\_XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi\_218001\_dbj\_BAA00570\_ (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 208591

Seq. ID LIB3135-003-Q1-K1-A10

Method BLASTX
NCBI GI g2274915
BLAST score 183
E value 1.0e-13
Match length 55
% identity 64

NCBI Description (AJ000081) beta-1,3-glucanase [Citrus sinensis]

Seq. No. 208592

Seq. ID LIB3135-003-Q1-K1-A11

Method BLASTX
NCBI GI g1814403
BLAST score 637
E value 1.0e-66
Match length 153
% identity 81

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 208593

Seq. ID LIB3135-003-Q1-K1-A3

```
Method
NCBI GI
                  q4455326
BLAST score
                  309
                  2.0e-28
E value
Match length
                  99
                  59
% identity
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
                  208594
Seq. No.
Seq. ID
                  LIB3135-003-Q1-K1-A4
Method
                  BLASTX
                  g3860315
NCBI GI
BLAST score
                  252
                  9.0e-22
E value
Match length
                  60
                  78
% identity
NCBI Description
                  (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
Seq. No.
                  208595
Seq. ID
                  LIB3135-003-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q1296816
BLAST score
                  576
E value
                  1.0e-59
Match length
                  132
                  85
% identity
NCBI Description
                  (X94995) naringenin-chalcone synthase [Juglans sp.]
Seq. No.
                  208596
Seq. ID
                  LIB3135-003-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q478389
BLAST score
                  363
                  1.0e-34
E value
                  109
Match length
% identity
                  61
NCBI Description
                  peroxidase (EC 1.11.1.7) precursor, anionic - Japanese
                  aspen x large-toothed aspen >gi 217997 dbj BAA01877
                  (D11102) peroxidase [Populus kitakamiensis]
                  >gi_444801_prf__1908234A anionic peroxidase [Populus
                  kitakamiensis]
Seq. No.
                  208597
Seq. ID
                  LIB3135-003-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q1086833
BLAST score
                  298
E value
                  6.0e-27
Match length
                  118
% identity
                  48
NCBI Description
                  (U41264) coded for by C. elegans cDNA CEESN26F; coded for
                  by C. elegans cDNA CEESI89F; similar to 60S acidic
```

ribosomal protein Po (L10) [Caenorhabditis elegans]

208598 Seq. No.

Seq. ID LIB3135-003-Q1-K1-B12

Method BLASTX

```
NCBI GI
BLAST score
                   295
                   1.0e-26
E value
                   116
Match length
                   52
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   208599
Seq. No.
                  LIB3135-003-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2832681
BLAST score
                   497
                   3.0e-50
E value
                   97
Match length
                   91
% identity
NCBI Description
                   (AL021712) putative protein [Arabidopsis thaliana]
                   208600
Seq. No.
Seq. ID
                   LIB3135-003-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g4262149
BLAST score
                   683
                   4.0e-72
E value
                   142
Match length
                   83
% identity
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
                   208601
Seq. No.
                   LIB3135-003-Q1-K1-B8
Seq. ID
                   {\tt BLASTX}
Method
NCBI GI
                   g1856971
BLAST score
                   594
                   8.0e-62
E value
                   127
Match length
                   89
% identity
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
                   208602
Seq. No.
                   LIB3135-003-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3201613
BLAST score
                   518
                   9.0e-53
E value
Match length
                   134
% identity
                   72
                  (AC004669) glutathione S-transferase [Arabidopsis thaliana]
NCBI Description
                   208603
Seq. No.
Seq. ID
                   LIB3135-003-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   q4539417
BLAST score
                   142
```

5.0e-09

28

E value Match length



% identity

(AL049171) putative protein [Arabidopsis thaliana] NCBI Description

208604 Seq. No.

Seq. ID LIB3135-003-Q1-K1-C7

BLASTX Method NCBI GI g1169009 BLAST score 353 E value 1.0e-65 Match length 143 81 % identity

CAFFEIC ACID 3-O-METHYLTRANSFERASE NCBI Description

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi 542009 pir S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi 437777 emb CAA52814 (X74814) 0-Methyltransferase

[Eucalyptus gunnii]

208605 Seq. No.

Seq. ID LIB3135-003-Q1-K1-C8

Method BLASTX NCBI GI g4567232 BLAST score 276 1.0e-24 E value 64 Match length 88 % identity

(AC007119) putative 40S ribosomal protein S25 [Arabidopsis NCBI Description

thaliana]

208606 Seq. No.

Seq. ID LIB3135-003-Q1-K1-D11

BLASTX Method NCBI GI g4454466 197 BLAST score 4.0e-15 E value 52 Match length

69 % identity

(AC006234) unknown protein [Arabidopsis thaliana] NCBI Description

208607 Seq. No.

LIB3135-003-Q1-K1-D4 Seq. ID

BLASTX Method NCBI GI g730129 BLAST score 269 1.0e-23 E value 53 Match length 91 % identity

NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) NCBI Description

>qi 3169310 (AF017641) nucleoside diphosphate kinase type 1

[Arabidopsis thaliana]

Seq. No. 208608

LIB3135-003-Q1-K1-D7 Seq. ID

Method BLASTX NCBI GI q1169009 BLAST score 327 E value 1.0e-59



```
Match length 144 % identity 76
```

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi\_542009\_pir\_S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi\_437777\_emb\_CAA52814\_ (X74814) 0-Methyltransferase

[Eucalyptus gunnii]

Seq. No. 208609

Seq. ID LIB3135-003-Q1-K1-E11

Method BLASTX
NCBI GI g4204695
BLAST score 393
E value 2.0e-38
Match length 109

% identity 77

NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase

At5P1 [Arabidopsis thaliana]

Seq. No. 208610

Seq. ID LIB3135-003-Q1-K1-E3

Method BLASTX
NCBI GI g585973
BLAST score 226
E value 3.0e-19
Match length 64
% identity 72

NCBI Description FRUCTOKINASE >gi\_626018\_pir\_\_S39997 fructokinase (EC 2.7.1.4) - potato >gi\_297015\_emb\_CAA78283\_ (Z12823)

fructokinase [Solanum tuberosum] >gi\_1095321\_prf\_\_2108342A

fructokinase [Solanum tuberosum]

Seq. No. 208611

Seq. ID LIB3135-003-Q1-K1-E8

Method BLASTX
NCBI GI g1346675
BLAST score 666
E value 4.0e-70
Match length 138
% identity 91

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)

>gi 499112 (U10283) nucleoside diphosphate kinase [Flaveria

bidentis]

Seq. No. 208612

Seq. ID LIB3135-003-Q1-K1-F1

Method BLASTX
NCBI GI g170076
BLAST score 506
E value 2.0e-51
Match length 110
% identity 58

NCBI Description (L01433) calmodulin [Glycine max] >gi\_1583770\_prf\_\_2121384D

calmodulin [Glycine max]

Seq. No. 208613

NCBI GI

BLAST score

q3915847

343



```
LIB3135-003-Q1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3393062
BLAST score
                  431
                  1.0e-42
E value
                  147
Match length
                  54
% identity
NCBI Description
                  (Y17386) putative In2.1 protein [Triticum aestivum]
                  208614
Seq. No.
Seq. ID
                  LIB3135-003-Q1-K1-F11
Method
                  BLASTX
                  g1370162
NCBI GI
BLAST score
                  587
                  5.0e-61
E value
Match length
                  115
% identity
                  97
                  (X97853) RAB1A [Lotus japonicus]
NCBI Description
                  208615
Seq. No.
Seq. ID
                  LIB3135-003-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3319882
                  745
BLAST score
                  2.0e-79
E value
                  150
Match length
% identity
                  96
NCBI Description
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
Seq. No.
                  208616
Seq. ID
                  LIB3135-003-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1076501
BLAST score
                  315
                  6.0e-29
E value
Match length
                  88
                  67
% identity
                  cell wall protein - alfalfa >gi 3818416 (AF028841)
NCBI Description
                  proline-rich cell wall protein [Medicago sativa]
                  208617
Seq. No.
Seq. ID
                  LIB3135-003-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1710078
BLAST score
                  570
                  7.0e-59
E value
Match length
                  142
                  72
% identity
                  RAB24 PROTEIN >gi 971280 dbj BAA09947 (D63917) RAB24
NCBI Description
                  protein [Oryza sativa]
                  208618
Seq. No.
Seq. ID
                  LIB3135-003-Q1-K1-F5
Method
                  BLASTX
```



2.0e-32 E value Match length 76 86 % identity NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana] Seq. No. 208619 Seq. ID LIB3135-003-Q1-K1-F6 Method BLASTX NCBI GI g625509 BLAST score 689 6.0e-73 E value Match length 140 28 % identity NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment) 208620 Seq. No. Seq. ID LIB3135-003-Q1-K1-F7 Method BLASTX NCBI GI g3914467 BLAST score 596 E value 5.0e-62 Match length 146 86 % identity 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) NCBI Description >gi 1864003 dbj BAA19252 (AB001422) 21D7 [Nicotiana tabacum] 208621 Seq. No. Seq. ID LIB3135-003-Q1-K1-G11 Method BLASTX NCBI GI g100351 BLAST score 522 3.0e-53 E value 122 Match length 79 % identity NCBI Description pathogenesis-related protein 4A - common tobacco >gi\_19962\_emb\_CAA41437 (X58546) pathogenesis-related protein 4A [Nicotiana tabacum] Seq. No. 208622 LIB3135-003-Q1-K1-G2 Seq. ID Method BLASTX NCBI GI g3779024 BLAST score 647 E value 7.0e-68 Match length 153

% identity 84

NCBI Description (AC005171) unknown protein [Arabidopsis thaliana]

Seq. No. 208623

Seq. ID LIB3135-003-Q1-K1-G3

Method BLASTX NCBI GI g629597 BLAST score 384 E value 4.0e-39 Match length 114

```
% identity
                  proline-rich protein - rape >gi 545029 bbs 142669 ($68113)
NCBI Description
                  proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                  Peptide, 147 aa] [Brassica napus]
Seq. No.
                  208624
Seq. ID
                  LIB3135-003-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1545805
BLAST score
                  161
E value
                  1.0e-11
Match length
                  101
                  48
% identity
                  (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
NCBI Description
Seq. No.
                  208625
Seq. ID
                  LIB3135-003-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g3319774
BLAST score
                  201
                  1.0e-15
E value
Match length
                  44
% identity
                  84
NCBI Description (Y16228) TOM7 protein [Solanum tuberosum]
                  208626
Seq. No.
                  LIB3135-003-Q1-K1-H2
                  BLASTX
                  g4150974
                  371
                  2.0e-35
                  95
```

Seq. ID

Method NCBI GI BLAST score E value Match length % identity 71

NCBI Description (AJ224331) cystatin [Castanea sativa]

208627 Seq. No.

Seq. ID LIB3135-003-Q1-K1-H4

Method BLASTX NCBI GI g4455194 BLAST score 311 E value 2.0e-28 Match length 70 % identity 83

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 208628

Seq. ID LIB3135-003-Q1-K1-H6

Method BLASTN NCBI GI q167366 BLAST score 148 E value 1.0e-77 Match length 252 % identity 91

NCBI Description Gossypium hirsutum peroxidase mRNA, complete cds

Seq. No. 208629

Seq. ID LIB3135-003-Q1-K1-H9



BLASTX Method NCBI GI g4056457 BLAST score 433 E value 8.0e-43Match length 127 % identity 63

(AC005990) ESTs gb 234051 and gb F13722 come from this NCBI Description

gene. [Arabidopsis thaliana]

Seq. No. 208630

Seq. ID LIB3135-004-Q1-K1-A1

Method BLASTN NCBI GI g16131 BLAST score 112 3.0e-56 E value Match length 119 % identity 98

Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with NCBI Description

18S rRNA fragment

Seq. No. 208631

Seq. ID LIB3135-004-Q1-K1-A11

Method BLASTN NCBI GI g1654276 BLAST score 143 E value 5.0e-75 Match length 159 97 % identity

Gossypium australe 5.8S ribosomal RNA gene and internal NCBI Description

transcribed spacer 1 and

Seq. No. 208632

Seq. ID LIB3135-004-Q1-K1-A4

Method BLASTX NCBI GI g1170606 BLAST score 574 E value 2.0e-59 Match length 141 79 % identity

NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)

> >gi\_629863\_pir\_\_S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi\_3114421\_pdb\_1ZAK\_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

>gi 3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize

In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

Seq. No. 208633

Seq. ID LIB3135-004-Q1-K1-A5

Method BLASTX NCBI GI g1706547 BLAST score 156 E value 7.0e-11 Match length 54 % identity 61

NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM





```
PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_2129912_pir__S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi_1184668 (U22147) beta-1,3-glucanase [Hevea brasiliensis]
```

```
208634
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                   q1107526
BLAST score
                   335
                   2.0e-31
E value
                   98
Match length
                   68
% identity
                  (X87931) SIEP1L protein [Beta vulgaris]
NCBI Description
                  208635
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                   g282994
BLAST score
                   613
                   5.0e-64
E value
                   132
Match length
                   81
% identity
                  Sip1 protein - barley >gi_167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
                   208636
Seq. No.
Seq. ID
                   LIB3135-004-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                   g3928543
                  Ī55
BLAST score
                   2.0e-10
E value
                   102
Match length
                   36
% identity
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   208637
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                   g3928086
BLAST score
                   232
E value
                   3.0e-19
Match length
                   93
% identity
                   53
NCBI Description
                  (AC005770) unknown protein [Arabidopsis thaliana]
```

Seq. No. 208638

Seq. ID LIB3135-004-Q1-K1-C3

Method BLASTX
NCBI GI g3201613
BLAST score 532
E value 2.0e-54
Match length 135
% identity 73

NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]



```
208639
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-C5
                  BLASTX
Method
NCBI GI
                  g2879811
                  343
BLAST score
                  2.0e-32
E value
                  84
Match length
                  70
% identity
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
Seq. No.
                  208640
                  LIB3135-004-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4559382
                  224
BLAST score
                  3.0e-18
E value
                  92
Match length
                  43
% identity
                  (AC006526) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  208641
Seq. ID
                  LIB3135-004-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3098571
BLAST score
                  203
E value
                  4.0e-16
Match length
                  96
                  43
% identity
                  (AF049028) BURP domain containing protein [Brassica napus]
NCBI Description
Seq. No.
                  208642
Seq. ID
                  LIB3135-004-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2911280
BLAST score
                  209
E value
                  1.0e-16
                  50
Match length
                  76
% identity
                  (U73937) PK12 protein kinase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  208643
Seq. ID
                  LIB3135-004-Q1-K1-D12
                  BLASTX
Method
                  g1076283
NCBI GI
BLAST score
                  315
                  4.0e-38
E value
                  116
Match length
                  73
% identity
                  adenylylsulfate kinase (EC 2.7.1.25) precursor -
NCBI Description
                  Arabidopsis thaliana >gi 414737 emb CAA53426 (X75782) APS
                  kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS
```

28757

kinase [Arabidopsis thaliana]

kinase [Arabidopsis thaliana] >gi\_1575322 (U59759) APS kinase [Arabidopsis thaliana] >gi\_3252812 (AC004705) APS



```
208644
Seq. No.
                  LIB3135-004-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  q3183088
NCBI GI
BLAST score
                  209
                  1.0e-16
E value
Match length
                  71
                  56
% identity
NCBI Description
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
                  (LTP) >gi_629658_pir_S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  208645
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g266690
BLAST score
                  345
E value
                  1.0e-32
Match length
                  99
% identity
                  72
                  OLEOSIN 18.2 KD >gi 167363 (L00935) 18.2 kDa oleosin
NCBI Description
                  [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin
                  _[Gossypium hirsutum]
Seq. No.
                  208646
Seq. ID
                  LIB3135-004-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3249099
BLAST score
                  470
E value
                  3.0e-47
                  137
Match length
                  68
% identity
NCBI Description
                  (AC003114) EST gb T21244 comes from this gene. [Arabidopsis
                  thaliana] >gi 4220616 dbj BAA74591 (AB021936)
                  nicotianamine synthase [Arabidopsis thaliana]
                  208647
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  q2997684
BLAST score
                  286
E value
                  1.0e-25
Match length
                  65
% identity
NCBI Description
                  (AF053302) putative transcriptional co-activator
                  [Arabidopsis thaliana]
Seq. No.
                  208648
                  LIB3135-004-Q1-K1-E6
```

Seq. ID Method BLASTN

NCBI GI g2264318 BLAST score 33 E value 5.0e-09 89 Match length 84 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

Seq. No.

208654



## MUP24, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  208649
                  LIB3135-004-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g559005
BLAST score
                  230
                  3.0e-19
E value
                  88
Match length
                  53
% identity
                  (U15933) ascorbate peroxidase [Nicotiana tabacum]
NCBI Description
                  208650
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-F1
Method
                  BLASTX
                  g4539660
NCBI GI
BLAST score
                  260
                  2.0e-22
E value
Match length
                  91
                  52
% identity
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
                  208651
Seq. No.
Seq. ID
                  LIB3135-004-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1351030
                  556
BLAST score
                  5.0e-57
E value
                  145
Match length
                  79
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
NCBI Description
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi 289365
                   (M35599) 60-kDa chaperonin-60 alpha-polypeptide precursor
                   [Brassica napus]
Seq. No.
                  208652
                  LIB3135-004-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4490705
                  398
BLAST score
E value
                  9.0e-44
Match length
                  110
% identity
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  208653
Seq. ID
                  LIB3135-004-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q2388575
BLAST score
                  170
E value
                  6.0e-12
Match length
                  75
                  48
% identity
NCBI Description
                  (AC000098) YUP8H12.18 [Arabidopsis thaliana]
```

```
Seq. ID
                   LIB3135-004-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                   g2213871
BLAST score
                   299
                   4.0e-27
E value
Match length
                   72
                   85
% identity
NCBI Description
                   (AF003126) poly(A)-binding protein [Mesembryanthemum
                  crystallinum]
Seq. No.
                  208655
Seq. ID
                  LIB3135-004-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                   q4220515
BLAST score
                  235
E value
                  1.0e-19
                   59
Match length
                  71
% identity
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  208656
Seq. ID
                  LIB3135-004-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2497752
BLAST score
                  294
E value
                  1.0e-26
Match length
                  96
% identity
                  59
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi_1321911_emb_CAA65475_ (X96714) lipid transfer protein
                   [Prunus dulcis]
Seq. No.
                  208657
Seq. ID
                  LIB3135-004-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1694621
BLAST score
                  352
E value
                  2.0e-33
Match length
                  75
% identity
                  88
NCBI Description
                  (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
Seq. No.
                  208658
Seq. ID
                  LIB3135-004-Q1-K1-G7
Method
                  BLASTX
                  g3924597
                  192
```

NCBI GI BLAST score E value 1.0e-14 Match length 86 % identity 47

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 208659

Seq. ID LIB3135-004-Q1-K1-H1

Method BLASTX NCBI GI g2342727 BLAST score 345

% identity

Seq. No.

NCBI Description

91

208665



```
2.0e-32
E value
Match length
                   89
% identity
                   71
NCBI Description
                   (AC002341) hypothetical protein [Arabidopsis thaliana]
                   208660
Seq. No.
Seq. ID
                   LIB3135-004-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                   g1743277
BLAST score
                   732
E value
                   8.0e-78
Match length
                   144
                   97
% identity
                  (Y09741) beta-tubulin 1 [Hordeum vulgare]
NCBI Description
                   208661
Seq. No.
Seq. ID
                   LIB3135-004-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                   g3157941
                   240
BLAST score
E value
                   4.0e-20
Match length
                   92
% identity
                   46
NCBI Description
                   (AC002131) Contains similarity to hypothetical protein
                   gb U95973 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   208662
Seq. ID
                   LIB3135-004-Q1-K1-H6
                   BLASTX
Method
NCBI GI
                   g2208944
BLAST score
                   362
E value
                   1.0e-39
                   114
Match length
                   74
% identity
NCBI Description
                  (Y11120) nodulin-35 homologue [Arabidopsis thaliana]
Seq. No.
                   208663
Seq. ID
                   LIB3135-005-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g3236248
BLAST score
                   457
E value
                   8.0e-46
Match length
                   117
% identity
                   75
NCBI Description
                  (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   208664
Seq. ID
                   LIB3135-005-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g3986110
BLAST score
                   467
E value
                   4.0e-47
Match length
                   102
```

28761

(AB012716) heat shock protein 70 cognate [Salix gilgiana]

```
LIB3135-005-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1854386
BLAST score
                  237
                  4.0e-20
E value
                   67
Match length
                   67
% identity
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                  vinifera]
Seq. No.
                  208666
Seq. ID
                  LIB3135-005-Q1-K1-A2
                  BLASTX
Method
                  q4335735
NCBI GI
BLAST score
                  349
E value
                   4.0e-33
Match length
                  123
                  58
```

% identity 58
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208667 LIB3135-005-Q1-K1-B10 Seq. ID Method BLASTX g2961352 NCBI GI BLAST score 427 4.0e-42 E value Match length 105 82 % identity

NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No. 208668

Seq. ID LIB3135-005-Q1-K1-B2

Method BLASTX
NCBI GI g1172811
BLAST score 375
E value 2.0e-36
Match length 76
% identity 91

NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)

>gi\_1076751\_pir\_\_S49575 ribosomal protein L10.e, cytosolic
- rice >gi\_575355\_emb\_CAA57339\_ (X81691) putative tumor

suppresser [Oryza satīva]

Seq. No. 208669

Seq. ID LIB3135-005-Q1-K1-B3

Method BLASTX
NCBI GI 94512698
BLAST score 261
E value 9.0e-23
Match length 127
% identity 43

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208670

Seq. ID LIB3135-005-Q1-K1-B5

Method BLASTX NCBI GI g3738320



BLAST score 7.0e-46E value Match length 116 % identity 75

(AC005170) putative cinnamoyl CoA reductase [Arabidopsis NCBI Description

208671 Seq. No.

LIB3135-005-Q1-K1-B6 Seq. ID

Method BLASTX NCBI GI g3738320 BLAST score 276 1.0e-24 E value Match length 109 55 % identity

(AC005170) putative cinnamoyl CoA reductase [Arabidopsis NCBI Description

thaliana]

Seq. No.

208672

Seq. ID LIB3135-005-Q1-K1-B7 Method BLASTX

NCBI GI q3913182 BLAST score 298 E value 4.0e-27 113 Match length 47 % identity

CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) NCBI Description

>gi\_2239258\_emb\_CAA74070\_ (Y13733) cinnamyl alcohol

dehydrogenase [Zea mays]

Seq. No. 208673

LIB3135-005-Q1-K1-B9 Seq. ID

Method BLASTX q465740 NCBI GI BLAST score 156 E value 2.0e-10 117 Match length % identity

HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III NCBI Description

> >qi 630513 pir S44609 hypothetical protein C02F5.7 -Caenorhabditis elegans >gi 289614 (L14745) homology with glucose induced repressor, GRR1; putative [Caenorhabditis

elegans]

208674 Seq. No.

Seq. ID LIB3135-005-Q1-K1-C2

Method BLASTX NCBI GI q1945611 BLAST score 266 2.0e-23 E value 129 Match length 43 % identity

(AB003103) 26S proteasome subunit p55 [Homo sapiens] NCBI Description

>gi 4506221\_ref\_NP\_002807.1\_pPSMD12\_ proteasome (prosome,

macropain) 26S subunit, non-ATPase,

208675 Seq. No.



```
LIB3135-005-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421104
BLAST score
                  360
E value
                  1.0e-58
Match length
                  139
% identity
                  (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  208676
Seq. ID
                  LIB3135-005-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q1881585
BLAST score
                  335
E value
                  2.0e-31
                  125
Match length
                  62
% identity
                  (U72489) remorin [Solanum tuberosum]
NCBI Description
                  208677
Seq. No.
Seq. ID
                  LIB3135-005-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q3377797
BLAST score
                  222
                  4.0e-18
E value
Match length
                  50
% identity
                  94
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                  208678
Seq. No.
Seq. ID
                  LIB3135-005-Q1-K1-C8
Method
                  {\tt BLASTX}
NCBI GI
                  g544242
BLAST score
                  389
E value
                  1.0e-37
Match length
                  121
                  69
% identity
NCBI Description
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                  >gi_485498_pir__S33533 heat shock protein 90 homolog
                  precursor - barley >gi 22652 emb CAA48143 (X67960) GRP94
                  homologue [Hordeum vulgare]
Seq. No.
                  208679
Seq. ID
                  LIB3135-005-Q1-K1-D11
Method
                  BLASTX
```

NCBI GI g2827528 BLAST score 493 E value 6.0e-50 133 Match length % identity 75

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

```
208680
Seq. No.
                  LIB3135-005-Q1-K1-D5
Seq. ID
                  BLASTX
NCBI GI
                  g1350984
BLAST score
                  133
```

9.0e-10

120

45 % identity 40S RIBOSOMAL PROTEIN S3A >gi 469248 (L31645) ribosomal NCBI Description

protein S3a [Helianthus annuus]

208681 Seq. No. Seq. ID LIB3135-005-Q1-K1-D7 Method BLASTX NCBI GI g3915826 BLAST score 404 1.0e-39

E value Match length 116 68 % identity

Method

E value Match length

NCBI Description 60S RIBOSOMAL PROTEIN L5

208682 Seq. No.

Seq. ID LIB3135-005-Q1-K1-E11

Method BLASTX NCBI GI q486784 BLAST score 337 E value 1.0e-31 97 Match length 25 % identity

NCBI Description Golgi-associated particle 102K chain - human

Seq. No. 208683

LIB3135-005-Q1-K1-E4 Seq. ID

Method BLASTX NCBI GI g3850571 BLAST score 329 E value 2.0e-35 Match length 83 95 % identity

(AC005278) Similar to gb U85207 snRNP core Sm protein NCBI Description

homolog Sm-X5 from Mus musculus. EST gb AA612141 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 208684

Seq. ID LIB3135-005-Q1-K1-E6

Method BLASTX NCBI GI g4539452 BLAST score 180 E value 2.0e-13 Match length 42 74 % identity

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 208685

LIB3135-005-Q1-K1-F11 Seq. ID

Method BLASTX

E value

Match length

% identity

2.0e-20

NCBI Description G.hirsutum metallothionein-like gene

90

90



```
NCBI GI
                   q2827528
BLAST score
                   487
                   3.0e-49
E value
Match length
                   139
                   72
% identity
NCBI Description
                  (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                   208686
Seq. ID
                  LIB3135-005-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                   g1076621
BLAST score
                   302
E value
                   2.0e-27
Match length
                   71
% identity
                   80
NCBI Description
                  cytochrome b5 - common tobacco >qi 296386 emb CAA50575
                   (X71441) cytochrome b5 [Nicotiana tabacum]
Seq. No.
                   208687
Seq. ID
                  LIB3135-005-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q542157
BLAST score
                   524
E value
                  2.0e-53
Match length
                  140
% identity
                   72
NCBI Description ribosomal 5S RNA-binding protein - Rice
                   208688
Seq. No.
Seq. ID
                  LIB3135-005-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2529683
BLAST score
                   503
E value
                   4.0e-51
Match length
                  136
% identity
                  71
NCBI Description
                  (AC002535) unknown protein [Arabidopsis thaliana]
Seq. No.
                  208689
Seq. ID
                  LIB3135-005-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2529683
BLAST score
                  164
E value
                  2.0e-11
Match length
                  50
% identity
                  64
NCBI Description
                  (AC002535) unknown protein [Arabidopsis thaliana]
                  208690
Seq. No.
Seq. ID
                  LIB3135-005-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                  g1418705
BLAST score
                  52
```



208691 Seq. No. Seq. ID LIB3135-005-Q1-K1-G10 Method BLASTX NCBI GI g3790587 BLAST score 212 6.0e-17 E value 92 Match length 55 % identity (AF079182) RING-H2 finger protein RHF2a [Arabidopsis NCBI Description thaliana] 208692 Seq. No. LIB3135-005-Q1-K1-G5 Seq. ID

Method BLASTX

NCBI GI g2267567 BLAST score 390 8.0e-38 E value Match length 85 % identity 89

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium

x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

Seq. No. 208693

Seq. ID LIB3135-005-Q1-K1-G7

Method BLASTX NCBI GI g2119043 BLAST score 294 1.0e-26 E value 70 Match length % identity 81

NCBI Description glycine-rich RNA-binding protein RGP-1c - wood tobacco

Seq. No. 208694

Seq. ID LIB3135-005-Q1-K1-G9

Method BLASTX NCBI GI q1731141 BLAST score 142 1.0e-08 E value 105 Match length 37 % identity

HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II NCBI Description

>gi\_3878112\_emb\_CAA87788\_ (Z47811) similar to

glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL: D27842 comes from this gene; cDNA EST EMBL: D27841 comes from this gene; cDNA EST EMBL:D32990 comes from this

gene; cDNA EST EMBL: D35712 comes...

>gi\_3879502\_emb\_CAA87796\_ (Z47812) similar to glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL: D27842 comes from this gene; cDNA EST EMBL: D27841 comes from this gene; cDNA EST EMBL: D32990 comes from this

gene; cDNA EST EMBL: D35712 comes

Seq. No. 208695

Seq. ID LIB3135-005-Q1-K1-H1

Method BLASTX



```
NCBI GI
                  g2739279
BLAST score
                  302
                  1.0e-27
E value
                  113
Match length
% identity
                  51
NCBI Description
                  (AJ223177) short chain alcohol dehydrogenase [Nicotiana
                  tabacum] >gi 2791348 emb CAA11154 (AJ223178) short chain
                  alcohol dehydrogenase [Nicotiana tabacum]
Seq. No.
                  208696
```

Seq. ID LIB3135-005-Q1-K1-H6

Method BLASTN NCBI GI q4220643 BLAST score 39 1.0e-12 E value Match length 89 92

% identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 208697 Seq. ID LIB3135-006-Q1-K1-A2 Method BLASTX NCBI GI q120669 BLAST score 536 E value 6.0e-55 Match length 106

% identity 94

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

208698 Seq. No.

Seq. ID LIB3135-006-Q1-K1-A3

Method BLASTX NCBI GI g4467359 BLAST score 304 1.0e-27 E value Match length 116 57 % identity

NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis

thaliana]

Seq. No. 208699

Seq. ID LIB3135-006-Q1-K1-B1

Method BLASTX NCBI GI q3868859 BLAST score 146 3.0e-09 E value Match length 71 49 % identity

(AB013887) RAV2 [Arabidopsis thaliana] NCBI Description

Seq. No. 208700

Seq. ID LIB3135-006-Q1-K1-B2



Method BLASTN
NCBI GI g1418705
BLAST score 77
E value 8.0e-36
Match length 118
% identity 92

NCBI Description G.hirsutum metallothionein-like gene

Seq. No. 208701

Seq. ID LIB3135-006-Q1-K1-B6

Method BLASTX
NCBI GI g2764941
BLAST score 385
E value 3.0e-37
Match length 101
% identity 67

NCBI Description (X98255) transcriptionally stimulated by gibberellins;

expressed in meristematic region, and style [Arabidopsis

thaliana]

Seq. No. 208702

Seq. ID LIB3135-006-Q1-K1-B8

Method BLASTX
NCBI GI g3176686
BLAST score 257
E value 3.0e-22
Match length 127
% identity 45

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 208703

Seq. ID LIB3135-006-Q1-K1-C1

Method BLASTX
NCBI GI g2244970
BLAST score 189
E value 8.0e-15
Match length 51
% identity 67

NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

>gi 2326365 emb CAA74765 (Y14423) putative cell wall

protein [Arabidopsis thaliana]

Seq. No. 208704

Seq. ID LIB3135-006-Q1-K1-C3

Method BLASTX
NCBI GI g4098321
BLAST score 703
E value 2.0e-74
Match length 136
% identity 99

NCBI Description (U76745) beta-tubulin 2 [Triticum aestivum]

Seq. No. 208705

Seq. ID LIB3135-006-Q1-K1-C6

Method BLASTX



```
NCBI GI
                   q3746069
BLAST score
                   143
                   7.0e-09
E value
Match length
                   86
% identity
                   38
NCBI Description
                   (AC005311) putative reverse transcriptase [Arabidopsis
                   thaliana]
                   208706
Seq. No.
Seq. ID
                   LIB3135-006-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   g464775
BLAST score
                   574
E value
                   2.0e-59
Match length
                   122
% identity
                   87
                   SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__$39492
NCBI Description
                   superoxide dismutase - Para rubber tree >gi 348137 (L11707)
                   superoxide dismutase (manganese) [Hevea brasiliensis]
Seq. No.
                   208707
Seq. ID
                   LIB3135-006-Q1-K1-D1
Method
                   BLASTX
NCBI GI
                   g122770
BLAST score
                   399
E value
                   8.0e-39
Match length
                   89
% identity
                   87
                   HEMOGLOBIN II >gi_99509_pir__S13378 hemoglobin II - swamp oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina
NCBI Description
                   glauca]
Seq. No.
                   208708
Seq. ID
                   LIB3135-006-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   q3599940
BLAST score
                   146
                   2.0e-09
E value
Match length
                   64
                   42
% identity
NCBI Description
                   (AF017368) faciogenital dysplasia protein 2 [Mus musculus]
Seq. No.
                   208709
Seq. ID
                   LIB3135-006-Q1-K1-G6
Method
                   BLASTN
NCBI GI
                   g434990
BLAST score
                   32
E value
                   8.0e-09
Match length
                   127
                   88
% identity
NCBI Description O.berteriana mitochondrial trnI gene
Seq. No.
                   208710
```

Seq. ID LIB3135-006-Q1-K1-H1

Method BLASTX NCBI GI q2894570 BLAST score 153



E value 5.0e-10

Match length 119
% identity 36

NCBI Description (AL021890) hypothetical protein [Arabidopsis thaliana]

>gi\_2961337\_emb\_CAA18095.1\_ (AL022140) hypothetical protein
[Arabidopsis thaliana]

 Seq. No.
 208711

 Seq. ID
 LIB3135-006-Q1-K1-H5

 Method
 BLASTX

 NCBI GI
 g3935167

 BLAST score
 385

 E value
 3.0e-37

Match length 119 % identity 68

NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No. 208712

Seq. ID LIB3135-006-Q1-K1-H7

Method BLASTX
NCBI GI g2459417
BLAST score 308
E value 3.0e-28
Match length 84
% identity 74

NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19

[Arabidopsis thaliana]

Seq. No. 208713

Seq. ID LIB3135-007-Q1-K1-A12

Method BLASTX
NCBI GI g1709498
BLAST score 525
E value 1.0e-53
Match length 144
% identity 63

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 208714

Seq. ID LIB3135-007-Q1-K1-A2

Method BLASTX
NCBI GI g3242722
BLAST score 221
E value 4.0e-18
Match length 100
% identity 46

NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis

thaliana]

Seq. No. 208715

Seq. ID LIB3135-007-Q1-K1-B2

Method BLASTX NCBI GI g3122388 BLAST score 300



E value 2.0e-27
Match length 66
% identity 55

NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi\_2394231 (AF016847) WD-40

repeat protein [Arabidopsis thaliana]

Seq. No. 208716

Seq. ID LIB3135-007-Q1-K1-B3

Method BLASTX
NCBI GI g3851636
BLAST score 428
E value 3.0e-42
Match length 105
% identity 78

NCBI Description (AF098519) unknown [Avicennia marina] >gi\_4128206

(AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 208717

Seq. ID LIB3135-007-Q1-K1-B5

Method BLASTX
NCBI GI g3885884
BLAST score 402
E value 3.0e-39
Match length 85
% identity 88

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 208718

Seq. ID LIB3135-007-Q1-K1-B6

Method BLASTX
NCBI GI g3885884
BLAST score 359
E value 2.0e-34
Match length 85
% identity 80

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 208719

Seq. ID LIB3135-007-Q1-K1-B8

Method BLASTX
NCBI GI g1710780
BLAST score 337
E value 1.0e-31
Match length 95
% identity 73

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433

(X96613) cytoplasmic ribosomal protein S7 [Podospora

anserina]

Seq. No. 208720

Seq. ID LIB3135-007-Q1-K1-C12

Method BLASTX
NCBI GI g2735246
BLAST score 256
E value 3.0e-29
Match length 120
% identity 59



```
NCBI Description
                  (U89678) protein kinase [Lycopersicon esculentum]
                  208721
Seq. No.
Seq. ID
                  LIB3135-007-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3914191
BLAST score
                  240
E value
                  2.0e-20
Match length
                  80
% identity
                   55
NCBI Description
                  UDP-N-ACETYLGLUCOSAMINE--PEPTIDE
                  N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC
                  TRANSFERASE P110 SUBUNIT) >gi 1931579 (U76557) O-GlcNAc
                  transferase, p110 subunit [Rattus norvegicus]
Seq. No.
                  208722
Seq. ID
                  LIB3135-007-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g549986
BLAST score
                  184
E value
                  1.0e-13
Match length
                  46
% identity
                  80
NCBI Description
                  (U13149) possible apospory-associated protein [Pennisetum
                  ciliare]
Seq. No.
                  208723
                  LIB3135-007-Q1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4455189
BLAST score
                  37
E value
                  2.0e-11
Match length
                  37
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSAII project)
Seq. No.
                  208724
Seq. ID
                  LIB3135-007-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3687251
BLAST score
                  144
E value
                  1.0e-09
Match length
                  48
% identity
                  56
NCBI Description
                  (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                  208725
```

Seq. ID LIB3135-007-Q1-K1-D5

Method BLASTX NCBI GI g629858 BLAST score 117 E value 4.0e-10 Match length 89 % identity 42

NCBI Description protein kinase C inhibitor - maize



```
208726
Seq. No.
Seq. ID
                  LIB3135-007-Q1-K1-D6
                  BLASTX
Method
NCBI GI
                  g629483
BLAST score
                  234
                  1.0e-19
E value
                  107
Match length
                  49
% identity
                  gene 1-Sc3 protein - European white birch
NCBI Description
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
                  208727
Seq. No.
Seq. ID
                  LIB3135-007-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1173209
BLAST score
                  271
                  3.0e-24
E value
Match length
                  63
% identity
                  89
NCBI Description
                  40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
                  protein S16 protein - upland cotton
                  >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                  [Gossypium hirsutum]
                  208728
Seq. No.
Seq. ID
                  LIB3135-007-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3805765
BLAST score
                  161
E value
                  2.0e-11
Match length
                  72
% identity
                  47
                  (AC005693) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  208729
Seq. ID
                  LIB3135-007-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2829923
BLAST score
                  441
E value
                  6.0e-44
Match length
                  112
% identity
                  48
NCBI Description
                  (AC002291) Similar to uridylyl transferases [Arabidopsis
                  thaliana]
                  208730
Seq. No.
                  LIB3135-007-01-K1-E4
Seq. ID
Method
                  BLASTX
```

NCBI GI g1350680 BLAST score 203 3.0e-21E value Match length 69 % identity 76

NCBI Description 60S RIBOSOMAL PROTEIN L1

NCBI Description



```
Seq. No.
                   208731
Seq. ID
                  LIB3135-007-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2829923
BLAST score
                   295
E value
                  5.0e-27
Match length
                  87
% identity
                   68
NCBI Description
                   (AC002291) Similar to uridylyl transferases [Arabidopsis
Seq. No.
                  208732
Seq. ID
                  LIB3135-007-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  q3024432
BLAST score
                   478
E value
                   3.0e-48
Match length
                   108
% identity
                  88
NCBI Description
                  PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                  COMPLEX ALPHA SUBUNIT) >gi_1930070 (U92540) proteasome
                  alpha subunit [Oryza sativa]
Seq. No.
                  208733
Seq. ID
                  LIB3135-007-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q82426
BLAST score
                   582
E value
                  2.0e-60
Match length
                  122
% identity
                   45
NCBI Description
                  ubiquitin precursor - barley (fragment)
                  >gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                   (171 aa) [Hordeum vulgare]
Seq. No.
                  208734
Seq. ID
                  LIB3135-007-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2462753
BLAST score
                  215
                  1.0e-17
E value
Match length
                  81
% identity
                  54
                   (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  208735
Seq. No.
Seq. ID
                  LIB3135-007-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q461987
BLAST score
                  163
E value
                  2.0e-11
Match length
                  99
% identity
                  43
```

>gi\_82042\_pir\_\_JS0719 translation elongation factor eEF-1
alpha chain - carrot >gi 217913 dbj BAA02205 (D12709)

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

E value

Match length





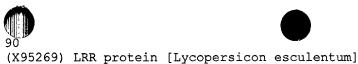
## elongation factor 1-alpha [Daucus carota]

208736 Seq. No. Seq. ID LIB3135-007-Q1-K1-G3 Method BLASTX NCBI GI g1703375 BLAST score 564 E value 3.0e-58 Match length 111 98 % identity NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420) DcARF1 [Daucus carota] 208737 Seq. No. Seq. ID LIB3135-007-Q1-K1-G4 Method BLASTX NCBI GI g2660664 BLAST score 164 E value 2.0e-11 Match length 54 % identity 56 NCBI Description (AC002342) unknown protein [Arabidopsis thaliana] 208738 Seq. No. Seq. ID LIB3135-007-Q1-K1-H11 Method BLASTX NCBI GI g730645 BLAST score 356 7.0e-34 E value Match length 129 % identity 58 NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679 (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi 313188 emb CAA80681 (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi 1903366 gb AAB70449 (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb\_R29788,gb\_ATTS0365 come from this gene. [Arabidopsis thaliana] Seq. No. 208739 LIB3135-007-Q1-K1-H12 Seq. ID Method BLASTX NCBI GI q1001755 BLAST score 143 E value 6.0e-09 Match length 79 % identity 11 NCBI Description (D64004) hypothetical protein [Synechocystis sp.] Seq. No. 208740 Seq. ID LIB3135-007-Q1-K1-H2 Method BLASTX NCBI GI g1619300 BLAST score 522

28776

Ç.

5.0e-58



208741 Seq. No.

NCBI Description

% identity

Seq. ID LIB3135-007-Q1-K1-H7

BLASTN Method NCBI GI g525331 BLAST score 46 7.0e-17 E value

66 Match length 92 % identity

Pisum sativum Alaska alpha-tubulin (TubA1) gene, complete NCBI Description

cds

208742 Seq. No.

Seq. ID LIB3135-008-Q1-K1-A10

Method BLASTX NCBI GI g1709498 BLAST score 545 E value 5.0e-56 Match length 129 % identity 78

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi 1362001 pir S57524 osmotin precursor - Arabidopsis

thaliana >gi 887390 emb CAA61411 (X89008) osmotin

[Arabidopsis thaliana]

208743 Seq. No.

Seq. ID LIB3135-008-Q1-K1-A2

Method BLASTX NCBI GI g4539324 BLAST score 222 E value 4.0e-18 143 Match length % identity 45

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

208744 Seq. No.

Seq. ID LIB3135-008-Q1-K1-A8

Method BLASTX NCBI GI g3080402 BLAST score 564 E value 3.0e-58 Match length 143 % identity 78

(AL022603) putative NADPH quinone oxidoreductase NCBI Description

[Arabidopsis thaliana] >gi 4455266 emb CAB36802.1\_ (AL035527) putative NADPH quinone oxidoreductase

[Arabidopsis thaliana]

Seq. No. 208745

Seq. ID LIB3135-008-Q1-K1-B1

BLASTX Method NCBI GI g1888357 BLAST score 262 E value 8.0e-23 Match length 112



```
% identity
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi 1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
                  208746
Seq. No.
Seq. ID
                  LIB3135-008-Q1-K1-B11
                  BLASTN
Method
                  q2558961
NCBI GI
BLAST score
                  111
                  1.0e-55
E value
Match length
                  135
% identity
                  96
NCBI Description Gossypium hirsutum histone H2B1 mRNA, complete cds
                  208747
Seq. No.
                  LIB3135-008-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1103318
BLAST score
                  160
                  5.0e-11
E value
Match length
                  116
% identity
                  (X78818) casein kinase I [Arabidopsis thaliana]
NCBI Description
                  >gi 2244791 emb CAB10213.1 (Z97336) casein kinase I
                  [Arabidopsis thaliana]
Seq. No.
                  208748
                  LIB3135-008-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                  g4455246
NCBI GI
                  220
BLAST score
E value
                  7.0e-18
                  90
Match length
% identity
                  49
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                  208749
Seq. No.
                  LIB3135-008-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g2262159
NCBI GI
                  142
BLAST score
                  9.0e-09
E value
                  46
Match length
% identity
                  (AC002329) predicted protein similar to S.pombe protein
NCBI Description
                  C5H10.03 [Arabidopsis thaliana]
Seq. No.
                  208750
Seq. ID
                  LIB3135-008-Q1-K1-C12
                  BLASTN
Method
                  g2924257
NCBI GI
```

BLAST score 190 1.0e-102 E value Match length 370 44 % identity

NCBI Description Tobacco chloroplast genome DNA



```
208751
Seq. No.
                  LIB3135-008-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4102861
BLAST score
                   460
                   5.0e-46
E value
Match length
                   92
                   91
% identity
                   (AF016893) copper/zinc-superoxide dismutase [Populus
NCBI Description
                   tremuloides]
Seq. No.
                   208752
                   LIB3135-008-Q1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g829169
BLAST score
                   136
                   2.0e-14
E value
Match length
                   95
                   63
% identity
                  (L33263) beta-tubulin [Oryza sativa]
NCBI Description
Seq. No.
                   208753
                   LIB3135-008-Q1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832677
BLAST score
                   298
E value
                   5.0e-27
Match length
                   120
                   50
% identity
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   208754
                   LIB3135-008-Q1-K1-D11
Seq. ID
Method
                   BLASTX
                   q2980770
NCBI GI
                   313
BLAST score
                   8.0e-29
E value
                   121
Match length
                   52
% identity
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   208755
Seq. No.
                   LIB3135-008-Q1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3193292
                   530
BLAST score
                   3.0e-54
E value
                   143
Match length
                   75
% identity
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
                   208756
Seq. No.
Seq. ID
                   LIB3135-008-Q1-K1-D2
```

28779

BLASTX

Method

```
q167367
NCBI GI
BLAST score
                   448
E value
                  1.0e-44
Match length
                  85
                  100
% identity
NCBI Description
                  (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  208757
                  LIB3135-008-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129651
BLAST score
                  467
E value
                  7.0e-47
Match length
                  124
% identity
                  myosin heavy chain ATM2 - Arabidopsis thaliana (fragment)
NCBI Description
                  >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis
                  thaliana]
Seq. No.
                  208758
Seq. ID
                  LIB3135-008-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g629483
BLAST score
                  348
                  7.0e-33
E value
Match length
                  124
                  57
% identity
NCBI Description
                  gene 1-Sc3 protein - European white birch
                  >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                  >gi_1584322_prf _2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
Seq. No.
                  208759
Seq. ID
                  LIB3135-008-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3451067
BLAST score
                  182
E value
                  2.0e-13
Match length
                  63
% identity
                  56
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                  208760
                  LIB3135-008-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4106538
BLAST score
                  509
E value
                  9.0e-52
Match length
                  141
% identity
                  71
NCBI Description
                  (AF104220) gamma-tocopherol methyltransferase [Arabidopsis
                  thaliana]
```

Seq. No. 208761

Seq. ID LIB3135-008-Q1-K1-E3

Method BLASTX NCBI GI g112972



BLAST score E value 5.0e-41 138 Match length % identity 58

NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi\_167546 (M92660) aspartate aminotransferase [Daucus

carota] >gi\_445587\_prf\_\_1909339A Asp aminotransferase

[Daucus carota]

208762 Seq. No.

Seq. ID LIB3135-008-Q1-K1-F1

Method BLASTX NCBI GI g4127456 BLAST score 357 5.0e-34 E value Match length 124 32 % identity

NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 208763

LIB3135-008-Q1-K1-F11 Seq. ID

Method BLASTX NCBI GI g1703108 BLAST score 707 E value 6.0e-75Match length 144 % identity 96

NCBI Description

ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis thaliana >gi\_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 208764

LIB3135-008-Q1-K1-F2 Seq. ID

Method BLASTX NCBI GI g286001 BLAST score 162 E value 3.0e-11 Match length 106 % identity 31

(D13630) KIAA0005 [Homo sapiens] NCBI Description

208765 Seq. No.

Seq. ID LIB3135-008-Q1-K1-F3

Method BLASTX NCBI GI q1732365 BLAST score 160 E value 7.0e-11 Match length 58 % identity

NCBI Description (U80271) proline rich protein [Malus domestica]

Seq. No. 208766

Seq. ID LIB3135-008-Q1-K1-F4

Method BLASTN g2829205 NCBI GI



BLAST score E value 1.0e-107 430 Match length % identity 22

Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein NCBI Description

precursor (PRP) mRNA, complete cds

Seq. No. 208767

LIB3135-008-Q1-K1-F7 Seq. ID

Method BLASTX NCBI GI g2244818 BLAST score 156 E value 2.0e-10 Match length 96 % identity

(Z97336) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 208768

LIB3135-008-Q1-K1-F9 Seq. ID

Method BLASTX NCBI GI q3367534 BLAST score 636 E value 1.0e-66 Match length 143 % identity

(AC004392) Strong similarity to coatamer alpha subunit NCBI Description

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]

208769 Seq. No.

Seq. ID LIB3135-008-Q1-K1-G1

Method BLASTX NCBI GI g2673868 175 BLAST score 8.0e-13 E value 36 Match length 89 % identity

(Y14856) fimbriata-associated protein [Antirrhinum majus] NCBI Description

208770 Seq. No.

Seq. ID LIB3135-008-Q1-K1-G10

Method BLASTX g267082 NCBI GI 363 BLAST score 1.0e-34 E value 114 Match length % identity 64

TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8 NCBI Description

chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

208771 Seq. No.

Seq. ID LIB3135-008-Q1-K1-G11

BLASTX Method NCBI GI q3598857 BLAST score 256 E value 1.0e-25



```
Match length
% identity
                   46
NCBI Description
                   (AF072447) short-chain alcohol dehydrogenase [Ipomoea
                  trifida]
                  208772
Seq. No.
Seq. ID
                  LIB3135-008-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3860308
BLAST score
                  170
                  5.0e-12
E value
Match length
                  53
% identity
                  68
NCBI Description
                  (AJ012681) hypothetical protein [Cicer arietinum]
Seq. No.
                  208773
Seq. ID
                  LIB3135-008-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1848212
BLAST score
                  306
E value
                  4.0e-28
Match length
                  108
% identity
                  39
                  (Y11209) protein disulfide-isomerase precursor [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  208774
Seq. ID
                  LIB3135-008-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2345148
BLAST score
                  144
E value
                  6.0e-09
Match length
                  56
% identity
                  52
NCBI Description
                  (AF014821) developmentally regulated GTP binding protein
                  [Pisum sativum]
Seq. No.
                  208775
                  LIB3135-008-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g584706
BLAST score
                  170
E value
                  3.0e-12
                  70
Match length
% identity
                  57
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                  >gi_2130066 pir__JC5124 aspartate transaminase (EC
                  2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
                  (D14673) aspartate aminotransferase [Oryza sativa]
```

Seq. No. 208776

LIB3135-008-Q1-K1-G6 Seq. ID

Method BLASTX NCBI GI g1169451 BLAST score 177 E value 8.0e-13 Match length 106



% identity NCBI Description PROBABLE GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi\_322510\_pir\_\_S31906 beta-1,3-glucanase homolog - Arabidopsis thaliana >gi\_22677\_emb\_CAA49853 (X70409) A6 [Arabidopsis thaliana] >gi\_2244764\_emb\_CAB10187\_ (Z97335) AMP-binding protein [Arabidopsis thaliana] Seq. No. 208777 Seq. ID LIB3135-008-Q1-K1-H2 Method BLASTX NCBI GI g2662341 BLAST score 537 3.0e-55 E value Match length 110 % identity 94 (D63580) EF-1 alpha [Oryza sativa] NCBI Description >gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza satīva] >gi 2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha [Oryza sativa] 208778 Seq. No. Seq. ID LIB3135-008-Q1-K1-H6 BLASTX Method q2244970 NCBI GI BLAST score 216 2.0e-17 E value Match length 89 48 % identity NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana] >gi\_2326365 emb CAA74765 (Y14423) putative cell wall protein [Arabidopsis thaliana] Seq. No. 208779 Seq. ID LIB3135-008-Q1-K1-H7 Method BLASTX NCBI GI q1488052 BLAST score 183 8.0e-14 E value Match length 96 % identity 46 NCBI Description (U63927) beta-tubulin 2 [Daucus carota] Seq. No. 208780 Seq. ID LIB3135-009-Q1-K1-A1 Method BLASTN NCBI GI q2829205 BLAST score 96 E value 1.0e-46 Match length 380

% identity 32

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 208781

Seq. ID LIB3135-009-Q1-K1-A2



```
Method
                   BLASTX
NCBI GI
                   g2760347
BLAST score
                   562
                   4.0e-58
E value
Match length
                  115
% identity
                  17
                  (U84968) ubiquitin [Arabidopsis thaliana]
NCBI Description
                  208782
Seq. No.
Seq. ID
                  LIB3135-009-Q1-K1-A4
                  BLASTX
Method
                  g2829899
NCBI GI
BLAST score
                  204
                   5.0e-16
E value
Match length
                  99
                   40
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp AJ001449 2465015 and major#latex protein,
                  gp X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                  208783
Seq. ID
                  LIB3135-009-Q1-K1-B1
                  BLASTX
Method
                  g4530585
NCBI GI
BLAST score
                   355
                  1.0e-33
E value
                  83
Match length
                  76
% identity
                  (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
Seq. No.
                  208784
Seq. ID
                  LIB3135-009-Q1-K1-C6
                  BLASTX
Method
NCBI GI
                  q4193382
BLAST score
                   389
E value
                  1.0e-37
Match length
                  86
% identity
                  85
NCBI Description
                   (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
                  >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                  thaliana]
Seq. No.
                  208785
Seq. ID
                  LIB3135-009-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g3914535
BLAST score
                  136
E value
                  1.0e-08
Match length
                  59
```

47 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb CAA11283 (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No. 208786

Seq. ID LIB3135-009-Q1-K1-D1

Method BLASTX NCBI GI g3250695



```
BLAST score
                   1.0e-27
E value
Match length
                   104
% identity
                   55
                   (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   208787
                   LIB3135-009-Q1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1946372
BLAST score
                   179
E value
                    3.0e-13
Match length
                    62
                    56
% identity
                    (U93215) yeast hypothetical protein YDB1_SCHPO isolog
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    208788
                   LIB3135-009-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                    q4337175
BLAST score
                    221
E value
                    3.0e-22
Match length
                    115
% identity
                    47
                    (AC006416) ESTs gb_T20589, gb T04648, gb AA597906,
NCBI Description
                    gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                    gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                    208789
                    LIB3135-009-Q1-K1-D4
Seq. ID
Method
                    BLASTX
                    g3386621
NCBI GI
BLAST score
                    196
                    4.0e-15
E value
Match length
                    41
% identity
                    93
                    (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                    208790
Seq. No.
                    LIB3135-009-Q1-K1-D6
Seq. ID
                    BLASTX
Method
NCBI GI
                    q4512667
BLAST score
                    194
                    4.0e-15
E value
Match length
                    83
% identity
                    54
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                    208791
Seq. No.
Seq. ID
                    LIB3135-009-Q1-K1-D8
                    BLASTX
Method
```

NCBI GI g1076427
BLAST score 513
E value 2.0e-52
Match length 112

```
% identity
NCBI Description
                  ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis
                  thaliana
                  208792
Seq. No.
Seq. ID
                  LIB3135-009-Q1-K1-E3
```

Method BLASTX NCBI GI g886362 BLAST score 141 E value 8.0e-09 66 Match length 3 % identity

NCBI Description (L42525) product unknown; 32 kd ORF [Plasmid pSW200]

208793 Seq. No. Seq. ID LIB3135-009-Q1-K1-E8 Method BLASTX NCBI GI g140185 BLAST score 232

2.0e-19 E value Match length 98 % identity 45

PROBABLE GYP7 PROTEIN >gi 173243 (M17741) unidentified NCBI Description

peptide [Yarrowia lipolytica]

208794 Seq. No.

Seq. ID LIB3135-009-Q1-K1-F1

Method BLASTX NCBI GI g3158476 BLAST score 543 E value 9.0e-56 Match length 120 90

% identity

NCBI Description (AF067185) aquaporin 2 [Samanea saman]

208795 Seq. No.

Seq. ID LIB3135-009-Q1-K1-F12

Method BLASTX NCBI GI g2129879 BLAST score 254 E value 7.0e-22 Match length 103 % identity 50

NCBI Description chlorophyll a/b-binding protein type II precursor,

photosystem I - garden pea >gi 602359 emb CAA57492 (X81962) Type II chlorophyll a/b binding protein from

photosystem I [Pisum sativum]

Seq. No. 208796

Seq. ID LIB3135-009-Q1-K1-F2

Method BLASTX NCBI GI g3928099 BLAST score 284 E value 2.0e-25 Match length 86

% identity 31

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]



```
208797
Seq. No.
Seq. ID
                  LIB3135-009-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                   g2792297
BLAST score
                   261
E value
                   1.0e-22
                   77
Match length
% identity
                   58
                  (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                   208798
Seq. No.
Seq. ID
                  LIB3135-009-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                   g113683
                  205
BLAST score
                   4.0e-16
E value
                   87
Match length
                   47
% identity
                  ALPHA-AMYLASE ISOZYME 3E PRECURSOR (1,4-ALPHA-D-GLUCAN
NCBI Description
                   GLUCANOHYDROLASE) >gi 100663 pir JT0946 alpha-amylase 3E -
                   rice >gi 169773 (M59352) alpha-amylase [Oryza sativa]
Seq. No.
                  208799
                  LIB3135-009-Q1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2465923
                   370
BLAST score
                   1.0e-35
E value
                   112
Match length
                   65
% identity
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   208800
Seq. ID
                   LIB3135-009-Q1-K1-G1
Method
                   BLASTX
                   g2465923
NCBI GI
BLAST score
                   456
                   1.0e-45
E value
Match length
                   134
% identity
                   68
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   208801
Seq. ID
                   LIB3135-009-Q1-K1-G4
```

Method BLASTN
NCBI GI g2829205
BLAST score 73
E value 7.0e-33
Match length 193
% identity 56

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 208802



```
LIB3135-009-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  410
                  4.0e-40
E value
Match length
                  88
                  91
% identity
NCBI Description
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                  208803
Seq. No.
Seq. ID
                  LIB3135-009-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q4102861
BLAST score
                  367
E value
                  4.0e-35
                  79
Match length
% identity
                  87
                  (AF016893) copper/zinc-superoxide dismutase [Populus
NCBI Description
                  tremuloides]
Seq. No.
                  208804
Seq. ID
                  LIB3135-010-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2213614
BLAST score
                  181
E value
                  1.0e-13
Match length
                  77
% identity
                  51
                  (AC000103) F21J9.8 [Arabidopsis thaliana]
NCBI Description
                  208805
Seq. No.
                  LIB3135-010-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351357
BLAST score
                  233
E value
                  2.0e-19
Match length
                  55
                  80
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN
NCBI Description
                  (CR14) >gi 633681 emb CAA55863 (X79276)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
Seq. No.
                  208806
Seq. ID
                  LIB3135-010-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3928079
BLAST score
                  230
E value
                  4.0e-19
Match length
                  91
% identity
                  51
NCBI Description (AC005770) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  208807
```

Seq. ID LIB3135-010-Q1-K1-A6

Method BLASTX NCBI GI q100519 BLAST score 297



E value 6.0e-27 Match length 115 % identity 50

NCBI Description hypothetical protein 873 - common sunflower

>gi\_12992\_emb\_CAA44478\_ (X62592) ORF 873 [Helianthus
annuus] >gi\_758363\_emb\_CAA37614\_ (X53537) orfH522

[Helianthus annuus]

Seq. No. 208808

Seq. ID LIB3135-010-Q1-K1-A7

Method BLASTX
NCBI GI g3928079
BLAST score 276
E value 2.0e-24
Match length 144
% identity 43

NCBI Description (AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208809

Seq. ID LIB3135-010-Q1-K1-A9

Method BLASTX
NCBI GI g1345979
BLAST score 617
E value 2.0e-64
Match length 125
% identity 86

NCBI Description OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR

>gi\_459962 (L29215) plastid omega-6 desaturase [Glycine

max]

Seq. No. 208810

Seq. ID LIB3135-010-Q1-K1-B1

Method BLASTX
NCBI GI g3928079
BLAST score 163
E value 3.0e-11
Match length 65
% identity 49

NCBI Description (AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208811

Seq. ID LIB3135-010-Q1-K1-B12

Method BLASTX
NCBI GI g1946360
BLAST score 184
E value 1.0e-13
Match length 122
% identity 39

NCBI Description (U93215) elicitor response element binding protein WRKY3

isolog [Arabidopsis thaliana]

Seq. No. 208812

Seq. ID LIB3135-010-Q1-K1-B5

Method BLASTX
NCBI GI g2687444
BLAST score 172
E value 7.0e-13

Haral Geller



Match length 59 % identity 46

NCBI Description (AF036567) alcohol dehydrogenase [Gossypium robinsonii]

Seq. No. 208813

Seq. ID LIB3135-010-Q1-K1-C12

59

Method BLASTX
NCBI GI g417542
BLAST score 422
E value 1.0e-41
Match length 133

% identity

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (PATHOGENESIS-RELATED

PROTEIN 1) >gi 169549 (J03679) glutathione S-transferase

[Solanum tuberosum]

Seq. No. 208814

Seq. ID LIB3135-010-Q1-K1-C2

Method BLASTX
NCBI GI g1706261
BLAST score 434
E value 4.0e-43
Match length 124
% identity 72

NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi 2118129 pir S59598

cysteine proteinase 2 precursor - maize

>gi\_644490\_dbj\_BAA08245\_ (D45403) cysteine proteinase [Zea

mays]

Seq. No. 208815

Seq. ID LIB3135-010-Q1-K1-C5

Method BLASTX
NCBI GI g2497702
BLAST score 158
E value 1.0e-10
Match length 110
% identity 36

NCBI Description OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR

>gi\_2121019\_pir\_\_I40710 outer membrane lipoprotein -Citrobacter freundii >gi 717136 (U21727) lipocalin

precursor [Citrobacter freundii]

Seq. No. 208816

Seq. ID LIB3135-010-Q1-K1-C6

Method BLASTX
NCBI GI g1706261
BLAST score 384
E value 3.0e-37
Match length 103
% identity 73

NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi\_2118129\_pir\_S59598

cysteine proteinase 2 precursor - maize

>gi\_644490\_dbj\_BAA08245\_ (D45403) cysteine proteinase [Zea

mays]

Seq. No. 208817

Seq. ID LIB3135-010-Q1-K1-D3



```
Method
                  BLASTX
NCBI GI
                  q4512698
BLAST score
                  575
                  2.0e-59
E value
Match length
                  146
% identity
                  76
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
                  208818
Seq. No.
Seq. ID
                  LIB3135-010-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q4512698
BLAST score
                  164
                  8.0e-16
E value
                  87
Match length
% identity
                  53
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  208819
Seq. ID
                  LIB3135-010-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2341032
BLAST score
                  353
E value
                  1.0e-33
Match length
                  94
                  69
% identity
NCBI Description (AC000104) EST gb ATTS0956 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  208820
Seq. ID
                  LIB3135-010-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3776581
BLAST score
                  143
                  3.0e-11
E value
Match length
                  71
% identity
                  58
NCBI Description (AC005388) Similar to Beta integral membrane protein
                  homolog gb U43629 from A. thaliana. [Arabidopsis thaliana]
```

Seq. No. 208821

Seq. ID LIB3135-010-Q1-K1-E3

Method BLASTX NCBI GI q4512698 BLAST score 245 E value 4.0e-21 Match length 94 % identity 53

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208822

Seq. ID LIB3135-010-Q1-K1-F3

Method BLASTX NCBI GI q2829899 BLAST score 278 E value 1.0e-24 Match length 115

28792



% identity 47

NCBI Description (AC002311) similar to ripening-induced protein, gp\_AJ001449\_2465015 and major#latex protein, gp\_X91961\_1107495 [Arabidopsis thaliana]

Seq. No. 208823

Seq. ID LIB3135-010-Q1-K1-G1

Method BLASTX
NCBI GI g2760837
BLAST score 276
E value 2.0e-24
Match length 118
% identity 45

NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 208824

Seq. ID LIB3135-010-Q1-K1-G4

Method BLASTX
NCBI GI g4337175
BLAST score 402
E value 3.0e-39
Match length 118
% identity 64

NCBI Description (AC006416) ESTs gb T20589, gb T04648, gb AA597906,

gb\_T04111, gb\_R84180, gb\_R65428, gb\_T444\overline{39}, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb\_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 208825

Seq. ID LIB3135-010-Q1-K1-G5

Method BLASTX
NCBI GI g2149955
BLAST score 139
E value 1.0e-08
Match length 39
% identity 67

NCBI Description (U97023) putative aquaporin-1 [Phaseolus vulgaris]

Seq. No. 208826

Seq. ID LIB3135-010-Q1-K1-H2

Method BLASTX
NCBI GI g3023685
BLAST score 443
E value 1.0e-50
Match length 115
% identity 90

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)

>gi\_1041245\_emb\_CAA63121\_ (X92377) enolase [Alnus

glutinosa]

Seq. No. 208827

Seq. ID LIB3135-010-Q1-K1-H7

Method BLASTX
NCBI GI g4049349
BLAST score 144
E value 1.0e-09



Match length 51 % identity 60

NCBI Description (AL034567) ubiquinol-cytochrome c reductase-like protein

[Arabidopsis thaliana]

Seq. No. 208828

Seq. ID LIB3135-011-Q1-K1-A11

Method BLASTX
NCBI GI g3023751
BLAST score 306
E value 4.0e-37
Match length 115
% identity 33

NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS

ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772 pir S55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

>gi\_854626\_emb\_CAA60505\_ (X86903) peptidylprolyl isomerase

[Triticum aestivum]

Seq. No. 208829

Seq. ID LIB3135-011-Q1-K1-A2

Method BLASTX
NCBI GI g3860272
BLAST score 522
E value 2.0e-53
Match length 119
% identity 79

NCBI Description (AC005824) putative suppressor protein [Arabidopsis

thaliana] >gi\_4314399\_gb\_AAD15609\_ (AC006232) putative skd1

protein [Arabidopsis thaliana]

Seq. No. 208830

Seq. ID LIB3135-011-Q1-K1-A3

Method BLASTX
NCBI GI g4105798
BLAST score 189
E value 3.0e-14
Match length 57
% identity 58

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 208831

Seq. ID LIB3135-011-Q1-K1-A6

Method BLASTX
NCBI GI g3608412
BLAST score 432
E value 9.0e-43
Match length 129
% identity 64

NCBI Description (AF079355) protein phosphatase-2c [Mesembryanthemum

crystallinum]

Seq. No. 208832

Seq. ID LIB3135-011-Q1-K1-A9

Method BLASTX NCBI GI g485393 BLAST score 510

NCBI Description

```
E value
                    7.0e-52
 Match length
                    132
 % identity
                    77
 NCBI Description
                    (D30653) peroxidase [Populus kitakamiensis]
 Seq. No.
                    208833
 Seq. ID
                   LIB3135-011-Q1-K1-B11
 Method
                   BLASTX
 NCBI GI
                   q1572681
 BLAST score
                   340
 E value
                   4.0e-32
 Match length
                   102
 % identity
 NCBI Description
                   (U69897) oligopeptidase B [Trypanosoma cruzi]
 Seq. No.
                   208834
 Seq. ID
                   LIB3135-011-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1256259
BLAST score
                   179
                   3.0e-13
E value
Match length
                   38
% identity
                   87
NCBI Description
                   (U50900) voltage-dependent anion channel protein [Spinacia
                   oleracea]
Seq. No.
                   208835
Seq. ID
                   LIB3135-011-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g3426048
BLAST score
                   157
E value
                   8.0e-11
Match length
                   58
% identity
                   62
NCBI Description
                   (AC005168) putative hydroxymethylglutaryl-CoA lyase
                   precursor [Arabidopsis thaliana]
Seq. No.
                   208836
Seq. ID
                   LIB3135-011-Q1-K1-B7
Method
                   BLASTN
NCBI GI
                   g2760172
BLAST score
                   37
E value
                   2.0e-11
Match length
                   73
% identity
                   88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   208837
Seq. ID
                  LIB3135-011-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3135254
BLAST score
                  224
E value
                  3.0e-18
Match length
                  74
% identity
                  66
```

28795

(AC003058) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  208838
Seq. ID
                  LIB3135-011-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3953479
BLAST score
                  518
E value
                  8.0e-53
Match length
                  125
% identity
NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]
                  208839
Seq. No.
                  LIB3135-011-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2344902
BLAST score
                  290
E value
                  4.0e-26
Match length
                  124
% identity
                  52
NCBI Description
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
                  >gi_3341701 (AC003672) hypothetical protein [Arabidopsis
                  thaliana]
Seq. No.
                  208840
Seq. ID
                  LIB3135-011-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2367431
                  250
BLAST score
E value
                  2.0e-21
Match length
                  83
% identity
NCBI Description (AF000403) putative cytochrome P450 [Lotus japonicus]
                  208841
Seq. No.
Seq. ID
                  LIB3135-011-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2827141
BLAST score
                  170
E value
                  1.0e-12
                  46
Match length
                  70
% identity
NCBI Description
                  (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                  208842
Seq. ID
                  LIB3135-011-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4314355
BLAST score
                  157
E value
                  2.0e-10
Match length
                  82
% identity
                  62
```

28796

NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

LIB3135-011-Q1-K1-D10

208843

BLASTX

Seq. No. Seq. ID

Method



NCBI GI g3023419
BLAST score 197
E value 8.0e-16
Match length 53
% identity 70

NCBI Description CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA

3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)

>gi\_1934859\_emb\_CAA72911\_ (Y12228) caffeoyl-CoA

O-methyltransferase [Eucalyptus gunnii]

Seq. No. 208844

Seq. ID LIB3135-011-Q1-K1-D2

Method BLASTN
NCBI GI g2264310
BLAST score 51
E value 1.0e-19
Match length 119

Match length 119 % identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MKP11, complete sequence [Arabidopsis thaliana]

Seq. No. 208845

Seq. ID LIB3135-011-Q1-K1-D4

Method BLASTX
NCBI GI g131015
BLAST score 235
E value 9.0e-20
Match length 50
% identity 78

NCBI Description PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR

(THAUMATIN-LIKE PROTEIN E22) >gi\_100385\_pir\_\_JH0230 pathogenesis-related protein R precursor - common tobacco >gi\_19855\_emb\_CAA33293\_ (X15224) thaumatin-like protein [Nicotiana tabacum] >gi\_19980\_emb\_CAA31235\_ (X12739) pathogenesis-related protein R (AA 1 - 226) [Nicotiana

tabacum]

Seq. No. 208846

Seq. ID LIB3135-011-Q1-K1-D5

Method BLASTX
NCBI GI g3335350
BLAST score 159
E value 1.0e-10
Match length 130
% identity 35

NCBI Description (AC004512) Similar to gb\_Z84386 anthranilate

N-hydroxycinnamoyl/benzoyltransferase from Dianthus

caryophyllus. [Arabidopsis thaliana]

Seq. No. 208847

Seq. ID LIB3135-011-Q1-K1-D6

Method BLASTX
NCBI GI g3986110
BLAST score 173
E value 5.0e-13
Match length 62
% identity 58

```
NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana]
 Seq. No.
                    208848
 Seq. ID
                    LIB3135-011-Q1-K1-D8
 Method
                    BLASTX
 NCBI GI
                    g2961372
 BLAST score
                    520
 E value
                    4.0e-53
                    126
 Match length
                    80
 % identity
 NCBI Description
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
                    thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                   protein L2 [Arabidopsis thaliana]
 Seq. No.
                    208849
 Seq. ID
                    LIB3135-011-Q1-K1-D9
                   BLASTN
 Method
 NCBI GI
                    g2829205
 BLAST score
                    37
                    2.0e-11
 E value
 Match length
                    191
" % identity
                    51
 NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
                    precursor (PRP) mRNA, complete cds
 Seq. No.
                    208850
 Seq. ID
                    LIB3135-011-Q1-K1-E12
 Method
                    BLASTX
 NCBI GI
                    g2244835
 BLAST score
                    145
                    1.0e-09
 E value
 Match length
                    41
 % identity
                    68
 NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
 Seq. No.
                    208851
 Seq. ID
                    LIB3135-011-Q1-K1-E7
 Method
                    BLASTN
 NCBI GI
                    g2687434
 BLAST score
                    44
 E value
                    1.0e-15
 Match length
                    124
                    90
 % identity
 NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                   partial sequence
                   208852
 Seq. No.
 Seq. ID
                   LIB3135-011-Q1-K1-E9
 Method
                   BLASTX
 NCBI GI
                    q3128195
 BLAST score
                    494
 E value
                    3.0e-50
 Match length
                    104
 % identity
                    94
 NCBI Description
                   (AC004521) putative phosphoribosyl pyrophosphate synthetase
                    [Arabidopsis thaliana] >gi_3341673 (AC003672) putative
```

28798

phosphoribosyl pyrophosphate synthetase [Arabidopsis



## thaliana]

```
Seq. No.
                   208853
Seq. ID
                  LIB3135-011-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2959370
BLAST score
                  235
E value
                  1.0e-19
Match length
                  116
% identity
                  36
NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  208854
Seq. ID
                  LIB3135-011-Q1-K1-F3
Method
                  BLASTN
NCBI GI
                  g2687432
BLAST score
                  33
E value
                  4.0e-09
Match length
                  117
% identity
                  82
                  Plumbago auriculata large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  208855
Seq. ID
                  LIB3135-011-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1730108
BLAST score
                  583
E value
                  2.0e-60
Match length
                  137
% identity
                  80
NCBI Description
                  LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
                  HYDROXYLASE) >gi_486848_pir__S36233 flavanone 3-hydroxylase
                  homolog - garden petunia
Seq. No.
                  208856
Seq. ID
                  LIB3135-011-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q2501578
BLAST score
                  510
E value
                  7.0e-52
Match length
                  139
% identity
                  74
NCBI Description
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__$60047
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi_1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
Seq. No.
                  208857
Seq. ID
                  LIB3135-011-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1877480
BLAST score
                  365
E value
                  6.0e-35
Match length
                  123
% identity
                  62
```

NCBI Description (U89270) short-chain alcohol dehydrogenase [Tripsacum



## dactyloides]

```
Seq. No.
                   208858
                   LIB3135-011-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1168728
BLAST score
                   281
E value
                   3.0e-25
Match length
                   79
% identity
                   68
NCBI Description
                   CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)
                   cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   208859
                   LIB3135-011-Q1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1168728
BLAST score
                   480
E value
                   2.0e-48
Match length
                   114
% identity
                   81
NCBI Description
                   CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)
                   cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   208860
Seq. ID
                   LIB3135-011-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   g902584
BLAST score
                   400
E value
                   3.0e-39
Match length
                   96
% identity
                   12
NCBI Description
                   (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
                  mays]
Seq. No.
                   208861
Seq. ID
                   LIB3135-011-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g1877480
BLAST score
                   305
E value
                   6.0e-28
Match length
                  123
% identity
NCBI Description
                   (U89270) short-chain alcohol dehydrogenase [Tripsacum
                  dactyloides]
Seq. No.
                  208862
Seq. ID
                  LIB3135-011-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  593
E value
                  9.0e-62
Match length
                  121
% identity
                  94
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473_pir _S46302
```

28800

heat shock cognate protein 70-1 - Arabidopsis thaliana >gi\_397482\_emb\_CAA52684 (X74604) heat shock protein 70



## cognate [Arabidopsis thaliana]

```
Seq. No.
                  208863
Seq. ID
                  LIB3135-011-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q1762935
BLAST score
                  143
                  3.0e-09
E value
Match length
                  36
% identity
                  81
NCBI Description (U66264) ubiquitin [Nicotiana tabacum]
                  208864
Seq. No.
Seq. ID
                  LIB3135-011-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3860323
BLAST score
                  248
E value
                  3.0e-21
Match length
                  59
% identity
                  78
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                  208865
Seq. ID
                  LIB3135-011-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g416649
BLAST score
                  327
E value
                  2.0e-30
Match length
                  111
                  59
% identity
                  PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
NCBI Description
                  PGNT1/PCNT110) >gi_100303_pir_ S16267 auxin-induced protein
                  (clone pGNT1) - common tobacco >gi_19789_emb_CAA39709_
                  (X56268) auxin-induced protein [Nicotiana tabacum]
                  >gi_19795_emb_CAA39705_ (X56264) auxin-induced protein
                  [Nicotiana tabacum]
Seq. No.
                  208866
                  LIB3135-012-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4559384
                  307
BLAST score
                  4.0e-28
E value
Match length
                  75
% identity
                  81
NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]
Seq. No.
                  208867
Seq. ID
                  LIB3135-012-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3885515
BLAST score
                  351
E value
                  2.0e-33
                  85
Match length
% identity
NCBI Description
                  (AF084202) similar to ribosomal protein S26 [Medicago
                  sativa]
```

BLAST score

E value

221

3.0e-18



```
Seq. No.
                    208868
                    LIB3135-012-Q1-K1-A9
Seq. ID
Method
                    BLASTX
                    g3775989
NCBI GI
BLAST score
                    250
                    2.0e-21
E value
Match length
                    68
                    69
% identity
NCBI Description (AJ010458) RNA helicase [Arabidopsis thaliana]
Seq. No.
                    208869
Seq. ID
                    LIB3135-012-Q1-K1-B11
Method
                    BLASTX
NCBI GI
                    q3599491
BLAST score
                    501
E value
                    5.0e-51
Match length
                    110
% identity
                    82
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]
Seq. No.
                    208870
                    LIB3135-012-Q1-K1-B12
Seq. ID
                    BLASTX
Method
                    g3201619
NCBI GI
BLAST score
                    280
                    6.0e-36
E value
                    106
Match length
                    74
% identity
NCBI Description (AC004669) dihydroxypolyprenylbenzoate methyltransferase
                     [Arabidopsis thaliana]
                     208871
Seq. No.
Seq. ID
                    LIB3135-012-Q1-K1-B4
Method
                    BLASTX
NCBI GI
                    g135159
BLAST score
                     227
E value
                     5.0e-19
Match length
                     60
% identity
                     68
NCBI Description ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE--TRNA LIGASE)
                     (ASNRS) >gi_68529_pir__SYECNT asparagine--tRNA ligase (EC
                     6.1.1.22) precursor - Escherichia coli
                    >gi_41000_emb_CAA48274_ (X68192) Asparaginyl-tRNA
synthetase [Escherichia coli] >gi_147935 (M33145)
                    asparaginyl-tRNA synthetase (asnS) [Escherichia coli] >gi_1651455_dbj_BAA35682_(D90731) Asparaginyl-tRNA synthetase (EC 6.1.1.22) (asparagine-tRNA ligase) (asnRS).
                     [Escherichia coli] >gi_1787161 (AE000195) asparagine tRNA
                     synthetase [Escherichia coli]
Seq. No.
                     208872
Seq. ID
                    LIB3135-012-Q1-K1-C12
Method
                    BLASTX
NCBI GI
                    g3608179
```

```
Match length
% identity
                  54
                  (AB008188) cyclin D [Pisum sativum]
NCBI Description
                  208873
Seq. No.
                  LIB3135-012-Q1-K1-D1
Seq. ID
Method
                  BLASTN
                   g2829205
NCBI GI
                   41
BLAST score
                   2.0e-14
E value
Match length
                   69
                   90
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
                   208874
Seq. No.
                   LIB3135-012-Q1-K1-D11
Seq. ID
Method
                   BLASTX
                   q1350956
NCBI GI
                   462
BLAST score
                                                                     2.0e-46
E value
                   97
Match length
                   93
% identity
                  40S RIBOSOMAL PROTEIN S20 (S22)
NCBI Description
                   208875
Seq. No.
                   LIB3135-012-Q1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1888357
                   436
BLAST score
E value
                   2.0e-43
                   90
Match length
% identity
                   82
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
```

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi\_1890154\_emb\_CAA72432\_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 208876

Seq. ID LIB3135-012-Q1-K1-E1

Method BLASTX
NCBI GI g1928981
BLAST score 499
E value 1.0e-50
Match length 106
% identity 93

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 208877

Seq. ID LIB3135-012-Q1-K1-F12

Method BLASTX
NCBI GI g170352
BLAST score 398
E value 1.0e-62
Match length 130
% identity 17

NCBI Description (M74101) hexameric polyubiquitin [Nicotiana sylvestris]



>gi\_870792 (L05361) polyubiquitin [Arabidopsis thaliana]
>gi\_4115333 (L81139) ubiquitin [Pisum sativum] >gi\_4115335
(L81140) ubiquitin [Pisum sativum]

208878 Seq. No. LIB3135-012-Q1-K1-F2 Seq. ID BLASTX Method g1808656 NCBI GI BLAST score 342 3.0e - 32E value 70 Match length 87 % identity (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum] NCBI Description 208879 Seq. No. LIB3135-012-Q1-K1-F3 Seq. ID BLASTX Method g1370589 NCBI GI 213 BLAST score 3.0e-17 E value 98 Match length % identity 51 (X98304) protein induced upon tuberization [Solanum NCBI Description demissum] 208880 Seq. No. LIB3135-012-Q1-K1-F4 Seq. ID BLASTX Method g3395436 NCBI GI 223 BLAST score 2.0e-18 E value 95 Match length % identity 43 (AC004683) unknown protein [Arabidopsis thaliana] NCBI Description 208881 Seq. No. LIB3135-012-Q1-K1-F9 Seq. ID BLASTX Method g1619300 NCBI GI 201 BLAST score 1.0e-15 E value 39 Match length 92 % identity (X95269) LRR protein [Lycopersicon esculentum] NCBI Description 208882 Seq. No. LIB3135-012-Q1-K1-G12 Seq. ID BLASTX Method g2983447 NCBI GI 241 BLAST score 1.0e-20 E value Match length 98 % identity

Seq. No. 208883

NCBI Description

[Aquifex aeolicus]

(AE000714) large subunit of isopropylmalate isomerase



```
LIB3135-012-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1771780
BLAST score
                  180
                  6.0e-29
E value
                  120
Match length
                  62
% identity
                  (Y10024) ubiquitin extension protein [Solanum tuberosum]
NCBI Description
                  208884
Seq. No.
Seq. ID
                  LIB3135-012-Q1-K1-G3
                  BLASTX
Method
NCBI GI
                  g2578033
                  255
BLAST score
                  1.0e-46
E value
Match length
                  98
% identity
                  94
NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]
                  208885
Seq. No.
Seq. ID
                  LIB3135-012-Q1-K1-G4
Method
                  BLASTN
                  g1418705
NCBI GI
                  108
BLAST score
                  1.0e-53
E value
Match length
                  340
                  92
% identity
NCBI Description G.hirsutum metallothionein-like gene
                  208886
Seq. No.
Seq. ID
                  LIB3135-012-Q1-K1-G5
Method
                  BLASTN
                  g167534
NCBI GI
BLAST score
                  168
                  1.0e-89
E value
                  259
Match length
                  92
% identity
NCBI Description Melon 17S rRNA, 5.8S rRNA, and 25S rRNA gene region
                  208887
Seq. No.
Seq. ID
                  LIB3135-012-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g585165
BLAST score
                  626
                  2.0e-65
E value
                  128
Match length
                  93
% identity
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                  (G6PD) >gi_2129985_pir S60287 glucose-6-phosphate
                  1-dehydrogenase (EC 1.1.1.49) - potato
                  >gi 471345 emb CAA52442 (X74421) glucose-6-phosphate
```

1-dehydrogenase [Solanum tuberosum]

208888 Seq. No.

Seq. ID LIB3135-012-Q1-K1-G8

Method BLASTX NCBI GI g3643608



BLAST score 289
E value 4.0e-26
Match length 101
% identity 56

NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 208889

Seq. ID LIB3135-012-Q1-K1-G9

Method BLASTX
NCBI GI g3334667
BLAST score 217
E value 9.0e-18
Match length 112
% identity 45

NCBI Description (Y10493) putative cytochrome P450 [Glycine max]

Seq. No. 208890

Seq. ID LIB3135-012-Q1-K1-H1

Method BLASTX
NCBI GI g508304
BLAST score 183
E value 1.0e-13
Match length 71
% identity 52

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 208891

Seq. ID LIB3135-012-Q1-K1-H10

Method BLASTN
NCBI GI g3334857
BLAST score 67
E value 2.0e-29
Match length 107
% identity 91

% identity 91
NCBI Description Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2

genes

Seq. No. 208892

Seq. ID LIB3135-012-Q1-K1-H2

Method BLASTX
NCBI GI g2745900
BLAST score 318
E value 9.0e-31
Match length 125
% identity 53

NCBI Description (AF039405) arsenite-translocating ATPase [Mus musculus]

Seq. No. 208893

Seq. ID LIB3135-012-Q1-K1-H5

Method BLASTX
NCBI GI g3393025
BLAST score 157
E value 8.0e-11
Match length 88
% identity 33

NCBI Description (AJ224000) tRNA (Guanine-N2-)-Methyltransferase

[Schizosaccharomyces pombe]



```
208894
Seq. No.
Seq. ID
                  LIB3135-012-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  408
E value
                  5.0e-40
                  89
Match length
% identity
                  87
                  (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
                  208895
Seq. No.
Seq. ID
                  LIB3135-013-Q1-K1-A12
                  BLASTN
Method
NCBI GI
                  g599722
                  36
BLAST score
                  6.0e-11
E value
Match length
                  76
                  87
% identity
                  C.melo mRNA for aconitase (UNI-ZAPxR)
NCBI Description
                  >gi 2300160 emb_A45787.1_A45787 Sequence 25 from Patent
                  WO9520046
                  208896
Seq. No.
Seq. ID
                  LIB3135-013-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q1173027
BLAST score
                  436
                  3.0e-43
E value
Match length
                  115
                  76
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
                  208897
Seq. No.
Seq. ID
                  LIB3135-013-Q1-K1-A7
                  BLASTX
Method
                  g3183088
NCBI GI
BLAST score
                  215
E value
                  3.0e-17
                  75
Match length
                  55
% identity
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                  (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
Seq. No.
                  208898
                  LIB3135-013-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006957
BLAST score
                  160
```

E value 4.0e-13
Match length 109
% identity 46

NCBI Description (AJ006910) pollen allergen Betv1, isoform at45 [Betula

pendula]



```
Seq. No.
                  208899
Seq. ID
                  LIB3135-013-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g267081
BLAST score
                  498
E value
                  2.0e-50
                  99
Match length
                  96
% identity
                  TUBULIN BETA-7 CHAIN >gi 320188 pir JQ1591 tubulin beta-7
NCBI Description
                  chain - Arabidopsis thalīana >gī_166906 (M84704) beta-7
                  tubulin [Arabidopsis thaliana] >gi 3980381 (AC004561)
                  tubulin beta-7 chain [Arabidopsis thaliana]
Seq. No.
                  208900
Seq. ID
                  LIB3135-013-Q1-K1-B5
                  BLASTX
Method
                  q120669
NCBI GI
BLAST score
                  435
                  4.0e-43
E value
Match length
                  87
                  92
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
                  208901
Seq. No.
Seq. ID
                  LIB3135-013-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4325324
BLAST score
                  157
                   6.0e-15
E value
Match length
                  95
                   51
% identity
                   (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  208902
Seq. ID
                  LIB3135-013-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2244834
BLAST score
                  106
                   1.0e-11
E value
Match length
                  72
% identity
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  208903
Seq. ID
                  LIB3135-013-Q1-K1-B8
```

Method BLASTX NCBI GI g1709498 BLAST score 461 2.0e-46 E value Match length 105 % identity 78

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis thaliana >gi 887390 emb\_CAA61411\_ (X89008) osmotin [Arabidopsis thaliana] Seq. No. 208904 LIB3135-013-Q1-K1-B9 Seq. ID Method BLASTX NCBI GI g4468050 BLAST score 442 E value 4.0e-44Match length 102 % identity 81 (X87099) S-adenosyl-L-methionine:caffeic acid NCBI Description 3-O-methyltransferase [Vanilla planifolia] Seq. No. 208905 Seq. ID LIB3135-013-Q1-K1-C2 Method BLASTX NCBI GI q462013 BLAST score 560 E value 1.0e-57 Match length 132 % identity 84 ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description >gi\_542022\_pir\_\_S39558 HSP90 homolog - Madagascar periwinkle >gi\_348696 (L14594) heat shock protein 90 [Catharanthus roseus] 208906 Seq. No.

Seq. ID LIB3135-013-Q1-K1-C4

Method BLASTX
NCBI GI g3334113
BLAST score 304
E value 1.0e-27
Match length 80
% identity 74

NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >qi 1006831 (U35015)

acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No. 208907

Seq. ID LIB3135-013-Q1-K1-C5

Method BLASTX
NCBI GI g1732204
BLAST score 220
E value 6.0e-18
Match length 124
% identity 40

NCBI Description (U65015) putative aldolase [Vibrio furnissii]

Seq. No. 208908

Seq. ID LIB3135-013-Q1-K1-C7

Method BLASTX
NCBI GI 94490292
BLAST score 350
E value 4.0e-33
Match length 99



208909

% identity (AL035678) putative protein [Arabidopsis thaliana] NCBI Description

LIB3135-013-Q1-K1-C8 Seq. ID BLASTX Method g2144186 NCBI GI BLAST score 719 2.0e-76 E value

145 Match length 93 % identity

Seq. No.

farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) 1 -NCBI Description

Glycyrrhiza glabra L >gi 1449163 dbj BAA13083 (D86409)

squalene synthase [Glycyrrhiza glabra]

208910 Seq. No.

LIB3135-013-Q1-K1-C9 Seq. ID

BLASTX Method g3123130 NCBI GI 155 BLAST score 1.0e-10 E value Match length 81 % identity 42

HYPOTHETICAL 61.8 KD TRP-ASP REPEATS CONTAINING PROTEIN NCBI Description

T32G6.2 IN CHROMOSOME II >gi 2618685 (AC002510) putative

small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana] >qi 3241948 (AC004625) putative small nuclear

ribonucleoprotein Prp4p [Arabidopsis thaliana]

208911 Seq. No.

Seq. ID LIB3135-013-Q1-K1-D11

BLASTX Method g2829899 NCBI GI 238 BLAST score 1.0e-23 E value 137 Match length 44 % identity

(AC002311) similar to ripening-induced protein, NCBI Description

gp\_AJ001449\_2465015 and major#latex protein,

gp X91961\_1107495 [Arabidopsis thaliana]

208912 Seq. No.

Seq. ID LIB3135-013-Q1-K1-D2

Method BLASTX NCBI GI g2262098 143 BLAST score 5.0e-09 E value 47 Match length % identity

(AC002343) HSP90 isolog [Arabidopsis thaliana] NCBI Description

Seq. No. 208913

LIB3135-013-Q1-K1-D3 Seq. ID

Method BLASTX NCBI GI q2088653 BLAST score 411 E value 3.0e-40



Match length 148 % identity 54

NCBI Description (AF002109) Hs1pro-1 related protein isolog [Arabidopsis

thaliana]

Seq. No. 208914

Seq. ID LIB3135-013-Q1-K1-D4

Method BLASTX
NCBI GI g2464852
BLAST score 241
E value 2.0e-20
Match length 109
% identity 50

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 208915

Seq. ID LIB3135-013-Q1-K1-D7

Method BLASTX
NCBI GI g4490292
BLAST score 330
E value 9.0e-31
Match length 99

% identity 66

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 208916

Seq. ID LIB3135-013-Q1-K1-E3

Method BLASTN
NCBI GI g2695738
BLAST score 146
E value 2.0e-76
Match length 205
% identity 93

NCBI Description Pisum sativum mitochondrial tRNA-Gly gene and flanking

sequences

Seq. No. 208917

Seq. ID LIB3135-013-Q1-K1-E4

Method BLASTX
NCBI GI 94539405
BLAST score 587
E value 7.0e-61
Match length 141
% identity 79

NCBI Description (AL049524) putative ribosomal protein L9, cytosolic

[Arabidopsis thaliana]

Seq. No. 208918

Seq. ID LIB3135-013-Q1-K1-F1

Method BLASTN
NCBI GI g2213876
BLAST score 49
E value 2.0e-18
Match length 77

% identity 91

NCBI Description Hevea brasiliensis glutamine synthetase mRNA, complete cds



Seq. No. 208919 Seq. ID LIB3135-013-Q1-K1-F10 Method BLASTX NCBI GI g4544399 BLAST score 260 E value 1.0e-22 98 Match length 50 % identity

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 208920

Seq. ID LIB3135-013-Q1-K1-F11

Method BLASTX
NCBI GI g3928758
BLAST score 437
E value 2.0e-43
Match length 113
% identity 76

NCBI Description (AB007987) Lipoic acid synthase [Arabidopsis thaliana]

>gi 4454462 gb AAD20909 (AC006234) putative lipoic acid

synthase [Arabidopsis thaliana]

Seq. No. 208921

Seq. ID LIB3135-013-Q1-K1-F2

Method BLASTX
NCBI GI g3096939
BLAST score 187
E value 2.0e-14
Match length 86
% identity 45

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 208922

Seq. ID LIB3135-013-Q1-K1-F4

Method BLASTX
NCBI GI g927428
BLAST score 606
E value 4.0e-63
Match length 130
% identity 85

NCBI Description (X86733) fis1 [Linum usitatissimum]

Seq. No. 208923

Seq. ID LIB3135-013-Q1-K1-F9

Method BLASTX
NCBI GI g2865175
BLAST score 312
E value 1.0e-28
Match length 79
% identity 70

NCBI Description (AB010945) AtRer1A [Arabidopsis thaliana]

Seq. No. 208924

Seq. ID LIB3135-013-Q1-K1-G10

Method BLASTX NCBI GI q2827528



```
BLAST score
                  5.0e-18
E value
                  136
Match length
                  39
% identity
                  (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                  208925
Seq. No.
                  LIB3135-013-Q1-K1-G2
Seq. ID
                  BLASTN
Method
                  q3334857
NCBI GI
BLAST score
                  249
E value
                  1.0e-138
Match length
                  348
                   93
% identity
                  Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2
NCBI Description
                  genes
                   208926
Seq. No.
                  LIB3135-013-Q1-K1-G4
Seq. ID
                  BLASTN
Method
                   g167366
NCBI GI
                   292
BLAST score
E value
                   1.0e-163
Match length
                   327
                   97
% identity
                  Gossypium hirsutum peroxidase mRNA, complete cds
NCBI Description
                   208927
Seq. No.
                   LIB3135-013-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g3885884
NCBI GI
                   739
BLAST score
                   1.0e-78
E value
                   149
Match length
                   91
% identity
                   (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                   208928
Seq. No.
                   LIB3135-013-Q1-K1-H1
Seq. ID
Method
                   BLASTX
                   q4388829
NCBI GI
                   200
BLAST score
                   2.0e-15
E value
Match length
                   86
 % identity
                   51
                   (AC006528) putative pol polyprotein with a Zn-finger CCHC
NCBI Description
                   type domain (prosite:QDOC50158) and a DDE integrase
                   signature motif [Arabidopsis thaliana]
                   208929
 Seq. No.
                   LIB3135-013-Q1-K1-H11
```

Seq. ID

BLASTX Method g3047123 NCBI GI 587 BLAST score 7.0e-61 E value 134 Match length 83 % identity



NCBI Description (AF058919) similar to the family of glycosyl hydrolases [Arabidopsis thaliana]

Seq. No. 208930

Seq. ID LIB3135-013-Q1-K1-H6

Method BLASTX
NCBI GI g100519
BLAST score 162
E value 5.0e-11
Match length 88
% identity 44

NCBI Description hypothetical protein 873 - common sunflower

>gi\_12992\_emb\_CAA44478\_ (X62592) ORF 873 [Helianthus
annuus] >gi\_758363\_emb\_CAA37614\_ (X53537) orfH522

[Helianthus annuus]

Seq. No. 208931

Seq. ID LIB3135-014-Q1-K1-A1

Method BLASTX
NCBI GI g2129772
BLAST score 405
E value 6.0e-40
Match length 82
% identity 87

NCBI Description xyloglucan endotransglycosylase-related protein XTR-7 -

Arabidopsis thaliana >gi\_1244760 (U43489) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No. 208932

Seq. ID LIB3135-014-Q1-K1-A10

Method BLASTX
NCBI GI g131773
BLAST score 225
E value 3.0e-27
Match length 95
% identity 73

NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)

>gi 82724\_pir\_\_B30097 ribosomal protein S14 (clone MCH2) -

maize

Seq. No. 208933

Seq. ID LIB3135-014-Q1-K1-A11

Method BLASTX
NCBI GI g4206197
BLAST score 166
E value 1.0e-11
Match length 50
% identity 62

NCBI Description (AF071527) putative pre-mRNA splicing factor [Arabidopsis

thaliana]

Seq. No. 208934

Seq. ID LIB3135-014-Q1-K1-A12

Method BLASTX
NCBI GI g100351
BLAST score 293
E value 1.0e-26



```
Match length 60
% identity 90
NCBI Description pathogenesis-related protein 4A - common tobacco
>gi_19962_emb_CAA41437_(X58546) pathogenesis-related
protein 4A [Nicotiana tabacum]

Seq. No. 208935
Seq. ID LIB3135-014-Q1-K1-A2
Method BLASTX

23461837
```

Method BLASTX
NCBI GI g3461837
BLAST score 418
E value 4.0e-41
Match length 90
% identity 83

NCBI Description (AC005315) putative expansin [Arabidopsis thaliana] >qi 3927842 (AC005727) expansin AtEx6 [Arabidopsis

thaliana]

Seq. No. 208936

Seq. ID LIB3135-014-Q1-K1-A3

Method BLASTX
NCBI GI 9416569
BLAST score 183
E value 4.0e-14
Match length 38
% identity 89

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE 1 (ACC OXIDASE)

(ETHYLENE-FORMING ENZYME) (EFE) (PMEL1)

>gi\_322412\_pir\_\_S29395 ethylene-forming enzyme - muskmelon >gi\_2129501\_pir\_\_JC6059 1-aminocyclopropane-1-carboxylic

acid oxidase (EC 1.-.-.) - muskmelon

>qi 2129502 pir S66174 ACC oxidase (clone ACO1) -

muskmelon >gi\_22663\_emb\_CAA49553\_ (X69935) enzyme-forming ethylene [Cucumis melo] >gi\_695400\_dbj\_BAA06526\_ (D31727) 1-aminocyclopropane-1-carboxylate oxidase [Cucumis melo] >gi\_1183896\_emb\_CAA64797\_ (X95551) ACC oxidase [Cucumis

melo]

Seq. No. 208937

Seq. ID LIB3135-014-Q1-K1-A4

Method BLASTX
NCBI GI g1129145
BLAST score 511
E value 4.0e-52
Match length 128
% identity 80

NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 208938

Seq. ID LIB3135-014-Q1-K1-A7

Method BLASTX
NCBI GI g2911073
BLAST score 267
E value 9.0e-24
Match length 89
% identity 58

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Match length

% identity

.93



```
208939
Seq. No.
Seq. ID
                  LIB3135-014-Q1-K1-B2
                  BLASTX
Method
                  g3122673
NCBI GI
                  150
BLAST score
                  7.0e-12
E value
                  56
Match length
                  71
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  208940
Seq. No.
                  LIB3135-014-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g3334244
NCBI GI
                   326
BLAST score
                   2.0e-39
E value
                   111
Match length
                   72
% identity
                  LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
NCBI Description
                   (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                   >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica
                   juncea]
                   208941
Seq. No.
                   LIB3135-014-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g4558672
NCBI GI
                   188
BLAST score
                   2.0e-14
E value
Match length
                   53
                   68
% identity
                   (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
                   thaliana]
                   208942
Seq. No.
                   LIB3135-014-Q1-K1-B8
Seq. ID
                   BLASTN
Method
                   g1389639
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
Match length
                   78
                   86
% identity
                   Pisum sativum mRNA for PNDKN1, complete cds
NCBI Description
                   >gi 3252749 dbj_E13982_E13982 Pisum sativum mRNA for
                   nucleoside-diphosphate kinase
                   208943
Seq. No.
                   LIB3135-014-Q1-K1-B9
Seq. ID
Method
                   BLASTX
                   q549063
NCBI GI
BLAST score
                   246
E value
                   3.0e-21
```



NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 208944

Seq. ID LIB3135-014-Q1-K1-C12

Method BLASTX
NCBI GI g2493495
BLAST score 336
E value 2.0e-31
Match length 82
% identity 74

NCBI Description SERINE CARBOXYPEPTIDASE-LIKE >gi\_2129878\_pir\_\_S72370

carboxypeptidase - garden pea (fragment)

>gi 1089904 emb CAA92216\_ (Z68130) carboxypeptidase [Pisum sativum] >gi 1587217\_prf 2206338A Ser carboxypeptidase

[Pisum sativum]

Seq. No. 208945

Seq. ID LIB3135-014-Q1-K1-C4

Method BLASTX
NCBI GI g4558556
BLAST score 182
E value 5.0e-14
Match length 58
% identity 60

NCBI Description (AC007138) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 208946

Seq. ID LIB3135-014-Q1-K1-C7

Method BLASTX
NCBI GI g2827544
BLAST score 325
E value 2.0e-30
Match length 81
% identity 77

NCBI Description (AL021635) HSP associated protein like [Arabidopsis

thaliana]

Seq. No. 208947

Seq. ID LIB3135-014-Q1-K1-C9

Method BLASTX
NCBI GI g1362078
BLAST score 385
E value 2.0e-37
Match length 97
% identity 69

NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)

- common nasturtium >gi 311835 emb CAA48324 (X68254)

cellulase [Tropaeolum majus]

Seq. No. 208948

Seq. ID LIB3135-014-Q1-K1-D1

Method BLASTX NCBI GI g3759177



BLAST score 190 E value 6.0e-15 Match length 65 % identity 62

NCBI Description (AB018408) 3-phosphoserine phosphatase [Arabidopsis

thaliana] >gi\_3759179\_dbj\_BAA33807\_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No. 208949

Seq. ID LIB3135-014-Q1-K1-D3

Method BLASTN
NCBI GI g871468
BLAST score 60
E value 3.0e-25

E value 3.0e-29
Match length 230
% identity 90

NCBI Description H.annuus mitochondrion genes trnH and trnE

Seq. No. 208950

Seq. ID LIB3135-014-Q1-K1-D9

Method BLASTX
NCBI GI g1350983
BLAST score 428
E value 3.0e-42
Match length 102
% identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYCO7 PROTEIN)

Seq. No. 208951

Seq. ID LIB3135-014-Q1-K1-E1

Method BLASTX
NCBI GI g2529665
BLAST score 389
E value 4.0e-38
Match length 82
% identity 90

% identity 90 NCBI Description (AC002535) putative ribosomal protein L7A [Arabidopsis

thaliana]

Seq. No. 208952

Seq. ID LIB3135-014-Q1-K1-E12

Method BLASTX
NCBI GI g3287834
BLAST score 393
E value 4.0e-41
Match length 92
% identity 95

NCBI Description (+)-DELTA-CADINENE SYNTHASE ISOZYME XC14 (D-CADINENE

SYNTHASE) >gi\_2147016\_pir\_\_S68366 (+)-delta-cadinene synthase isozyme XC14 - Gossypium arboreum >gi\_1045314

ر پیشیر

(U23205) (+)-delta-cadinene synthase isozyme XC14

[Gossypium arboreum]

Seq. No. 208953

Seq. ID LIB3135-014-Q1-K1-E4

Method BLASTN NCBI GI g18506

Match length

% identity

103

85



```
BLAST score
                  1.0e-61
E value
Match length
                  203
                   90
% identity
                  Cotton mRNA for malate synthase (EC 4.1.3.2)
NCBI Description
                  208954
Seq. No.
                  LIB3135-014-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529665
BLAST score
                  170
                  2.0e-12
E value
                  52
Match length
                   67
% identity
                   (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                  thaliana]
                   208955
Seq. No.
Seq. ID
                  LIB3135-014-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  q3892054
BLAST score
                  185
                   2.0e-14
E value
                   54
Match length
% identity
                   61
                   (AC002330) putative glycosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                   208956
Seq. No.
Seq. ID
                  LIB3135-014-Q1-K1-E7
                  BLASTX
Method
NCBI GI
                   g3738323
BLAST score
                   411
                   2.0e-40
E value
                   96
Match length
                   76
% identity
                  (AC005170) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   208957
Seq. No.
                  LIB3135-014-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3064039
BLAST score
                   273
                   4.0e-24
E value
Match length
                   127
% identity
                   43
NCBI Description
                   (AF054445) major latex protein homolog [Mesembryanthemum
                   crystallinum]
Seq. No.
                   208958
Seq. ID
                   LIB3135-014-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   g2341032
BLAST score
                   472
E value
                   1.0e-47
```



NCBI Description (AC000104) EST gb\_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No. 208959

Seq. ID LIB3135-014-Q1-K1-F11

Method BLASTX
NCBI GI g4185143
BLAST score 369
E value 1.0e-35
Match length 103
% identity 71

NCBI Description (AC005724) putative signal recognition particle receptor

beta subunit [Arabidopsis thaliana]

Seq. No. 208960

Seq. ID LIB3135-014-Q1-K1-F2

Method BLASTX
NCBI GI g81624
BLAST score 202
E value 2.0e-16
Match length 46
% identity 80

NCBI Description glycine-rich protein 2 - Arabidopsis thaliana

>gi\_259445\_bbs\_117608 (S47408) glycine-rich protein, atGRP {clone atGRP-2} [Arabidopsis thaliana, C24, Peptide, 203 aa] [Arabidopsis thaliana] >gi\_4467155\_emb\_CAB37524\_ (AL035540) glycine-rich protein 2 (GRP2) [Arabidopsis

thaliana]

Seq. No. 208961

Seq. ID LIB3135-014-Q1-K1-F3

Method BLASTX
NCBI GI g3643607
BLAST score 491
E value 1.0e-49
Match length 132
% identity 70

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 208962

Seq. ID LIB3135-014-Q1-K1-F4

Method BLASTX
NCBI GI g1709498
BLAST score 296
E value 8.0e-27
Match length 111
% identity 57

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis

thaliana  $>gi_887390$ \_emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 208963

Seq. ID LIB3135-014-Q1-K1-F9

Method BLASTN NCBI GI g2829205 BLAST score 101

```
E value
                  350
Match length
                  23
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  208964
Seq. No.
                  LIB3135-014-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q134792
                  155
BLAST score
E value
                  2.0e-10
                  76
Match length
                  43
% identity
                  MICROSOMAL SIGNAL PEPTIDASE 21 KD SUBUNIT (SPC21)
NCBI Description
                  >gi_89064_pir__A34229 signal peptidase (EC 3.4.99.-) 21K
                  chain - dog >gi 164084 (J05069) signal peptidase 21 kDa
                  subunit [Canis familiaris]
                  208965
Seq. No.
                  LIB3135-014-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                  g2146797
NCBI GI
                  336
BLAST score
                   2.0e-31
E value
                   91
Match length
                   38
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                   >gi_1134968 (U41385) protein disulphide isomerase PDI
                   [Ricinus communis] >gi_1587210_prf__2206331A protein
                   disulfide isomerase [Ricinus communis]
                   208966
Seq. No.
                   LIB3135-014-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   g2739004
NCBI GI
                   156
BLAST score
                   8.0e-11
E value
                   67
Match length
                   40
% identity
                  (AF022461) CYP82C1p [Glycine max]
NCBI Description
                   208967
Seq. No.
                   LIB3135-014-Q1-K1-G2
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g2258135
BLAST score 335
E value 5.0e-32
Match length 68
% identity 97

NCBI Description (Z83830) porin [Picea abies]

Seq. No. 208968

Seq. ID LIB3135-014-Q1-K1-G3

Method BLASTX NCBI GI g3747050

BLAST score 278

NCBI GI

E value Match length

BLAST score

g1703375

233 9.0e-20



```
E value
                   4.0e-25
Match length
                  75
% identity
                  75
NCBI Description
                  (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                  208969
Seq. ID
                  LIB3135-014-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2739389
BLAST score
                  181
E value
                  1.0e-21
Match length
                  91
                  34
% identity
NCBI Description (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
                  208970
Seq. No.
                  LIB3135-014-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  g1717949
NCBI GI
BLAST score
                  310
E value
                  1.0e-28
Match length
                  73
% identity
                  77
NCBI Description
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1)
                  >gi_100375_pir__B41607 ubiquinol--cytochrome-c reductase
                  (EC 1.10.2.2) iron-sulfur protein precursor - common
                  tobacco (fragment) >gi 170322 (M77225) Rieske Fe-S protein
                  [Nicotiana tabacum]
Seq. No.
                  208971
Seq. ID
                  LIB3135-014-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  173
                  3.0e-22
E value
Match length
                  88
% identity
                  65
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  208972
                  LIB3135-014-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1853968
BLAST score
                  182
E value
                  2.0e-13
Match length
                  68
% identity
                  53
NCBI Description (D88121) CPRD12 protein [Vigna unguiculata]
Seq. No.
                  208973
Seq. ID
                  LIB3135-014-Q1-K1-H2
Method
                  BLASTX
```



Seq. No. 208974

Seq. ID LIB3135-014-Q1-K1-H3

Method BLASTX
NCBI GI 94210332
BLAST score 311
E value 1.0e-28
Match length 103
% identity 65

NCBI Description (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit

[Arabidopsis thaliana]

Seq. No. 208975

Seq. ID LIB3135-014-Q1-K1-H4

Method BLASTX
NCBI GI g2586153
BLAST score 225
E value 4.0e-19
Match length 61
% identity 70

NCBI Description (AF001530) ripening-associated protein [Musa acuminata]

Seq. No. 208976

Seq. ID LIB3135-014-Q1-K1-H5

Method BLASTX
NCBI GI g3204103
BLAST score 198
E value 1.0e-15
Match length 60
% identity 67

NCBI Description (AJ006761) hypothetical protein [Cicer arietinum]

Seq. No. 208977

Seq. ID LIB3135-014-Q1-K1-H7

Method BLASTX
NCBI GI g2462929
BLAST score 231
E value 3.0e-19
Match length 59
% identity 69

NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 208978

Seq. ID LIB3135-014-Q1-K1-H8

Method BLASTX
NCBI GI g3935169
BLAST score 190
E value 7.0e-15
Match length 53
% identity 68

NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No. 208979

Seq. ID LIB3135-018-Q1-K1-A10



```
BLASTN
Method
                  g2829205
NCBI GI
BLAST score
                  187
                  1.0e-101
E value
                  423
Match length
                  19
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  208980
Seq. No.
                  LIB3135-018-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567197
                  260
BLAST score
                   1.0e-22
E value
                   115
Match length
% identity
                  (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   208981
Seq. No.
                   LIB3135-018-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2369766
BLAST score
                   234
E value
                   1.0e-19
                   45
Match length
                   96
% identity
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   208982
Seq. No.
Seq. ID
                   LIB3135-018-Q1-K1-A7
Method
                   BLASTX
                   g2459420
NCBI GI
BLAST score
                   442
                   6.0e-44
E value
Match length
                   89
% identity
                   94
                   (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                   thaliana]
                   208983
Seq. No.
                   LIB3135-018-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703446
BLAST score
                   246
                   3.0e-21
E value
Match length
                   84
                   62
% identity
                   L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi 1076292 pir S53127 asparaginase - Arabidopsis thaliana
                   thaliana]
```

>qi 735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis

208984 Seq. No.

LIB3135-018-Q1-K1-B2 Seq. ID

BLASTX Method g2924781 NCBI GI

```
BLAST score 498
E value 3.0e-52
Match length 134
% identity 77
NCBI Description (AC002334 thaliana)
```

ICBI Description (AC002334) putative cellulose synthase [Arabidopsis

Seq. No. 208985

Seq. ID LIB3135-018-Q1-K1-B3

Method BLASTX
NCBI GI g124224
BLAST score 250
E value 2.0e-30
Match length 120
% identity 62

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi 100345\_pir\_\_S21060 translation initiation factor eIF-5A

- common tobacco >gi\_19887\_emb\_CAA45105\_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 208986

Seq. ID LIB3135-018-Q1-K1-B5

Method BLASTX
NCBI GI g3892051
BLAST score 186
E value 6.0e-14
Match length 45
% identity 78

NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit

[Arabidopsis thaliana]

Seq. No. 208987

Seq. ID LIB3135-018-Q1-K1-C10

Method BLASTX
NCBI GI g132944
BLAST score 542
E value 1.0e-55
Match length 107
% identity 93

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi\_81658\_pir\_\_JQ0772 ribosomal

protein L3 (ARP2) - Arabidopsis thaliana >gi\_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 208988

Seq. ID LIB3135-018-Q1-K1-C11

Method BLASTX
NCBI GI g461812
BLAST score 164
E value 3.0e-14
Match length 101
% identity 46

NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE

GERANIOL-10-HYDROXYLASE) (GE10H) >gi 167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]

>gi 445604\_prf\_\_1909351A cytochrome P450 [Catharanthus

roseus]



```
208989
Seq. No.
                  LIB3135-018-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                  g3861189
NCBI GI
                  236
BLAST score
                  6.0e-20
E value
Match length
                  105
                  50
% identity
                  (AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia
NCBI Description
                  prowazekii]
Seq. No.
                  208990
                  LIB3135-018-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g133793
NCBI GI
                  146
BLAST score
                  2.0e-09
E value
Match length
                  54
                   65
% identity
                  40S RIBOSOMAL PROTEIN S15A (PPCB8) >gi 99825 pir S20945
NCBI Description
                   ribosomal protein S15a - rape >gi_17863_emb_CAA42599_
                   (X59983) r-protein BnS15a [Brassica napus]
Seq. No.
                   208991
                   LIB3135-018-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                   g2894109
NCBI GI
                   213
BLAST score
                   8.0e-24
E value
Match length
                   70
                   77
% identity
                   (AJ002391) high mobility group protein [Solanum tuberosum]
NCBI Description
                   208992
Seq. No.
                   LIB3135-018-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   q300265
NCBI GI
                   509
BLAST score
                   9.0e-52
E value
                   144
Match length
                   76
% identity
                   HSP68=68 kda heat-stress DnaK homolog [Lycopersicon
NCBI Description
                   peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]
                   208993
Seq. No.
                   LIB3135-018-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   g2708314
NCBI GI
                   231
BLAST score
                   3.0e-19
E value
                   128
Match length
                   30
 % identity
                   (AF027727) protein disulfide isomerase RB60 [Chlamydomonas
 NCBI Description
                   reinhardtii] >gi 4104541 (AF036939) protein disulfide
                   isomerase [Chlamydomonas reinhardtii]
```

Seq. No. 208994

```
LIB3135-018-Q1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q434990
                  45
BLAST score
                  4.0e-16
E value
                  120
Match length
% identity
                  93
NCBI Description O.berteriana mitochondrial trnI gene
                  208995
Seq. No.
                  LIB3135-018-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024020
                   437
BLAST score
                   2.0e-43
E value
                   97
Match length
                   86
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation
                   factor 5A3 [Solanum tuberosum]
                   208996
Seq. No.
Seq. ID
                   LIB3135-018-Q1-K1-D3
Method
                   BLASTX
                   q3334115
NCBI GI
                   610
BLAST score
                   2.0e-70
E value
                   141
Match length
% identity
                   48
                   ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
                   208997
Seq. No.
                   LIB3135-018-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   q3236253
NCBI GI
                   629
BLAST score
                   7.0e-66
E value
                   138
Match length
                   85
% identity
                   (AC004684) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   208998
Seq. No.
                   LIB3135-018-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   q3860323
NCBI GI
BLAST score
                   223
                   4.0e-19
E value
                   63
Match length
                   81
 % identity
                  (AJ012688) hypothetical protein [Cicer arietinum]
NCBI Description
```

28827

208999

LIB3135-018-Q1-K1-E11

Seq. No.

Seq. ID

```
Method
                   BLASTX
NCBI GI
                   q2880051
BLAST score
                   148
E value
                   2.0e-09
Match length
                   44
% identity
                   64
NCBI Description
                   (AC002340) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   209000
Seq. ID
                   LIB3135-018-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   q629597
BLAST score
                   349
E value
                   6.0e-33
Match length
                   83
% identity
                   77
NCBI Description
                   proline-rich protein - rape >gi 545029 bbs 142669 (S68113)
                   proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                   Peptide, 147 aa] [Brassica napus]
Seq. No.
                   209001
Seq. ID
                   LIB3135-018-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g1086263
BLAST score
                   152
E value
                   4.0e-13
Match length
                   79
% identity
                   57
NCBI Description
                   TMV resistance protein N - tobacco (Nicotiana glutinosa)
                   >gi_558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                   209002
                   LIB3135-018-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3892058
BLAST score
                   312
E value
                   1.0e-28
Match length
                   107
% identity
                   55
NCBI Description
                   (AC002330) putative glutamate-/aspartate-binding peptide
                   [Arabidopsis thaliana]
Seq. No.
                   209003
Seq. ID
                  LIB3135-018-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                   q3914442
BLAST score
                  279
E value
                   1.0e-36
Match length
                  104
% identity
                  68
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
```

Seq. No. 209004

Seq. ID LIB3135-018-Q1-K1-F12

Method BLASTX

```
q2995384
NCBI GI
BLAST score
                  284
                  1.0e-25
E value
                  92
Match length
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  209005
Seq. No.
                  LIB3135-018-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g3647335
NCBI GI
                  153
BLAST score
                  5.0e-10
E value
Match length
                  70
                  43
% identity
                  (AL031644) possible zinc-finger protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   209006
Seq. No.
                  LIB3135-018-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g3549691
NCBI GI
BLAST score
                   626
E value
                   2.0e-65
Match length
                   142
                   75
% identity
NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
                   209007
Seq. No.
                   LIB3135-018-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g2558962
NCBI GI
                   229
BLAST score
E value
                   5.0e-19
                   67
Match length
% identity
                   73
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
Seq. No.
                   209008
                   LIB3135-018-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3128180
BLAST score
                   447
                   2.0e-44
E value
Match length
                   96
                   86
% identity
NCBI Description (AC004521) citrate synthetase [Arabidopsis thaliana]
                   209009
Seq. No.
                   LIB3135-018-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                   g1170949
NCBI GI
BLAST score
                   349
                   3.0e-33
E value
                   88
Match length
                   70
% identity
NCBI Description SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir__S38327
```

E value

Match length



protein kinase - Arabidopsis thaliana >gi 166811 (L07249) protein kinase [Arabidopsis thaliana]

```
209010
Seq. No.
                  LIB3135-018-Q1-K1-G4
Seq. ID
                  {\tt BLASTX}
Method
                  g2245060
NCBI GI
                  304
BLAST score
                  5.0e-28
E value
                  89
Match length
                  62
% identity
                  (Z97342) allergen homolog [Arabidopsis thaliana]
NCBI Description
                   209011
Seq. No.
                  LIB3135-018-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g2505867
NCBI GI
                   253
BLAST score
                   8.0e-22
E value
Match length
                   88
% identity
                   28
                  (Y12227) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   209012
Seq. No.
                   LIB3135-018-Q1-K1-G9
Seq. ID
Method
                   BLASTX
                   q4580397
NCBI GI
                   234
BLAST score
                   2.0e-19
E value
                   129
Match length
% identity
                   42
                  (AC007171) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
                   209013
Seq. No.
                   LIB3135-018-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   q2497737
NCBI GI
                   156
BLAST score
                   7.0e-11
E value
                   60
Match length
                   52
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                   >gi 732524 (U22175) germination-specific lipid transfer
                   protein 3 [Brassica napus]
                   209014
Seq. No.
                   LIB3135-018-Q1-K1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2129820
                   177
BLAST score
```

% identity 48 chitinase (EC 3.2.1.14) class II - peanut NCBI Description

>gi 1237025\_emb\_CAA57773\_ (X82329) chitinase (class II) [Arachis hypogaea]

3.0e-13

```
209015
Seq. No.
Seq. ID
                   LIB3135-018-Q1-K1-H2
                   BLASTX
Method
                   q4455242
NCBI GI
                   401
BLAST score
                   3.0e-39
E value
                   91
Match length
                   79
% identity
                   (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis
NCBI Description
                   thaliana]
                   209016
Seq. No.
                   LIB3135-018-Q1-K1-H5
Seq. ID
Method
                   BLASTX
                   q2213643
NCBI GI
                   280
BLAST score
                   2.0e-25
E value
Match length
                   78
                   73
% identity
                   (U57338) glossyl homolog [Oryza sativa]
NCBI Description
                   209017
Seq. No.
                   LIB3135-018-Q1-K1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3128139
BLAST score
                   50
                   2.0e-19
E value
                    94
Match length
                    88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIK19, complete sequence [Arabidopsis thaliana]
                    209018
Seq. No.
Seq. ID
                    LIB3135-019-Q1-K1-A11
                    BLASTX
Method
NCBI GI
                    g120669
BLAST score
                    531
                    2.0e-54
E value
                    105
Match length
% identity
                    94
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                    >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                    >gi 19566 emb CAA42905_ (X60347) glyceraldehyde
                    3-phosphate dehydrogenase [Magnolia liliiflora]
                    209019
Seq. No.
Seq. ID
                    LIB3135-019-Q1-K1-A12
                    BLASTX
Method
NCBI GI
                    q122770
                    543
BLAST score
```

Match length 123 % identity 85

E value

NCBI Description HEMOGLOBIN II >gi\_99509\_pir\_\_S13378 hemoglobin II - swamp oak >gi\_18015\_emb\_CAA37898\_ (X53950) hemoglobin [Casuarina

glauca]

1.0e-55



```
209020
Seq. No.
                  LIB3135-019-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g602076
NCBI GI
BLAST score
                  552
                  6.0e-57
E value
Match length
                  113
                  23
% identity
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
Seq. No.
                  209021
                  LIB3135-019-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1903034
                  238
BLAST score
                  4.0e-20
E value
Match length
                  105
                   45
% identity
NCBI Description (X94625) amp-binding protein [Brassica napus]
                   209022
Seq. No.
Seq. ID
                  LIB3135-019-Q1-K1-A8
Method
                  BLASTX
                   q3493172
NCBI GI
                   289
BLAST score
                   2.0e-26
E value
                   81
Match length
% identity
                   72
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
                   209023
Seq. No.
                   LIB3135-019-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g730324
                   376
BLAST score
                   1.0e-36
E value
                   83
Match length
% identity
                   80
                   DEOXYRIBODIPYRIMIDINE PHOTOLYASE (DNA PHOTOLYASE)
NCBI Description
                   (PHOTOREACTIVATING ENZYME) >gi_1084356_pir__S48120
                   deoxyribodipyrimidine photo-lyase (EC \overline{4.1.99.3}) - white
                   mustard >gi_414196_emb_CAA50898_ (X72019) photolyase
                   [Sinapis alba]
                   209024
 Seq. No.
                   LIB3135-019-Q1-K1-B10
 Seq. ID
                   BLASTX
Method
                   g4062934
NCBI GI
                   335
BLAST score
                   2.0e-31
E value
                   123
Match length
 % identity
 NCBI Description (D88272) formate dehydrogenase [Hordeum vulgare]
```

209025

LIB3135-019-Q1-K1-B5

Seq. No.

Seq. ID



```
Method
                   BLASTX
                  g3901018
NCBI GI
BLAST score
                   164
                   1.0e-11
E value
Match length
                   82
                   46
% identity
                   (AJ130889) stress and pathogenesis-related protein [Fagus
NCBI Description
                   sylvatica]
                   209026
Seq. No.
                   LIB3135-019-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g485393
NCBI GI
BLAST score
                   259
                   4.0e-23
E value
                   65
Match length
                   80
% identity
                   (D30653) peroxidase [Populus kitakamiensis]
NCBI Description
                 209027
Seq. No.
                   LIB3135-019-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g4558665
NCBI GI
                   150
BLAST score
                   9.0e-11
E value
                   64
Match length
                   60
% identity
                   (AC007063) putative white protein [Arabidopsis thaliana]
NCBI Description
                   209028
Seq. No.
                   LIB3135-019-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   q3334112
NCBI GI
BLAST score
                   265
                   1.0e-23
E value
Match length
                   77
                   65
% identity
                   ACYL-COA-BINDING PROTEIN (ACBP) >gi 1938236 emb CAA70200
NCBI Description
                   (Y08996) acyl-CoA-binding protein [Ricinus communis]
                   209029
Seq. No.
                   LIB3135-019-Q1-K1-C7
Seq. ID
                   BLASTN
Method
                   g2341023
NCBI GI
BLAST score
                   54
                   1.0e-21
E value
                   90
Match length
                   91
 % identity
                   Sequence of BAC F19P19 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   209030
 Seq. No.
                   LIB3135-019-Q1-K1-D1
 Seq. ID
                   BLASTX
 Method
```

Method BLASTX
NCBI GI g1134957
BLAST score 144
E value 4.0e-09

NCBI Description

Seq. No.

209036



```
Match length
% identity
                   34
NCBI Description
                  (U41162) unidentified ORF [Burkholderia cepacia]
Seq. No.
                   209031
Seq. ID
                  LIB3135-019-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4165323
BLAST score
                  459
                  3.0e-46
E value
Match length
                  92
% identity
                  89
NCBI Description
                  (AB022442) p-type H+-ATPase [Vicia faba]
                  209032
Seq. No.
                  LIB3135-019-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469025
BLAST score
                  178
                  5.0e-16
E value
Match length
                  70
% identity
                  39
NCBI Description
                  (AL035602) putative protein [Arabidopsis thaliana]
                  209033
Seq. No.
Seq. ID
                  LIB3135-019-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3075394
BLAST score
                   274
E value
                  1.0e-24
                  87
Match length
                  70
% identity
                   (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
                  209034
Seq. No.
                  LIB3135-019-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1477428
BLAST score
                  346
E value
                  9.0e-41
Match length
                  106
% identity
                  88
NCBI Description
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
                  209035
Seq. No.
                  LIB3135-019-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  410
                  3.0e-40
E value
Match length
                  103
% identity
```

28834

(AC004665) unknown protein [Arabidopsis thaliana]

```
LIB3135-019-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2462753
BLAST score
                   419
                   3.0e-41
E value
Match length
                  125
% identity
                   62
                   (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  209037
Seq. ID
                  LIB3135-019-Q1-K1-E9
Method
                  BLASTX
                  q1084393
NCBI GI
                   471
BLAST score
                  3.0e-47
E value
                  139
Match length
% identity
                   66
                  peroxidase (EC 1.11.1.7) precursor - parsley >gi 559235
NCBI Description
                   (L36981) anionic peroxidase [Petroselinum crispum]
                   209038
Seq. No.
Seq. ID
                  LIB3135-019-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                   q629483
                   297
BLAST score
                   7.0e-27
E value
Match length
                   122
% identity
                   51
                  gene 1-Sc3 protein - European white birch
NCBI Description
                  >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                   >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
Seq. No.
                   209039
                   LIB3135-019-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1495251
BLAST score
                   591
E value
                   2.0e-61
Match length
                   137
% identity
                   81
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   209040
Seq. No.
Seq. ID
                   LIB3135-019-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   g629483
BLAST score
                   314
E value
                   7.0e-29
```

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula] >gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

125

54

Match length % identity

Seq. ID

Method



```
Seq. No.
Seq. ID
                  LIB3135-019-Q1-K1-F5
                  BLASTN
Method
                  g2829205
NCBI GI
                  72
BLAST score
E value
                  1.0e-32
Match length
                  132
% identity
                  16
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  209042
Seq. No.
Seq. ID
                  LIB3135-019-Q1-K1-F8
                  BLASTN
Method
                  q3687405
NCBI GI
BLAST score
                  51
                   8.0e-20
E value
                  71
Match length
                   93
% identity
NCBI Description Lycopersicon esculentum mRNA for hypothetical protein
                   209043
Seq. No.
                  LIB3135-019-Q1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2829899
                   184
BLAST score
                   1.0e-13
E value
Match length
                   81
                   44
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp_AJ001449_2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   209044
                   LIB3135-019-Q1-K1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1129145
BLAST score
                   294
E value
                   1.0e-26
Match length
                   107
% identity
                   (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
NCBI Description
                   209045
Seq. No.
                   LIB3135-019-Q1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g421810
BLAST score
                   467
                   5.0e-47
E value
Match length
                   107
% identity
                   acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor -
NCBI Description
                   cucumber
                   209046
Seq. No.
```

28836

LIB3135-019-Q1-K1-G4

BLASTX



```
g2369766
NCBI GI
                  304
BLAST score
                  9.0e-28
E value
                  125
Match length
% identity
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   209047
Seq. No.
                  LIB3135-019-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                   g167367
NCBI GI
BLAST score
                   391
                   3.0e-38
E value
                   74
Match length
                   96
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   209048
Seq. No.
                   LIB3135-019-Q1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3193323
BLAST score
                   240
E value
                   2.0e-20
Match length
                   51
                   88
% identity
                   (AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm,
NCBI Description
                   score: 78.35); identical to Arabidopsis 40S ribosomal
                   protein S13 (fragment) (SW: P49203A) except the first 32
                   amino acids are different [Arabidopsis thaliana]
                   209049
Seq. No.
                   LIB3135-019-Q1-K1-H10
Seq. ID
Method
                   BLASTX
                   g3150407
NCBI GI
                   222
BLAST score
                   4.0e-18
E value
                   73
Match length
                   66
% identity
                   (AC004165) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   209050
Seq. No.
                   LIB3135-019-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g3150407
NCBI GI
                   268
BLAST score
                   2.0e-23
E value
                   73
Match length
                   75
 % identity
                  (AC004165) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   209051
 Seq. No.
 Seq. ID
                   LIB3135-019-Q1-K1-H4
                   BLASTN
Method
                   g2829205
NCBI GI
BLAST score
                   35
```

28837

2.0e-10

93

E value

Match length



% identity 21

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No. 209052

Seq. ID LIB3135-019-Q1-K1-H7

Method BLASTX
NCBI GI g1076678
BLAST score 161
E value 1.0e-11
Match length 44
% identity 82

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 209053

Seq. ID LIB3135-019-Q1-K1-H8

Method BLASTX
NCBI GI 9730645
BLAST score 333
E value 2.0e-31
Match length 82
% identity 82

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi\_629556\_pir\_\_S43412 ribosomal protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi\_313188\_emb\_CAA80681\_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi\_1903366\_gb\_AAB70449\_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb\_R29788,gb\_ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 209054

Seq. ID LIB3135-019-Q1-K1-H9

Method BLASTX
NCBI GI g3461848
BLAST score 439
E value 1.0e-43
Match length 121
% identity 69

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No. 209055

Seq. ID LIB3135-020-Q1-K1-A2

Method BLASTX
NCBI GI g2244734
BLAST score 563
E value 3.0e-58
Match length 116
% identity 97

NCBI Description (D88414) actin [Gossypium hirsutum]

Seq. No. 209056

Seq. ID LIB3135-020-Q1-K1-A4

MethodBLASTXNCBI GIg3420051BLAST score609E value2.0e-63



```
Match length
                   97
% identity
                  (AC004680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   209057
Seq. No.
                  LIB3135-020-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4336205
BLAST score
                   522
E value
                   2.0e-53
Match length
                   114
% identity
                   83
                  (AF077372) cytochrome b5 reductase [Zea mays]
NCBI Description
Seq. No.
                   209058
                   LIB3135-020-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1498338
BLAST score
                   215
                   1.0e-17
E value
Match length
                   94
                   51
% identity
                  (U60502) actin [Glycine max]
NCBI Description
                   209059
Seq. No.
                   LIB3135-020-Q1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244749
BLAST score
                   153
                   5.0e-10
E value
                   39
Match length
                   69
% identity
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209060
                   LIB3135-020-Q1-K1-B5
Seq. ID
                   BLASTX
Method
                   q3334320
NCBI GI
                   454
BLAST score
                   1.0e-45
E value
                   87
Match length
                   97
% identity
                   40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [Glycine max]
                   209061
Seq. No.
                   LIB3135-020-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g3342211
NCBI GI
BLAST score
                   195
                   3.0e-15
E value
Match length
                   58
% identity
                   (U89255) Pti4 [Lycopersicon esculentum]
NCBI Description
```

Seq. No. 209062

Seq. ID LIB3135-020-Q1-K1-B7



Method BLASTX NCBI GI g1363492 BLAST score 178 E value 3.0e-13 Match length 40 % identity 82

NCBI Description outer envelope membrane protein OEP75 precursor - garden pea >gi 576507 (L36858) outer membrane protein [Pisum

sativum] >gi 633607\_emb CAA58720 (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No.

209063

Seq. ID LIB3135-020-Q1-K1-C1 Method BLASTX NCBI GI g3128228 BLAST score 511 E value 5.0e-52 Match length 108 % identity 88

NCBI Description

(AC004077) putative ribosomal protein L18A [Arabidopsis

thaliana] >gi\_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 209064

Seq. ID LIB3135-020-Q1-K1-C7

Method BLASTX NCBI GI g120673 BLAST score 724 E value 7.0e-77 Match length 153 % identity 90

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66013\_pir\_\_DEPJG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - garden petunia >gi 20551 emb CAA42904 (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

Seq. No. 209065

Seq. ID LIB3135-020-Q1-K1-C9

Method BLASTX NCBI GI g1429226 BLAST score 189 E value 3.0e-14 Match length 46 % identity 83

NCBI Description (X98861) TFIIA [Arabidopsis thaliana]

Seq. No. 209066

Seq. ID LIB3135-020-Q1-K1-D3

Method BLASTX NCBI GI g1166450 BLAST score 190 E value 2.0e-14 Match length 41 % identity 83

NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

```
209067
Seq. No.
Seq. ID
                  LIB3135-020-Q1-K1-D4
                  BLASTX
Method
                  g3184281
NCBI GI
                   142
BLAST score
                   2.0e-09
E value
                   64
Match length
                   47
% identity
                   (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  209068
Seq. No.
                  LIB3135-020-Q1-K1-D9
Seq. ID
                  BLASTX
                   q3075399
                   170
```

Method BLASTX
NCBI GI g3075399
BLAST score 170
E value 3.0e-12
Match length 70
% identity 50

NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 209069 Seq. ID LIB3135-020-Q1-K1-E10

Method BLASTX
NCBI GI g1370589
BLAST score 189
E value 2.0e-14
Match length 79
% identity 53

NCBI Description (X98304) protein induced upon tuberization [Solanum

demissum]

Seq. No. 209070

Seq. ID LIB3135-020-Q1-K1-E11

Method BLASTN
NCBI GI g19212
BLAST score 49
E value 2.0e-18
Match length 130
% identity 27

NCBI Description Tomato extensin mRNA (clone w17-1)

Seq. No. 209071

Seq. ID LIB3135-020-Q1-K1-E12

Method BLASTN
NCBI GI g3869075
BLAST score 50
E value 4.0e-19
Match length 118
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 209072

Seq. ID LIB3135-020-Q1-K1-E4

Method BLASTX NCBI GI g2746719 BLAST score 324



```
2.0e-30
E value
                  93
Match length
                  74
% identity
                  (AF038386) histone H2B [Capsicum annuum]
NCBI Description
                  209073
Seq. No.
                  LIB3135-020-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  g3915037
NCBI GI
                  355
BLAST score
                  9.0e-34
E value
                   91
Match length
                   70
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi 2570067_emb_CAA04512_ (AJ001071) second sucrose
                   synthase [Pisum sativum]
                   209074
Seq. No.
                   LIB3135-020-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g3024020
NCBI GI
BLAST score
                   594
E value
                   1.0e-61
Match length
                   121
                   93
% identity
                   INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation
                   factor 5A3 [Solanum tuberosum]
                   209075
Seq. No.
                   LIB3135-020-Q1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4006827
                   515
BLAST score
                   1.0e-52
E value
                   124
Match length
                   80
% identity
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   209076
Seq. No.
                   LIB3135-020-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g282963
NCBI GI
BLAST score
                   498
                   1.0e-50
E value
                   103
Match length
                   85
 % identity
                   transforming protein (myb) homolog (clone myb.Ph2) - garden
NCBI Description
                   petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia
                   x hybrida]
                   209077
 Seq. No.
```

Seq. ID LIB3135-020-Q1-K1-F8

Method BLASTX
NCBI GI g116923
BLAST score 397
E value 1.0e-38



Match length 140 % identity 61

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi\_111414\_pir\_\_S13520 beta-COP protein - rat
>gi\_55819\_emb\_CAA40505\_ (X57228) beta COP [Rattus

norvegicus]

Seq. No. 209078

Seq. ID LIB3135-020-Q1-K1-G1

Method BLASTX
NCBI GI g3860277
BLAST score 382
E value 6.0e-37
Match length 113
% identity 72

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi\_4314394\_gb\_AAD15604\_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 209079

Seq. ID LIB3135-020-Q1-K1-G11

Method BLASTX
NCBI GI g558143
BLAST score 205
E value 4.0e-16
Match length 67
% identity 60

NCBI Description (L36946) orf 143 [Vicia faba]

Seq. No. 209080

Seq. ID LIB3135-020-Q1-K1-G5

Method BLASTX
NCBI GI g2160166
BLAST score 323
E value 6.0e-30
Match length 128
% identity 51

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 209081

Seq. ID LIB3135-020-Q1-K1-G6

Method BLASTX
NCBI GI g4191788
BLAST score 224
E value 8.0e-19
Match length 60
% identity 63

NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate

oxidase [Arabidopsis thaliana]

Seq. No. 209082

Seq. ID LIB3135-020-Q1-K1-G7

Method BLASTX
NCBI GI g3608140
BLAST score 146
E value 3.0e-09
Match length 118

% identity 34 NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 209083

Seq. ID LIB3135-020-Q1-K1-G8

Method BLASTX
NCBI GI g2827715
BLAST score 143
E value 7.0e-09
Match length 107

Match length 107 % identity 41

NCBI Description (AL021684) receptor protein kinase - like protein

1

[Arabidopsis thaliana]

Seq. No. 209084

Seq. ID LIB3135-020-Q1-K1-H2

Method BLASTX
NCBI GI g3928086
BLAST score 243
E value 1.0e-20
Match length 94
% identity 55

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 209085

Seq. ID LIB3135-020-Q1-K1-H5

Method BLASTX
NCBI GI g1161566
BLAST score 494
E value 5.0e-50
Match length 133
% identity 71

NCBI Description (X94943) peroxidase [Lycopersicon esculentum]

Seq. No. 209086

Seq. ID LIB3135-020-Q1-K1-H9

Method BLASTX
NCBI GI g1276977
BLAST score 474
E value 8.0e-48
Match length 108
% identity 85

NCBI Description (U47143) nonsymbiotic hemoglobin [Glycine max]

Seq. No. 209087

Seq. ID LIB3135-021-Q1-K1-A1

Method BLASTX
NCBI GI g2695711
BLAST score 315
E value 3.0e-29
Match length 98
% identity 61

NCBI Description (AJ001370) cytochome b5 [Olea europaea]

Seq. No. 209088

Seq. ID LIB3135-021-Q1-K1-A10

Method BLASTX



```
q3080428
NCBI GI
                  148
BLAST score
                  2.0e-09
E value
Match length
                  74
% identity
                  34
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                  209089
Seq. No.
                  LIB3135-021-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136057
BLAST score
                  153
E value
                  3.0e-10
Match length
                  72
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 99499 pir A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi 556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
                  209090
Seq. No.
Seq. ID
                  LIB3135-021-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3876465
BLAST score
                  298
E value
                   4.0e-27
Match length
                  81
% identity
                  70
                   (Z81071) predicted using Genefinder; Similarity to Human
NCBI Description
                   small nuclear ribonucleoprotein E (SW:P08578); cDNA EST
                   yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes
                   from this gene; cDNA EST yk435f5.3 comes from this gene;
Seq. No.
                   209091
Seq. ID
                  LIB3135-021-Q1-K1-B1
                  BLASTX
Method
                   q3885343
NCBI GI
BLAST score
                   185
                   5.0e-14
E value
                  70
Match length
                   49
% identity
                  (AC005623) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   209092
Seq. No.
Seq. ID
                  LIB3135-021-Q1-K1-B11
Method
                   BLASTX
                   g1279654
NCBI GI
BLAST score
                   424
                   9.0e-42
E value
                   146
Match length
                   57
% identity
                   (X97351) peroxidase [Populus balsamifera subsp.
NCBI Description
                   trichocarpa]
```

28845

209093

BLASTX

LIB3135-021-Q1-K1-B3

Seq. No. Seq. ID

Method

```
g3122724
NCBI GI
                  161
BLAST score
                  4.0e-11
E value
                  53
Match length
                  66
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
NCBI Description
                  protein L38 isolog [Arabidopsīs thaliana]
                  209094
Seq. No.
                  LIB3135-021-Q1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4185819
                  192
BLAST score
                  1.0e-14
E value
                  47
Match length
                  68
% identity
                  (AF116845) metallothionein-like type 1 protein [Ipomoea
NCBI Description
                  batatas]
                  209095
Seq. No.
                  LIB3135-021-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1729760
                   331
BLAST score
                   6.0e - 31
E value
                   60
Match length
                  100
% identity
NCBI Description (Z68152) chitinase [Gossypium hirsutum]
                   209096
Seq. No.
                  LIB3135-021-Q1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g643469
                   213
BLAST score
                   3.0e-17
E value
                   92
Match length
                   54
% identity
NCBI Description (U19886) unknown [Lycopersicon esculentum]
                   209097
Seq. No.
Seq. ID
                   LIB3135-021-Q1-K1-C5
                   BLASTX
Method
                   g4027891
NCBI GI
BLAST score
                   338
                   9.0e-32
E value
                   84
Match length
                   71
% identity
                  (AF049350) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
```

Seq. No. 209098

Seq. ID LIB3135-021-Q1-K1-C6

Method BLASTX
NCBI GI g542200
BLAST score 444
E value 3.0e-44
Match length 124
% identity 71



```
hypothetical protein - garden asparagus
NCBI Description
                  >gi 452714 emb CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
                  209099
Seq. No.
                  LIB3135-021-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3452263
BLAST score
                  557
                   2.0e-57
E value
Match length
                   132
% identity
                   (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
NCBI Description
                   thaliana]
                   209100
Seq. No.
                   LIB3135-021-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   g3850778
NCBI GI
                   427
BLAST score
                   4.0e-42
E value
                   106
Match length
% identity
                   (Y18346) gluaredoxin [Lycopersicon esculentum]
NCBI Description
                   209101
Seq. No.
                   LIB3135-021-Q1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g441457
                   343
BLAST score
                   2.0e-32
E value
                   64
Match length
                   97
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                   esculentum]
                   209102
Seq. No.
                   LIB3135-021-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   g1946360
NCBI GI
                   285
BLAST score
                   1.0e-25
E value
                   102
Match length
                   59
% identity
                   (U93215) elicitor response element binding protein WRKY3
NCBI Description
                   isolog [Arabidopsis thaliana]
                   209103
 Seq. No.
                   LIB3135-021-Q1-K1-D11
 Seq. ID
                   BLASTX
Method
                   g3128195
 NCBI GI
                   518
 BLAST score
                   6.0e-53
 E value
                   112
 Match length
```

28847

(AC004521) putative phosphoribosyl pyrophosphate synthetase

[Arabidopsis thaliana] >gi\_3341673 (AC003672) putative

93

% identity

NCBI Description



phosphoribosyl pyrophosphate synthetase [Arabidopsis thalianal

 Seq. No.
 209104

 Seq. ID
 LIB3135-021-Q1-K1-D6

 Method
 BLASTX

 NCBI GI
 g2828280

 BLAST score
 248

E value 3.0e-36
Match length 90
% identity 80

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

>gi 2832633 emb CAA16762 (AL021711) putative protein

[Arabidopsis thaliana]

Seq. No. 209105

Seq. ID LIB3135-021-Q1-K1-E11

Method BLASTN
NCBI GI g167350
BLAST score 110
E value 2.0e-55
Match length 110
% identity 100

NCBI Description Cotton late embryogenesis-abundant protein (Lea5-D) gene

exons 1-2, complete cds

Seq. No. 209106

Seq. ID LIB3135-021-Q1-K1-E12

Method BLASTX
NCBI GI g629483
BLAST score 299
E value 4.0e-27
Match length 113
% identity 54

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula] >gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 209107

Seq. ID LIB3135-021-Q1-K1-E3

Method BLASTX
NCBI GI g3219858
BLAST score 362
E value 2.0e-40
Match length 94
% identity 89

NCBI Description DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE

>gi\_2129724\_pir\_\_S71204 RNA polymerase II 13.6 kDa chain Arabidopsis thaliana >gi\_881501 (U28048) RNA polymerase II

13.6 kDa subunit [Arabidopsis thaliana]

Seq. No. 209108

Seq. ID LIB3135-021-Q1-K1-E4

Method BLASTX NCBI GI g1173043 BLAST score 302



1.0e-27 E value 65 Match length 91 % identity 60S RIBOSOMAL PROTEIN L38 >gi\_479441\_pir\_\_S33899 ribosomal NCBI Description protein L38 - tomato (cv. Moneymaker) >gi 313027\_emb\_CAA49599\_ (X69979) ribosomal protein L38 [Lycopersicon esculentum] 209109 Seq. No. Seq. ID LIB3135-021-Q1-K1-E5 Method BLASTX g3123745 NCBI GI 471 BLAST score 2.0e-47 E value Match length 122 73 % identity (AB013447) aluminum-induced [Brassica napus] NCBI Description Seq. No. 209110 LIB3135-021-Q1-K1-E7 Seq. ID Method BLASTN NCBI GI q2829205 BLAST score 104 3.0e-51 E value Match length 382 16 % identity Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein NCBI Description precursor (PRP) mRNA, complete cds Seq. No. 209111 LIB3135-021-Q1-K1-F1 Seq. ID Method BLASTX NCBI GI g133940 BLAST score 389 1.0e-37 E value 93 Match length % identity 81 40S RIBOSOMAL PROTEIN S3A (S1A) >gi 70851\_pir\_\_R3XL3A NCBI Description ribosomal protein S3a - African clawed frog >gi 65091\_emb\_CAA40592\_ (X57322) ribosomal protein S1a [Xenopus laevis] 209112 Seq. No. Seq. ID LIB3135-021-Q1-K1-F11 Method BLASTX NCBI GI g585110 BLAST score 384 E value 4.0e-37 132 Match length 58 % identity ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) NCBI Description

>gi\_479194\_pir\_\_S32482 electron transfer flavoprotein beta

chain - human >gi\_2781203\_pdb\_1EFV\_B Chain B,

Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution >gi\_297902\_emb\_CAA50441\_(X7129) electron transfer flavoprotein beta subunit [Homo

sapiens] >gi\_4503609\_ref\_NP\_001976.1\_pETFB\_

NCBI GI BLAST score

E value

455

2.0e-45



## electron-transfer-flavoprotein, beta polypeptide

```
Seq. No.
                   209113
                   LIB3135-021-Q1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1943694
BLAST score
                   55
                   1.0e-22
E value
                   63
Match length
                   97
% identity
                   Clerodendrum inerme 18S ribosomal RNA gene, partial
NCBI Description
                   sequence, internal transcribed spacer 1, 5.8S ribosomal RNA
                   gene and internal transcribed spacer 2, complete sequence,
                   and 26S ribosomal RNA gene, partial sequence
                   209114
Seq. No.
                   LIB3135-021-Q1-K1-F8
Seq. ID
Method
                   BLASTX
                   q120669
NCBI GI
                   155
BLAST score
                   2.0e-11
E value
                   73
Match length
                   66
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >qi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   209115
Seq. No.
                   LIB3135-021-Q1-K1-G3
Seq. ID
Method
                   BLASTX
                   g1931647
NCBI GI
BLAST score
                   158
E value
                   5.0e-11
Match length
                   61
% identity
                   52
                    (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                    [Arabidopsis thaliana]
                   209116
Seq. No.
                   LIB3135-021-Q1-K1-G5
Seq. ID
                   BLASTN
Method
                   g2829205
NCBI GI
                   36
BLAST score
                   7.0e-11
E value
                   56
Match length
                    91
% identity
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
                   209117
Seq. No.
Seq. ID
                   LIB3135-021-Q1-K1-G6
                   BLASTX
Method
                   g294668
```



```
Match length
% identity
                   95
                   (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]
NCBI Description
                   209118
Seq. No.
                   LIB3135-021-Q1-K1-H12
Seq. ID
Method
                   BLASTX
                   q728744
NCBI GI
                   500
BLAST score
                   9.0e-51
E value
Match length
                   120
                   79
% identity
                   AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir__S16390
NCBI Description
                   auxin-induced protein - common tobacco >gi_19799 emb_CAA39708_ (X56267) auxin-induced protein
                    [Nicotiana tabacum]
                   209119
Seq. No.
                   LIB3135-021-Q1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q445613
                   454
BLAST score
                   7.0e-53
E value
Match length
                   118
% identity
                    86
                   ribosomal protein L7 [Solanum tuberosum]
NCBI Description
                    209120
Seq. No.
                    LIB3135-021-Q1-K1-H6
Seq. ID
                    BLASTX
Method
                    g1771780
NCBI GI
                    316
BLAST score
                    3.0e-29
E value
Match length
                    111
                    58
% identity
                   (Y10024) ubiquitin extension protein [Solanum tuberosum]
NCBI Description
                    209121
Seq. No.
                    LIB3135-022-Q1-K1-A2
Seq. ID
Method
                    BLASTX
                    g133867
NCBI GI
                    399
BLAST score
                    5.0e-39
E value
Match length
                    97
                    79
 % identity
                    40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                    protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                    ribosomal protein S11 [Zea mays]
                    209122
 Seq. No.
                    LIB3135-022-Q1-K1-A7
 Seq. ID
                    BLASTX
Method
NCBI GI
                    g2088651
                    260
BLAST score
```

28851

1.0e-22

95

52

E value

Match length

% identity

```
(AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                  [Arabidopsis thaliana]
                  209123
Seq. No.
                  LIB3135-022-Q1-K1-B6
Seq. ID
Method
                  BLASTN
                  g2879810
NCBI GI
                  45
BLAST score
                  4.0e-16
E value
                  121
Match length
% identity
                  Lupinus luteus mRNA for ribosomal protein L30
NCBI Description
                  209124
Seq. No.
                  LIB3135-022-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g629483
NCBI GI
BLAST score
                  232
                  3.0e-19
E value
                  85
Match length
                  55
% identity
                  gene 1-Sc3 protein - European white birch
NCBI Description
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi_1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
                   209125
Seq. No.
                   LIB3135-022-Q1-K1-B8
Seq. ID
Method
                   BLASTX
                   g3805842
NCBI GI
BLAST score
                   454
                   3.0e-45
E value
Match length
                   138
                   70
% identity
                   (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                   209126
Seq. No.
                   LIB3135-022-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g419779
NCBI GI
                   232
BLAST score
                   1.0e-19
E value
                   92
Match length
                   58
% identity
                   ferredoxin--nitrite reductase (EC 1.7.7.1) nir-2 - common
NCBI Description
                   tobacco (fragment) >gi 445051_prf__1908371C nitrite
                   reductase [Nicotiana tabacum]
                   209127
Seq. No.
                   LIB3135-022-Q1-K1-C2
Seq. ID
```

BLASTX Method g2495365 NCBI GI BLAST score 269 6.0e-24E value 86 Match length 65 % identity

NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi\_445127\_prf\_\_1908431B



heat shock protein HSP81-2 [Arabidopsis thaliana]

```
209128
Seq. No.
                  LIB3135-022-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                  g3281846
NCBI GI
                  176
BLAST score
                  9.0e-13
E value
                  76
Match length
% identity
                  50
                  (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
NCBI Description
                  209129
Seq. No.
                  LIB3135-022-Q1-K1-C7
Seq. ID
                  {\tt BLASTX}
Method
                  g2245138
NCBI GI
BLAST score
                  501
                  7.0e-51
E value
                  134
Match length
                  69
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  209130
                  LIB3135-022-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                   q1173456
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   112
Match length
                   54
% identity
                  SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN
NCBI Description
                   D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]
Seq. No.
                   209131
Seq. ID
                   LIB3135-022-Q1-K1-D2
                   BLASTX
Method
NCBI GI
                   q169989
BLAST score
                   646
                   7.0e-68
E value
                   135
Match length
                   90
% identity
                   (L12157) NADPH-specific isocitrate dehydrogenase [Glycine
NCBI Description
                   max]
                   209132
Seq. No.
Seq. ID
                   LIB3135-022-Q1-K1-D5
                   BLASTX
Method
NCBI GI
                   q1706547
BLAST score
                   220
                   6.0e-18
E value
                   75
Match length
                   57
% identity
                   GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
NCBI Description
                   PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                   ((1->3)-BETA-GLUCANASE) (BETA-1, 3-ENDOGLUCANASE)
                   >gi 2129912 pir S65077 beta-1,3-glucanase class I
```

28853

precursor - Para rubber tree >gi 1184668 (U22147)

BLAST score

E value

233 9.0e-37



## beta-1,3-glucanase [Hevea brasiliensis]

```
209133
Seq. No.
                  LIB3135-022-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1345975
BLAST score
                  218
                  1.0e-17
E value
                  59
Match length
% identity
                  69
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_1084421_pir__JC2555 omega-3 fatty acid desaturase -
                  Common tobacco (cv. SR1) >gi_599592_dbj_BAA05515_ (D26509)
                  microsomal omega-3 acid desaturase [Nicotiana tabacum]
Seq. No.
                  209134
Seq. ID
                  LIB3135-022-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g113742
                  278
BLAST score
                  8.0e-25
E value
Match length
                  107
% identity
                  50
                  AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)
NCBI Description
                  >gi_147142 (M15273) peptidase N [Escherichia coli]
                      147144 (M15676) aminopeptidase N [Escherichia coli]
                  >gi 1787163 (AE000195) aminopeptidase N [Escherichia coli]
                  >gi 4062498 dbj BAA35684 (D90731) Aminopeptidase n (EC
                  3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia
                  coli]
                  209135
Seq. No.
                  LIB3135-022-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                  g4262250
NCBI GI
                  403
BLAST score
                  1.0e-39
E value
Match length
                  101
                  76
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                  209136
Seq. No.
                  LIB3135-022-Q1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4008159
BLAST score
                   276
                  1.0e-24
E value
Match length
                   95
                   46
% identity
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
Seq. No.
                   209137
                   LIB3135-022-Q1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1345975
```



```
Match length
                  85
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_1084421_pir__JC2555 omega-3 fatty acid desaturase -
                  Common tobacco (cv. SR1) >gi_599592_dbj BAA05515_ (D26509)
                  microsomal omega-3 acid desaturase [Nicotiana tabacum]
                  209138
Seq. No.
                  LIB3135-022-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3687246
BLAST score
                  164
                  2.0e-11
E value
                  94
Match length
                  37
% identity
                  (AC005169) putative suppressor protein [Arabidopsis
NCBI Description
                  thaliana]
                  209139
Seq. No.
                  LIB3135-022-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738283
                  350
BLAST score
                  3.0e-33
E value
                  81
Match length
                  77
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  209140
Seq. No.
Seq. ID
                  LIB3135-022-Q1-K1-F12
                  BLASTX
Method
NCBI GI
                  g3153154
BLAST score
                  210
                  5.0e-17
E value
                  88
Match length
                  50
% identity
                  (AJ006225) small GTP-binding protein [Mesembryanthemum
NCBI Description
                  crystallinum]
                  209141
Seq. No.
Seq. ID
                  LIB3135-022-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2497752
                  297
BLAST score
E value
                  6.0e-27
Match length
                  105
% identity
                   55
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1321911 emb CAA65475 (X96714) lipid transfer protein
                   [Prunus dulcis]
```

Seq. No. 209142

Seq. ID LIB3135-022-Q1-K1-G5

BLASTN Method NCBI GI q2829205 BLAST score 37 E value 2.0e-11



Match length 214 % identity 49

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 209143

Seq. ID LIB3135-022-Q1-K1-H3

Method BLASTX
NCBI GI 94455256
BLAST score 454
E value 2.0e-45
Match length 122
% identity 68

NCBI Description (AL035523) protein-methionine-S-oxide reductase

[Arabidopsis thaliana]

Seq. No. 209144

Seq. ID LIB3135-022-Q1-K1-H4

Method BLASTX
NCBI GI g4204313
BLAST score 272
E value 6.0e-24
Match length 123
% identity 47

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 209145

Seq. ID LIB3135-022-Q1-K1-H6

Method BLASTX
NCBI GI g4454033
BLAST score 550
E value 1.0e-56
Match length 147
% identity 64

NCBI Description (AL035394) putative potassium transport protein

[Arabidopsis thaliana]

Seq. No. 209146

Seq. ID LIB3135-022-Q1-K1-H9

Method BLASTX
NCBI GI g3334245
BLAST score 354
E value 1.0e-33
Match length 108
% identity 62

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi\_2909424\_emb\_CAA12028\_ (AJ224520) Glyoxalase I [Cicer

arietinum]

Seq. No. 209147

Seq. ID LIB3135-023-Q1-K1-A12

Method BLASTX NCBI GI g4062934 BLAST score 701



E value 3.0e-74 Match length 141 % identity 89

NCBI Description (D88272) formate dehydrogenase [Hordeum vulgare]

Seq. No. 209148

Seq. ID LIB3135-023-Q1-K1-A3

Method BLASTX
NCBI GI g3212610
BLAST score 219
E value 6.0e-18
Match length 92
% identity 51

NCBI Description Chain A, Sulfite Oxidase From Chicken Liver

>gi\_3212611\_pdb\_1SOX\_B Chain B, Sulfite Oxidase From

Chicken Liver

Seq. No. 209149

Seq. ID LIB3135-023-Q1-K1-A8

Method BLASTX
NCBI GI g3075391
BLAST score 204
E value 2.0e-16
Match length 80
% identity 51

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 209150

Seq. ID LIB3135-023-Q1-K1-A9

Method BLASTX
NCBI GI g2493133
BLAST score 234
E value 2.0e-19
Match length 113
% identity 49

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT)

>gi\_2183244 (AF002134) Vma8p [Candida albicans]

Seq. No. 209151

Seq. ID LIB3135-023-Q1-K1-B10

Method BLASTX
NCBI GI g1498053
BLAST score 366
E value 6.0e-35
Match length 110
% identity 67

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 209152

Seq. ID LIB3135-023-Q1-K1-B12

Method BLASTX
NCBI GI g1168470
BLAST score 168
E value 8.0e-12
Match length 112
% identity 42

NCBI Description PROTEIN KINASE APK1A >gi\_282877\_pir\_\_S28615 protein kinase,



tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi\_217829\_dbj\_BAA02092\_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

209153 Seq. No. Seq. ID LIB3135-023-Q1-K1-B6 BLASTN Method g871468 NCBI GI BLAST score 44 1.0e-15 E value 205 Match length 85 % identity NCBI Description H.annuus mitochondrion genes trnH and trnE 209154 Seq. No. LIB3135-023-Q1-K1-B8 Seq. ID BLASTX Method g2292917 NCBI GI 172 BLAST score 4.0e-22 E value Match length 78 % identity NCBI Description (X99851) galactokinase [Arabidopsis thaliana] 209155 Seq. No. LIB3135-023-Q1-K1-B9 Seq. ID Method BLASTX g2511541 NCBI GI 624 BLAST score 3.0e-65 E value Match length 139 % identity 87 (AF020787) DNA-binding protein GBP16 [Oryza sativa] NCBI Description 209156 Seq. No. Seq. ID LIB3135-023-Q1-K1-C10 BLASTX Method g134892 NCBI GI BLAST score 261 7.0e-33 E value Match length 142 % identity SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT NCBI Description (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi 88607 pir\_A29440 signal recognition particle receptor - human  $> \overline{g}i$  30866 emb CAA29608 (X06272) docking protein [Homo sapiens] >gi 4507223 ref NP 003130.1\_pSRPR\_ signal recognition particle receptor ('docking protein')

 Seq. No.
 209157

 Seq. ID
 LIB3135-023-Q1-K1-C12

 Method
 BLASTX

 NCBI GI
 g136057

 BLAST score
 234

 E value
 2.0e-19

 Match length
 71



% identity 63

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi\_99499\_pir\_\_A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi\_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 209158

Seq. ID LIB3135-023-Q1-K1-C5

Method BLASTX
NCBI GI g267075
BLAST score 359
E value 1.0e-34
Match length 77
% identity 92

NCBI Description TUBULIN BETA-2 CHAIN >gi\_388254\_emb\_CAA38614\_ (X54845)

beta-tubulin 2 [Pisum sativum]

Seq. No. 209159

Seq. ID LIB3135-023-Q1-K1-C7

Method BLASTN
NCBI GI g18058
BLAST score 242
E value 1.0e-134
Match length 274
% identity 97

NCBI Description Citrus limon cistron for 26S ribosomal RNA

Seq. No. 209160

Seq. ID LIB3135-023-Q1-K1-D10

Method BLASTN
NCBI GI g3449327
BLAST score 40
E value 3.0e-13
Match length 52
% identity 94

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCA23, complete sequence [Arabidopsis thaliana]

Seq. No. 209161

Seq. ID LIB3135-023-Q1-K1-D12

Method BLASTX
NCBI GI g136057
BLAST score 197
E value 3.0e-15
Match length 67
% identity 58

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi\_99499\_pir\_\_A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi 556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 209162

Seq. ID LIB3135-023-Q1-K1-E10

Method BLASTX
NCBI GI g3386621
BLAST score 369
E value 8.0e-37



Match length 92 % identity 86

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 209163

Seq. ID LIB3135-023-Q1-K1-E9

Method BLASTX
NCBI GI g3643594
BLAST score 357
E value 6.0e-34
Match length 99
% identity 75

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 209164

Seq. ID LIB3135-023-Q1-K1-F10

Method BLASTX
NCBI GI g629483
BLAST score 314
E value 7.0e-29
Match length 125
% identity 53

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula]
>gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 209165

Seq. ID LIB3135-023-Q1-K1-F12

Method BLASTX
NCBI GI g3786016
BLAST score 208
E value 2.0e-16
Match length 51
% identity 76

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 209166

Seq. ID LIB3135-023-Q1-K1-F9

Method BLASTX
NCBI GI g113029
BLAST score 395
E value 2.0e-38
Match length 118
% identity 69

NCBI Description ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)

>gi\_68209\_pir\_\_WZCNIU isocitrate lyase (EC 4.1.3.1) upland cotton >gi\_18486\_emb\_CAA36381\_ (X52136) isocitrate

lyase (AA 1-576) [Gossypium hirsutum]

Seq. No. 209167

Seq. ID LIB3135-023-Q1-K1-G10

Method BLASTX NCBI GI g421810 BLAST score 558 E value 1.0e-57



Match length % identity

acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor -NCBI Description

cucumber

209168 Seq. No.

LIB3135-023-Q1-K1-G11 Seq. ID

BLASTX Method NCBI GI g3868758 BLAST score 373 8.0e-36 E value 143 Match length

53 % identity

(D89802) elongation factor 1B gamma [Oryza sativa] NCBI Description

209169 Seq. No.

Seq. ID LIB3135-023-Q1-K1-G12

Method BLASTX NCBI GI g4115377 BLAST score 159 E value 3.0e-11 49 Match length

% identity 63

(AC005967) unknown protein [Arabidopsis thaliana] NCBI Description

. .

Seq. No. 209170

LIB3135-023-Q1-K1-G2 Seq. ID

Method BLASTX g421826 NCBI GI BLAST score 315 E value 1.0e-29 Match length 68 82 % identity

chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description

>gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis

thaliana]

209171 Seq. No.

LIB3135-023-Q1-K1-G4 Seq. ID

Method BLASTX NCBI GI q1346524 308 BLAST score E value 3.0e-28 60 Match length % identity 93

S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE NCBI Description

> ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >qi 497900 (M73430) S-adenosyl methionine synthetase [Populus

deltoides]

Seq. No. 209172

LIB3135-023-Q1-K1-G9 Seq. ID

Method BLASTX NCBI GI q1172635 BLAST score 281 E value 3.0e-25 Match length 77



```
% identity
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
                  209173
Seq. No.
                  LIB3135-023-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3150407
                  268
BLAST score
E value
                  2.0e-23
Match length
                  73
% identity
NCBI Description (AC004165) hypothetical protein [Arabidopsis thaliana]
                  209174
Seq. No.
                  LIB3135-023-Q1-K1-H11
Seq. ID
Method
                  BLASTN
                  g2829205
NCBI GI
                  159
BLAST score
                  4.0e-84
E value
                  414
Match length
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                  209175
Seq. No.
                  LIB3135-023-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  g3980393
NCBI GI
BLAST score
                  358
                  4.0e-34
E value
Match length
                  105
% identity
                  63
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                  thaliana]
                  209176
Seq. No.
                  LIB3135-023-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                  g2213867
NCBI GI
                   343
BLAST score
                   3.0e-32
E value
Match length
                  145
% identity
                   50
                   (AF003124) fructose-biphosphate aldolase [Mesembryanthemum
NCBI Description
                   crystallinum]
                   209177
Seq. No.
Seq. ID
                  LIB3135-024-Q1-K1-A11
                   BLASTN
Method
                   g434989
NCBI GI
BLAST score
                   198
                   1.0e-107
E value
```

28862

NCBI Description O.berteriana mitochondrial trnC and trnN genes

356

91

Match length

% identity



```
209178
Seq. No.
                  LIB3135-024-Q1-K1-B11
Seq. ID
Method
                  BLASTN
                  g514323
NCBI GI
                  38
BLAST score
                  6.0e-12
E value
Match length
                   50
                   94
% identity
                  Arabidopsis thaliana RNA polymerase subunit (isoform B)
NCBI Description
                  mRNA, complete cds
                   209179
Seq. No.
                  LIB3135-024-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                   q2677828
NCBI GI
BLAST score
                   299
E value
                   3.0e-27
Match length
                   107
                   60
% identity
                  (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                   209180
Seq. No.
                   LIB3135-024-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129639
                   649
BLAST score
                   3.0e-68
E value
                   131
Match length
% identity
                   luminal binding protein (BiP) - Arabidopsis thaliana
NCBI Description
                   >gi 1303695 dbj BAA12348 (D84414) luminal binding protein
                   (BiP) [Arabidopsis thaliana]
                   209181
Seq. No.
                   LIB3135-024-Q1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512653
BLAST score
                   255
E value
                   1.0e-29
                   100
Match length
                   68
% identity
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
Seq. No.
                   209182
                   LIB3135-024-Q1-K1-B9
Seq. ID
Method
                   BLASTX
                   g548852
NCBI GI
                   358
BLAST score
                   4.0e-34
E value
                   82
Match length
                   79
% identity
                   40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal
NCBI Description
                   protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
```

Seq. No. 209183

subunit ribosomal protein [Oryza sativa]

NCBI GI

BLAST score



```
Seq. ID
                      LIB3135-024-Q1-K1-C10
 Method
                      BLASTX
 NCBI GI
                      g2558654
 BLAST score
                      353
 E value
                      2.0e-33
 Match length
                      127
 % identity
                      56
 NCBI Description
                     (AC002354) No definition line found [Arabidopsis thaliana]
 Seq. No.
                     209184
 Seq. ID
                     LIB3135-024-Q1-K1-C5
 Method
                     BLASTX
 NCBI GI
                     g266972
 BLAST score
                     198
 E value
                     2.0e-15
 Match length
                     54
 % identity
                     65
                     40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal
 NCBI Description
                     protein S29 - rat >gi_1362934_pir_ S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610)
                     homologous to antisense sequence of krev-1, anti oncogene
                     [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein
                     [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29
                     [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein
                     S29 [Homo sapiens] >gi_4506717 ref_NP_001023.1 pRPS29
                     ribosomal protein S29
Seq. No.
                     209185
Seq. ID
                     LIB3135-024-Q1-K1-C9
Method
                     BLASTX
NCBI GI
                     g2494415
BLAST score
                     590
E value
                     2.0e-61
Match length
                     133
% identity
                     91
NCBI Description
                     FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                     (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                     >gi_515747 (L34841) fructose-1,6-bisphosphatase [Glycine
                    max]
Seq. No.
                     209186
Seq. ID
                    LIB3135-024-Q1-K1-D1
Method
                    BLASTX
NCBI GI
                    g4426565
BLAST score
                    166
E value
                    2.0e-11
Match length
                    84
% identity
                    39
NCBI Description (AF031483) unknown [Rattus norvegicus]
Seq. No.
                    209187
Seq. ID
                    LIB3135-024-Q1-K1-D12
Method
                    BLASTX
```

28864

g4467095



```
E value
                   132
Match length
                   39
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                   209188
                   LIB3135-024-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2618721
BLAST score
                   368
E value
                   3.0e-35
Match length
                   74
% identity
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
Seq. No.
                   209189
Seq. ID
                   LIB3135-024-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3068809
BLAST score
                   219
E value
                   4.0e-18
Match length
                   74
% identity
                   62
                   (AF059295) Skp1 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209190
Seq. ID
                   LIB3135-024-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   g2501231
BLAST score
                   454
                   3.0e-45
E value
Match length
                   137
% identity
                   64
                   HYPOTHETICAL 38.1 KD PROTEIN >gi 99505 pir S24930
NCBI Description
                   hypothetical protein - pink corydalis >gi_18258_emb_CAA45139_ (X63595) protein of unknown
                   function [Corydalis sempervirens] >gi 444333 prf_1906382A
                   pCSC71 protein [Corydalis sempervirens]
                   209191
Seq. No.
Seq. ID
                   LIB3135-024-Q1-K1-D9
                   BLASTX
Method
NCBI GI
                   g2244792
                   592
BLAST score
                   2.0e-61
E value
                   130
Match length
% identity
                   46
                   (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209192
Seq. ID
                   LIB3135-024-Q1-K1-E3
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3297819
BLAST score 534
E value 1.0e-54
Match length 132
% identity 73



```
(AL031032) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  209193
Seq. No.
                  LIB3135-024-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g500837
                  299
BLAST score
E value
                  4.0e-27
Match length
                  125
% identity
                  43
NCBI Description
                  (U10556) Irelp: Probable protein kinase [Saccharomyces
                  cerevisiae]
                  209194
Seq. No.
                  LIB3135-024-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1518855
BLAST score
                   143
                  3.0e-09
E value
                  84
Match length
                  42
% identity
NCBI Description (U65960) HASPP28 [Homo sapiens]
                 209195
Seq. No.
                  LIB3135-024-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3123264
BLAST score
                   527
                   7.0e-54
E value
Match length
                   130
                   77
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   209196
Seq. No.
                   LIB3135-024-Q1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2388575
                   254
BLAST score
                   8.0e-22
E value
                   133
Match length
% identity
                   41
                  (AC000098) YUP8H12.18 [Arabidopsis thaliana]
NCBI Description
                   209197
Seq. No.
                   LIB3135-024-Q1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1362615
                   259
BLAST score
                   2.0e-22
E value
                   113
Match length
                   51
% identity
                   iswi protein - fruit fly (Drosophila melanogaster)
NCBI Description
```

Seq. No. 209198

28866

>gi 439197 (L27127) ISWI protein [Drosophila melanogaster]

```
LIB3135-024-Q1-K1-F8
Seq. ID
Method
                  BLASTN
                  g2829205
NCBI GI
                  90
BLAST score
                  7.0e-43
E value
                  366
Match length
% identity
                  23
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
```

Seq. No. 209199

Seq. ID LIB3135-024-Q1-K1-G1

Method BLASTN
NCBI GI g2829205
BLAST score 150
E value 9.0e-79
Match length 409
% identity 21

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

precursor (PRP) mRNA, complete cds

Seq. No. 209200

Seq. ID LIB3135-024-Q1-K1-G11

Method BLASTX
NCBI GI g1362093
BLAST score 213
E value 5.0e-17
Match length 53
% identity 77

NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)

>gi\_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 209201

Seq. ID LIB3135-024-Q1-K1-G12

Method BLASTX
NCBI GI g4218120
BLAST score 159
E value 1.0e-10
Match length 81
% identity 40

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 209202

Seq. ID LIB3135-024-Q1-K1-G2

Method BLASTN
NCBI GI g3821780
BLAST score 33
E value 6.0e-09
Match length 35
% identity 59

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 209203

Seq. ID LIB3135-024-Q1-K1-G8

Method BLASTX NCBI GI g719291

Match length

102



```
BLAST score
                    1.0e-48
 E value
                    128
 Match length
                    74
 % identity
                    (U19134) unknown [Arabidopsis thaliana]
 NCBI Description
                    >gi 1095007 prf__2107236A SABRE gene [Arabidopsis thaliana]
                    209204
 Seq. No.
                    LIB3135-024-Q1-K1-G9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g3158474
 BLAST score
                    447
                    2.0e-44
 E value
 Match length
                    111
                    79
 % identity
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                    209205
 Seq. No.
                    LIB3135-024-Q1-K1-H1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3688123
 BLAST score
                    288
                    8.0e-26
 E value
 Match length
                    67
                    79
% identity
                    (AJ006293) granule-bound starch synthase [Antirrhinum
 NCBI Description
                    majus]
 Seq. No.
                    209206
                    LIB3135-024-Q1-K1-H10
 Seq. ID
 Method
                    BLASTX
                    g2654358
 NCBI GI
 BLAST score
                    462
                    3.0e-46
 E value
 Match length
                    134
                    63
 % identity
                    (Y15522) MNUDC protein [Mus musculus]
 NCBI Description
                    >gi_2808636_emb_CAA57201_ (X81443) Sig 92 [Mus musculus]
                    209207
 Seq. No.
 Seq. ID
                    LIB3135-024-Q1-K1-H2
                    BLASTX
 Method
 NCBI GI
                    g719291
                    506
 BLAST score
                    2.0e-51
 E value
                    126
 Match length
                    79
  % identity
                    (U19134) unknown [Arabidopsis thaliana]
 NCBI Description
                    >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]
                    209208
  Seq. No.
  Seq. ID
                    LIB3135-024-Q1-K1-H9
                    BLASTX
 Method
 NCBI GI
                    g3493172
 BLAST score
                    290
                    3.0e-26
  E value
```



```
% identity
                   (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
                   209209
Seq. No.
                   LIB3135-025-Q1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q400976
                   477
BLAST score
                   4.0e-48
E value
Match length
                   101
% identity
                   RAS-RELATED PROTEIN RHA1 >gi_478671_pir__S23727 GTP-binding protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_
NCBI Description
                    (X59152) RHA1 [Arabidopsis thaliana]
                   >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein
                    [Arabidopsis thaliana]
Seq. No.
                   209210
                   LIB3135-025-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   q3702339
NCBI GI
                   156
BLAST score
E value
                   2.0e-10
Match length
                   81
% identity
                    41
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                    209211
Seq. No.
Seq. ID
                   LIB3135-025-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                    g1708313
BLAST score
                    524
E value
                    2.0e-53
Match length
                    110
% identity
                    95
                   HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637
NCBI Description
                    (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                    thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                    thaliana]
                    209212
Seq. No.
                    LIB3135-025-Q1-K1-B1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2924772
BLAST score
                    435
                    2.0e-43
E value
Match length
                    95
```

% identity 88

(AC002334) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

209213

Seq. ID LIB3135-025-Q1-K1-B11

BLASTX Method g3212854 NCBI GI BLAST score 168 8.0e-12 E value Match length 92



```
% identity
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  209214
Seq. ID
                  LIB3135-025-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3281851
BLAST score
                  177
E value
                   6.0e-16
Match length
                  68
% identity
                   62
NCBI Description
                  (AL031004) RNA lariat debranching enzyme - like protein
                   [Arabidopsis thaliana]
Seq. No.
                  209215
Seq. ID
                  LIB3135-025-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g4455329
BLAST score
                  212
E value
                  5.0e-17
Match length
                  87
% identity
                  52
NCBI Description
                  (AL035525) lysine-ketoglutarate reductase/saccharopine
                   [Arabidopsis thaliana]
Seq. No.
                  209216
Seq. ID
                  LIB3135-025-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q4455329
BLAST score
                  315
E value
                  5.0e-29
                  97
Match length
% identity
                   64
NCBI Description
                  (AL035525) lysine-ketoglutarate reductase/saccharopine
                   [Arabidopsis thaliana]
                  209217 ~
Seq. No.
Seq. ID
                  LIB3135-025-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2982432
BLAST score
                  296
                  8.0e-27
E value
Match length
                  66
% identity
                  82
NCBI Description
                  (AL022224) putative protein [Arabidopsis thaliana]
Seq. No.
                  209218
                  LIB3135-025-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g897761
BLAST score
                  194
E value
                  3.0e-15
Match length
                  88
% identity
                  43
                  (X89416) protein phosphatase 5 [Homo sapiens]
NCBI Description
```

Seq. No. 209219



Seq. ID LIB3135-025-Q1-K1-C7 Method BLASTX

NCBI GI g3914403

BLAST score 208

E value 9.0e-24
Match length 74
% identity 74

NCBI Description PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II)

(PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II) >gi\_2370335\_emb\_CAA73866\_ (Y13466) protoporphyrinogen oxidase [Nicotiana tabacum] >gi\_3929920\_dbj\_BAA34712\_ (AB020500) mitochondrial protoporphyrinogen oxidase

[Nicotiana tabacum] >gi 4105188 (AF044129)

protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]

Seq. No. 209220

Seq. ID LIB3135-025-Q1-K1-D1

Method BLASTX
NCBI GI g3914403
BLAST score 504
E value 3.0e-51
Match length 125
% identity 76

NCBI Description PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II)

(PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II) >gi\_2370335\_emb\_CAA73866\_ (Y13466) protoporphyrinogen oxidase [Nicotiana tabacum] >gi\_3929920\_dbj\_BAA34712\_ (AB020500) mitochondrial protoporphyrinogen oxidase

[Nicotiana tabacum] >gi 4105188 (AF044129)

protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]

Seq. No. 209221

Seq. ID LIB3135-025-Q1-K1-D2

Method BLASTX
NCBI GI g3850579
BLAST score 317
E value 1.0e-29
Match length 89
% identity 69

NCBI Description (AC005278) Strong similarity to gb\_D14550 extracellular

dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470,

gb\_R65072, gb\_N76373, gb\_F15470, gb\_Z35182, gb\_H76373,

gb\_Z34678 an

Seq. No. 209222

Seq. ID LIB3135-025-Q1-K1-D3

Method BLASTX
NCBI GI g1709990
BLAST score 229
E value 4.0e-19
Match length 50
% identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L35A

Seq. No. 209223

Seq. ID LIB3135-025-Q1-K1-D4



```
Method
                  BLASTX
                  q2687726
NCBI GI
BLAST score
                  315
                  4.0e-29
E value
                  108
Match length
                  56
% identity
                  (AJ003246) 2'-hydroxydihydrodaidzein reductase [Glycine
NCBI Description
                  209224
Seq. No.
                  LIB3135-025-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914403
                  283
BLAST score
                  2.0e-25
E value
                  86
Match length
                   64
% identity
                  PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II)
NCBI Description
                   (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II)
                  >gi 2370335 emb_CAA73866_ (Y13466) protoporphyrinogen
                   oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_
                   (AB020500) mitochondrial protoporphyrinogen oxidase
                   [Nicotiana tabacum] >gi 4105188 (AF044129)
                  protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]
                   209225
Seq. No.
                   LIB3135-025-Q1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3643600
                   174
BLAST score
                   9.0e-14
E value
                   102
Match length
                   52
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   209226
Seq. No.
                   LIB3135-025-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3901018
                   151
BLAST score
                   2.0e-10
E value
Match length
                   55
% identity
                   58
                   (AJ130889) stress and pathogenesis-related protein [Fagus
NCBI Description
                   sylvatica]
                   209227
Seq. No.
Seq. ID
                   LIB3135-025-Q1-K1-E10
                   BLASTX
Method
                   q3337366
NCBI GI
                   150
BLAST score
                   1.0e-09
E value
```

148 Match length 16 % identity

NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No. 209228

BLAST score

E value

306 2.0e-28



```
LIB3135-025-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g3643600
NCBI GI
                  196
BLAST score
                  1.0e-30
E value
                  114
Match length
                  74
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                  209229
Seq. No.
                  LIB3135-025-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  q3334144
NCBI GI
                  188
BLAST score
                  1.0e-16
E value
                  65
Match length
% identity
                  72
                  G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698_dbj BAA13181
NCBI Description
                   (D86925) C-type cyclin [Oryza sativa]
                  209230
Seq. No.
                  LIB3135-025-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  q551444
NCBI GI
                  -148
BLAST score
                  1.0e-09
E value
                  89
Match length
% identity
                  35
NCBI Description (X79365) protein MFP-b [Cucumis sativus]
                   209231
Seq. No.
Seq. ID
                  LIB3135-025-Q1-K1-E7
Method
                  BLASTX
                   g3769673
NCBI GI
                   446
BLAST score
                   2.0e-44
E value
                   102
Match length
                   73
% identity
NCBI Description (AF095285) Tic20 [Pisum sativum]
                   209232
Seq. No.
                   LIB3135-025-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g3334147
NCBI GI
BLAST score
                   747
                   1.0e-79
E value
Match length
                   153
                   90
% identity
                  ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
NCBI Description
                   chitinase [Gossypium hirsutum]
                   209233
Seq. No.
Seq. ID
                   LIB3135-025-Q1-K1-F11
                   BLASTX
Method
NCBI GI
                   g3249105
```



```
Match length
                  75
% identity
                  (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  209234
                  LIB3135-025-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3294469
                  223
BLAST score
E value
                  3.0e-18
Match length
                  51
% identity
                  88
                  (U89342) phosphoglucomutase 2 [Zea mays]
NCBI Description
                  209235
Seq. No.
                  LIB3135-025-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  q1418331
NCBI GI
                  268
BLAST score
                   9.0e-24
E value
                   95
Match length
                   58
% identity
                   (X95909) receptor like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   209236
Seq. No.
                   LIB3135-025-Q1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3164222
                   153
BLAST score
                   4.0e-10
E value
                   98
Match length
% identity
                   40
                   (AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205
NCBI Description
                   (AF071527) RMA1 RING zinc finger protein [Arabidopsis
                   thaliana]
                   209237
Seq. No.
                   LIB3135-025-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                   g475602
NCBI GI
BLAST score
                   175
E value
                   8.0e-13
Match length
                   82
                   49
% identity
NCBI Description (U08384) BiP isoform A [Glycine max]
Seq. No.
                   209238
                   LIB3135-025-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   g1052973
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
Match length
                   128
```

28874

30

NCBI Description (U37838) fructokinase [Beta vulgaris]

% identity



```
209239
Seq. No.
Seq. ID
                  LIB3135-025-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g729618
BLAST score
                  455
                  2.0e-45
E value
Match length
                  112
                  81
% identity
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2)
NCBI Description
                  (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP
                  2) >gi 82172 pir PQ0262 luminal binding protein BLP-2 -
                  common tobacco (fragment) >gi 100338 pir S21878 heat shock
                  protein BiP homolog blp2 - common tobacco (fragment)
                  >gi 19807 emb CAA42661 (X60059) luminal binding protein
                  (BiP) [Nicotiana tabacum]
                  209240
Seq. No.
Seq. ID
                  LIB3135-025-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3335353
BLAST score
                  460
E value
                  5.0e-46
                  124
Match length
% identity
                  63
                  (AC004512) Similar to cytochrome P450 gb X90458 from A.
NCBI Description
                  thaliana. [Arabidopsis thaliana]
                  209241
Seq. No.
Seq. ID
                  LIB3135-025-Q1-K1-H2
                  BLASTX
Method
NCBI GI
                  g3183088
BLAST score
                  217
                  1.0e-17
E value
                  68
Match length
                  63
% identity
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                  (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
Seq. No.
                  209242
Seq. ID
                  LIB3135-025-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g112717
BLAST score
                  168
                  7.0e-13
E value
                  97
Match length
                  42
% identity
                  21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911
NCBI Description
                  hypothetical protein precursor - carrot
                  >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA
```

-22 to 171) [Daucus carota]

Seq. No. 209243

Seq. ID LIB3135-025-Q1-K1-H4

Method BLASTX

NCBI GI

BLAST score

```
NCBI GI
                   q3193285
BLAST score
                  153
E value
                  3.0e-10
Match length
                  92
                  33
% identity
                  (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  209244
                  LIB3135-025-Q1-K1-H5
Seq. ID
Method
                  BLASTX
                  g231573
NCBI GI
BLAST score
                  152
E value
                  6.0e-10
Match length
                  72
                  50
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                  >gi_99970_pir__S24757 asparaginase (EC 3.5.1.1) -
                  narrow-leaved blue lupine >gi_19135_emb_CAA43099_ (X60691)
                  developing seed L-asparaginase [Lupinus angustifolius]
                  209245
Seq. No.
Seq. ID
                  LIB3135-025-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q4454014
BLAST score
                  252
                  1.0e-21
E value
                  96
Match length
                  57
% identity
                 (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  209246
                  LIB3135-025-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415930
BLAST score
                  143
E value
                  3.0e-09
Match length
                  40
% identity
                  65
NCBI Description
                  (AC006418) unknown protein [Arabidopsis thaliana]
                  >gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                  209247
Seq. No.
Seq. ID
                  LIB3135-026-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2388575
BLAST score
                  253
E value
                  9.0e-22
Match length
                  104
% identity
                  47
NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]
Seq. No.
                  209248
Seq. ID
                  LIB3135-026-Q1-K1-A11
Method
                  BLASTX
```

28876

g1402912



```
E value
Match length
                  126
% identity
                  (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
                  209249
Seq. No.
                  LIB3135-026-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                  q2677830
NCBI GI
                  477
BLAST score
E value
                  5.0e-48
Match length
                  107
% identity
                  (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                  209250
Seq. No.
                  LIB3135-026-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  g3860323
NCBI GI
                  367
BLAST score
E value
                   4.0e-35
                  78
Match length
                  86
% identity
                  (AJ012688) hypothetical protein [Cicer arietinum]
NCBI Description
                  209251
Seq. No.
                  LIB3135-026-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4008544
                   168
BLAST score
                   7.0e-12
E value
                   104
Match length
                   37
% identity
                   (AL034492) putative nucleotide-sugar dehydratase
NCBI Description
                   [Streptomyces coelicolor]
                   209252
Seq. No.
                   LIB3135-026-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3335347
BLAST score
                   507
                   1.0e-51
E value
Match length
                   128
% identity
                   (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
                   gb_X98309 from Drosophila melanogaster. ESTs gb_T44383,
                   gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and
                   gb_AA042359 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   209253
                   LIB3135-026-Q1-K1-A8
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g585165
BLAST score 486
E value 2.0e-49
Match length 99
% identity 91



```
NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
                  (G6PD) >gi 2129985 pir S60287 glucose-6-phosphate
                  1-dehydrogenase (EC 1.1.1.49) - potato
                  >gi_471345_emb_CAA52442 (X74421) glucose-6-phosphate
                  1-dehydrogenase [Solanum tuberosum]
                  209254
Seq. No.
                  LIB3135-026-Q1-K1-A9
Seq. ID
Method
                  BLASTX
```

NCBI GI g2351097 BLAST score 386 E value 1.0e-37 90 Match length 80 % identity

(AB006810) ATMRK1 [Arabidopsis thaliana] NCBI Description

209255 Seq. No. LIB3135-026-Q1-K1-B1 Seq. ID Method BLASTX NCBI GI q116359 BLAST score 594

9.0e-62 E value Match length 139 % identity 76

HEVAMINE A (CHITINASE / LYSOZYME >gi\_82026\_pir\_\_S17205 NCBI Description chitinase (EC 3.2.1.14) hevamine - Para rubber tree

>gi 234388 bbs 52808 hevamine [Hevea brasiliensis, Peptide Partial, 273 aa] >gi 1311006 pdb 1HVQ Glycosidase, Chitin Degradation, Multifunctional Enzyme Mol\_id: 1; Molecule: Hevamine A; Chain: Null; Ec: 3.2.1.14,  $\overline{3}.2.1.17$ ; Heterogen: N-,N'-,N''-Triacetyl-Chitotriose; Other\_details: Plant EndochitinaseLYSOZYME >gi 1421554\_pdb\_1LLO\_ Hevamine A (A Plant EndochitinaseLYSOZYME) COMPLEXED WITH Allosamidin >qi 1942537 pdb 2HVM Hevamine A At 1.8 Angstrom

Resolution

209256 Seq. No.

LIB3135-026-Q1-K1-B11 Seq. ID

Method BLASTX q3747050 NCBI GI BLAST score 291 3.0e-26 E value 60 Match length % identity 88

(AF093540) ribosomal protein L26 [Zea mays] NCBI Description

209257 Seq. No.

Seq. ID LIB3135-026-Q1-K1-B12

BLASTX Method q1352821 NCBI GI 460 BLAST score 5.0e-46 E value Match length 85 96 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT) >qi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain



precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

```
209258
Seq. No.
                  LIB3135-026-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g117291
                  509
BLAST score
                  8.0e-52
E value
                  122
Match length
% identity
                  CHLOROPLAST PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) (P36)
NCBI Description
                   (E29) >gi_81464_pir__S03638 triose
                  phosphate/3-phosphoglycerate/phosphate translocator
                  precursor - spinach >gi 21274 emb_CAA32016_ (X13754)
                  phosphate translocator protein (AA 1 - 404) [Spinacia
                  oleracea]
                  209259
Seq. No.
                  LIB3135-026-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                  g2832672
NCBI GI
BLAST score
                  490
E value
                  1.0e-49
Match length
                  122
% identity
                  80
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                   209260
Seq. No.
                  LIB3135-026-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                   q231660
NCBI GI
                   344
BLAST score
E value
                   2.0e-32
                   128
Match length
% identity
                   57
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
                   209261
Seq. No.
                   LIB3135-026-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832683
BLAST score
                   537
E value
                   2.0e-55
Match length
                   131
                   74
% identity
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209262
                   LIB3135-026-Q1-K1-C3
Seq. ID
Method
                   BLASTX
                   q167311
NCBI GI
BLAST score
                   601
                   1.0e-62
E value
Match length
                   132
```

28879

NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]

88

% identity

Seq. No.

Seq. ID

209268

LIB3135-026-Q1-K1-D3



```
209263
Seq. No.
Seq. ID
                  LIB3135-026-Q1-K1-C5
                  BLASTX
Method
NCBI GI
                  g3834307
                  151
BLAST score
                  8.0e-10
E value
                  42
Match length
% identity
                  69
                   (AC005679) Strong similarity to gene T10I14.120 gi_2832679
NCBI Description
                  putative protein from Arabidopsis thaliana BAC gb AL021712.
                  ESTs gb N65887 and gb N65627 come from this gene.
                   [Arabidopsis thaliana]
                  209264
Seq. No.
Seq. ID
                  LIB3135-026-Q1-K1-C6
Method
                  BLASTX
                  g2760086
NCBI GI
BLAST score
                   320
                  1.0e-29
E value
Match length
                   94
% identity
                   46
NCBI Description
                  (Y16046) leucine-rich repeat protein [Arabidopsis thaliana]
                   209265
Seq. No.
                  LIB3135-026-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4567304
BLAST score
                   160
                   7.0e-11
E value
                   99
Match length
                   43
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                   209266
Seq. No.
Seq. ID
                   LIB3135-026-Q1-K1-C9
                   BLASTX
Method
NCBI GI
                   q445613
                   443
BLAST score
                   4.0e-44
E value
                   111
Match length
                   76
% identity
                  ribosomal protein L7 [Solanum tuberosum]
NCBI Description
Seq. No.
                   209267
Seq. ID
                   LIB3135-026-Q1-K1-D2
                   BLASTX
Method
NCBI GI
                   q4455223
BLAST score
                   483
                   1.0e-48
E value
Match length
                   139
                   33
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
```

NCBI GI BLAST score

E value

332

4.0e-31



```
Method
NCBI GI
                  q1619300
BLAST score
                   430
E value
                   9.0e-43
                   97
Match length
                   86
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  209269
Seq. No.
                  LIB3135-026-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4415941
BLAST score
                   175
                   1.0e-12
E value
                   47
Match length
                   30
% identity
                   (AC006418) putative arginine-serine rich splicing factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   209270
                   LIB3135-026-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3355311
BLAST score
                   443
                   3.0e-44
E value
                   105
Match length
% identity
                   85
                   (AJ009737) eukaryotic translation initiation factor 6 [Beta
NCBI Description
                   vulgaris]
                   209271
Seq. No.
                   LIB3135-026-Q1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3337352
BLAST score
                   328
E value
                   1.0e-30
Match length
                   107
% identity
                   61
                   (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
                   209272
Seq. No.
Seq. ID
                   LIB3135-026-Q1-K1-D8
Method
                   BLASTX
                   g2564066
NCBI GI
BLAST score
                   511
                   5.0e-52
E value
Match length
                   120
% identity
                   81
                   (D45900) LEDI-3 protein [Lithospermum erythrorhizon]
NCBI Description
                   209273
Seq. No.
Seq. ID
                   LIB3135-026-Q1-K1-E12
Method
                   BLASTX
                  g2832898
```



Match length 78 % identity (AJ000886) Tetrafunctional protein of glyoxysomal fatty NCBI Description acid beta-oxidation [Brassica napus] 209274 Seq. No. LIB3135-026-Q1-K1-E4 Seq. ID BLASTX Method g3169180 NCBI GI 391 BLAST score 6.0e-38 E value Match length 138 % identity 61 (AC004401) putative casein kinase II catalytic subunit NCBI Description [Arabidopsis thaliana] 209275 Seq. No. LIB3135-026-Q1-K1-E6 Seq. ID BLASTX Method g1076746 NCBI GI 150 BLAST score E value 3.0e-10 Match length 35 83 % identity heat shock protein 70 - rice (fragment) NCBI Description >gi 763160 emb CAA47948 (X67711) heat shock protein 70 [Oryza sativa] 209276 Seq. No. LIB3135-026-Q1-K1-F11 Seq. ID BLASTN Method NCBI GI g3402695 BLAST score 36 1.0e-10 E value 136 Match length 82 % identity Arabidopsis thaliana chromosome II BAC T3K9 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 209277 Seq. No. Seq. ID LIB3135-026-Q1-K1-F12 Method BLASTX g95985 NCBI GI BLAST score 170 5.0e-12 E value 109 Match length 36 % identity hypothetical protein (mrr 3' region) - Escherichia coli NCBI Description

(fragment) >gi 42021 emb CAA38118 (X54198) downstream ORF;

unknown function [Escherichia coli]

209278 Seq. No.

Seq. ID LIB3135-026-Q1-K1-F7

Method BLASTX NCBI GI g2959781 BLAST score 664 6.0e - 70E value



```
Match length
                   92
% identity
                  (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                  209279
Seq. No.
                  LIB3135-026-Q1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4558462
                   196
BLAST score
                   4.0e-15
E value
                   39
Match length
                   92
% identity
                  (AF079404) cell cycle switch protein [Medicago sativa
NCBI Description
                   subsp. X varia]
                   209280
Seq. No.
                   LIB3135-026-Q1-K1-G1
Seq. ID
                   BLASTN
Method
                   g4567193
NCBI GI
                   79
BLAST score
                   2.0e-36
E value
                   335
Match length
                   81
% identity
                  Arabidopsis thaliana chromosome II BAC T26C19 genomic
NCBI Description
                   sequence, complete sequence
                   209281
Seq. No.
                   LIB3135-026-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   q1079652
NCBI GI
BLAST score
                   220
                   7.0e-18
E value
                   63
Match length
                   65
% identity
NCBI Description (U38247) late embryogenesis abundant protein [Glycine soja]
                   209282
Seq. No.
                   LIB3135-026-Q1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2062173
                   366
BLAST score
E value
                   5.0e-35
                   99
Match length
                   69
 % identity
                   (AC001645) cell division protein FtsH isolog [Arabidopsis
NCBI Description
                   thaliana]
                   209283
 Seq. No.
                   LIB3135-026-Q1-K1-G2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q126078
                   345
 BLAST score
```

NCBI GI g126078 BLAST score 345 E value 1.0e-32 Match length 136 % identity 55

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
>gi 81554 pir S04046 embryonic abundant protein gD-34 -



upland cotton >gi\_18501\_emb\_CAA31594\_ (X13206) D-34 Lea protein [Gossypium hirsutum] >gi\_167385 (M19389) storage protein [Gossypium hirsutum] >gi\_226556\_prf\_\_1601521F Lea D-34 gene [Saguinus oedipus]

209284 Seq. No. Seq. ID LIB3135-026-Q1-K1-G6 Method BLASTX g3386615 NCBI GI 309 BLAST score 3.0e-28 E value 86 Match length 71 % identity (AC004665) putative phosphomannomutase [Arabidopsis NCBI Description thaliana] 209285 Seq. No. LIB3135-026-Q1-K1-G8 Seq. ID BLASTX Method g3641834 NCBI GI BLAST score 627 E value 1.0e-65 Match length 143 83 % identity (AJ007312) pyruvate dehydrogenase kinase [Arabidopsis NCBI Description thaliana] 209286 Seq. No.

Seq. ID LIB3135-026-Q1-K1-G9

Method BLASTX
NCBI GI g3738320
BLAST score 184
E value 1.0e-13
Match length 88
% identity 42

NCBI Description (AC005170) putative cinnamoyl CoA reductase [Arabidopsis

thaliana]

Seq. No. 209287

Seq. ID LIB3135-026-Q1-K1-H11

Method BLASTX
NCBI GI g3128228
BLAST score 307
E value 3.0e-28
Match length 66
% identity 85

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis

thaliana] >gi 3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 209288

Seq. ID LIB3135-026-Q1-K1-H6

Method BLASTX
NCBI GI g3643598
BLAST score 216
E value 2.0e-17
Match length 105

Seq. ID

Method NCBI GI



```
% identity-
                  (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  209289
Seq. No.
                  LIB3135-027-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  q1076511
NCBI GI
                  484
BLAST score
                  7.0e-49
E value
                  124
Match length
                  79
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                  >qi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase
                  [Phaseolus vulgaris]
Seq. No.
                  209290
                  LIB3135-027-Q1-K1-A9
Seq. ID
Method
                  BLASTX
                  g3913791
NCBI GI
                  278
BLAST score
E value
                  8.0e-25
Match length
                  102
% identity
                   60
                  GLUTAMATE--CYSTEINE LIGASE PRECURSOR
NCBI Description
                   (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS)
                  >gi 2407615 (AF017983) gamma-glutamylcysteine synthetase
                   [Lycopersicon esculentum]
                  209291
Seq. No.
                  LIB3135-027-Q1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g464734
                   718
BLAST score
                   3.0e-76
E value
                   145
Match length
                   93
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi 481237 pir S38379
                   adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle
                   >qi 407412 emb CAA81527 (Z26881) S-adenosyl-L-homocysteine
                   hydrolase [Catharanthus roseus]
                   209292
Seq. No.
Seq. ID
                   LIB3135-027-Q1-K1-B12
Method
                  BLASTX
                   g3342211
NCBI GI
BLAST score
                   287
                   9.0e-26
E value
                   105
Match length
                   59
% identity
                  (U89255) Pti4 [Lycopersicon esculentum]
NCBI Description
                   209293
Seq. No.
```

28885

LIB3135-027-Q1-K1-C12

BLASTX

q1313968



```
BLAST score 422
E value 2.0e-41
Match length 146
% identity 58
```

NCBI Description (Z72426) major allergen Mal d 1 [Malus domestica]

Seq. No. 209294

Seq. ID LIB3135-027-Q1-K1-D10

Method BLASTX
NCBI GI g4006934
BLAST score 136
E value 6.0e-09
Match length 87
% identity 43

NCBI Description (AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No. 209295

Seq. ID LIB3135-027-Q1-K1-D9

Method BLASTX
NCBI GI g3928099
BLAST score 436
E value 4.0e-43
Match length 154
% identity 31

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 209296

Seq. ID LIB3135-027-Q1-K1-E10

Method BLASTX
NCBI GI g3367517
BLAST score 225
E value 2.0e-18
Match length 130
% identity 34

NCBI Description (AC004392) Similar to F4I1.26 putative beta-glucosidase

gi\_3128187 from A. thaliana BAC gb\_AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene.

[Arabidopsis thaliana]

Seq. No. 209297

Seq. ID LIB3135-027-Q1-K1-E12

Method BLASTX
NCBI GI g4115948
BLAST score 159
E value 2.0e-12
Match length 64
% identity 62

NCBI Description (AF118223) contains similarity to CDP-alcohol

phosphatidyltransferases (Pfam: PF01066, score=13.7, E=

0.00016, n=1) [Arabidopsis thaliana]

Seq. No. 209298

Seq. ID LIB3135-027-Q1-K1-E9

Method BLASTX
NCBI GI g3096919
BLAST score 223
E value 3.0e-18



Match length % identity 44 (AL023094) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] Seq. No. 209299 LIB3135-027-Q1-K1-F12 Seq. ID Method BLASTX NCBI GI q3165536 BLAST score 543 E value 8.0e-56 Match length 130 % identity (AF067608) similar to DEAD-box helicases (Pfam: DEAD.hmm, NCBI Description score: 262.89) (Pfam: helicase C.hmm, score: 76.21) [Caenorhabditis elegans] Seq. No. 209300 LIB3135-027-Q1-K1-F9 Seq. ID Method BLASTX q1086651 NCBI GI 146 BLAST score E value 3.0e-09 Match length 66 45 % identity (U41015) similar to cystic fibrosis transmembrane NCBI Description conductance regulator and other ABC transporters (MDR subfamily) [Caenorhabditis elegans] Seq. No. 209301 LIB3135-027-Q1-K1-G11 Seq. ID Method BLASTX NCBI GI g1915974 BLAST score 441 E value 5.0e-44Match length 105 % identity 80 (U62329) fructokinase [Lycopersicon esculentum] >gi\_2102693 NCBI Description (U64818) fructokinase [Lycopersicon esculentum] 209302 Seq. No. LIB3135-027-Q1-K1-H10 Seq. ID BLASTX Method NCBI GI g4539405 188 BLAST score 3.0e-14E value 83 Match length

% identity 51

(AL049524) putative ribosomal protein L9, cytosolic NCBI Description

[Arabidopsis thaliana]

209303 Seq. No.

Seq. ID LIB3135-027-Q1-K1-H11

Method BLASTX NCBI GI g4510363 BLAST score 393 E value 4.0e-38



Match length 87 % identity (AC007017) putative DNA-binding protein [Arabidopsis NCBI Description thaliana] 209304 Seq. No.

LIB3135-028-Q1-K1-A10 Seq. ID BLASTX Method g480450 NCBI GI 414 BLAST score 1.0e-40 E value

89 Match length 90 % identity

ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis NCBI Description thaliana >gi 402552 emb CAA49506\_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

209305 Seq. No.

LIB3135-028-Q1-K1-A4 Seq. ID

BLASTX Method g3386621 NCBI GI BLAST score 264 4.0e-23 E value 62 Match length % identity

(AC004665) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 209306

LIB3135-028-Q1-K1-A5 Seq. ID

BLASTX Method g3036798 NCBI GI 157 BLAST score E value 2.0e-10 129 Match length

% identity 36

(AL022373) putative protein [Arabidopsis thaliana] NCBI Description

>gi 3805860 emb CAA21480 (AL031986) putative protein

[Arabidopsis thaliana]

209307 Seq. No.

Seq. ID LIB3135-028-Q1-K1-A7

Method BLASTX NCBI GI g2459417 BLAST score 389 E value 9.0e-38 103 Match length % identity

(AC002332) putative pre-mRNA splicing factor PRP19 NCBI Description

[Arabidopsis thaliana]

209308 Seq. No.

Seq. ID LIB3135-028-Q1-K1-A8

BLASTX Method q3386621 NCBI GI BLAST score 202 E value 7.0e-16 56 Match length



% identity NCBI Description (AC004665) unknown protein [Arabidopsis thaliana] 209309 Seq. No. LIB3135-028-Q1-K1-A9 Seq. ID Method BLASTX NCBI GI g3913791 BLAST score 598 4.0e-62 E value 128 Match length % identity GLUTAMATE--CYSTEINE LIGASE PRECURSOR NCBI Description (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi 2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum] 209310 Seq. No. Seq. ID LIB3135-028-Q1-K1-B10 Method BLASTX q480450 NCBI GI 298 BLAST score 5.0e-27 E value Match length 84 % identity 71 ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis NCBI Description thaliana >gi\_402552\_emb CAA49506\_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana] Seq. No. 209311 LIB3135-028-Q1-K1-B12 Seq. ID Method BLASTX NCBI GI g3869088 BLAST score 625 E value 2.0e-65 Match length 120 % identity 99 NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata] Seq. No. 209312 LIB3135-028-Q1-K1-B2 Seq. ID Method BLASTX NCBI GI g3874214 BLAST score 162 E value 3.0e-11 Match length 88 % identity 41 (Z83217) Similarity to Yeast E1-E2 ATPase YEL031W NCBI Description (SW:YED1\_YEAST); cDNA EST EMBL:D27574 comes from this gene;

cDNA EST EMBL: D33757 comes from this gene; cDNA EST EMBL: D34256 comes from this gene; cDNA EST EMBL: D37288

comes from

209313 Seq. No.

Seq. ID LIB3135-028-Q1-K1-B3

BLASTX Method g2129871 NCBI GI BLAST score 165



```
3.0e-12
E value
                  83
Match length
% identity
                  proline-rich protein, 14K - kidney bean >gi_1420885
NCBI Description
                   (U34333) proline-rich 14 kDa protein [Phaseolus vulgaris]
                  209314
Seq. No.
                  LIB3135-028-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  272
E value
                  6.0e-24
Match length
                  55
% identity
                   91
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                   209315
                  LIB3135-028-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3128228
BLAST score
                   455
                   2.0e-45
E value
                   92
Match length
                   92
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   209316
Seq. No.
                   LIB3135-028-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g3044214
NCBI GI
                   328
BLAST score
                   1.0e-30
E value
                   126
Match length
                   54
% identity
                  (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]
NCBI Description
                   209317
Seq. No.
Seq. ID
                   LIB3135-028-Q1-K1-C3
                   BLASTX
Method
                   g2497752
NCBI GI
BLAST score
                   192
                   2.0e-14
E value
                   68
Match length
```

% identity 57

NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description >qi 1321911 emb CAA65475 (X96714) lipid transfer protein

[Prunus dulcis]

209318 Seq. No.

LIB3135-028-Q1-K1-C5 Seq. ID

Method BLASTX NCBI GI q1076809 BLAST score 586

```
E value
Match length
                  141
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                  >qi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase
                  [Zea mays]
                  209319
Seq. No.
                  LIB3135-028-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3287824
BLAST score
                  311
E value
                  1.0e-28
                  68
Match length
                  93
% identity
                  (+)-DELTA-CADINENE SYNTHASE ISOZYME XC1 (D-CADINENE
NCBI Description
                  SYNTHASE) >gi_2147015_pir__S68365 (+)-delta-cadinene
                  synthase isozyme XC1 - Gossypium arboreum >gi 1045312
                  (U23206) (+)-delta-cadinene synthase isozyme XC1 [Gossypium
                  arboreum]
                  209320
Seq. No.
Seq. ID
                  LIB3135-028-Q1-K1-C9
Method
                  BLASTX
                  q3044214
NCBI GI
                  400
BLAST score
                  5.0e-39
E value
                  124
Match length
% identity
                  (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]
NCBI Description
                  209321
Seq. No.
                  LIB3135-028-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2828296
BLAST score
                  439
                  1.0e-43
E value
Match length
                  93
                  61
% identity
NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]
                  209322
Seq. No.
                  LIB3135-028-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2828296
BLAST score
                  428
E value
                  3.0e-42
Match length
                  93
                  59
% identity
NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]
```

Seq. No. 209323

Seq. ID LIB3135-028-Q1-K1-D2

Method BLASTX
NCBI GI g2262172
BLAST score 395
E value 2.0e-38



```
Match length
                   58
% identity
                   (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   209324
Seq. No.
Seq. ID
                   LIB3135-028-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                   g4106061
BLAST score
                   142
                   5.0e-09
E value
                   63
Match length
                   49
% identity
                  (AF053318) CCR4-associated factor 1 [Homo sapiens]
NCBI Description
Seq. No.
                   209325
Seq. ID
                   LIB3135-028-Q1-K1-D6
Method
                   BLASTN
NCBI GI
                   g18511
                   318
BLAST score
E value
                   1.0e-179
Match length
                   362
% identity
                   97
NCBI Description G.hirsutum light regulated unknown reading frame DNA
                   209326
Seq. No.
                   LIB3135-028-Q1-K1-D7
Seq. ID
Method
                   BLASTN
                   g18511
NCBI GI
                   114
BLAST score
                   2.0e-57
E value
                   222
Match length
% identity
                   88
NCBI Description G.hirsutum light regulated unknown reading frame DNA
                   209327
Seq. No.
Seq. ID
                   LIB3135-028-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   q3128228
BLAST score
                   565
E value
                   2.0e-58
Match length
                   114
                   91
% identity
NCBI Description
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
                   thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
Seq. No.
                   209328
Seq. ID
                   LIB3135-028-Q1-K1-E1
                   BLASTX
Method
NCBI GI
                   g3183088
```

Method BLASTX
NCBI GI g3183088
BLAST score 209
E value 2.0e-16
Match length 71
% identity 56

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi 629658 pir S47084 lipid transfer like protein -

Seq. ID

Method

NCBI GI



cowpea >gi\_499034\_emb\_CAA56113\_ (X79604) lipid transfer like protein [Vigna unguiculata]

209329 Seq. No. Seq. ID LIB3135-028-Q1-K1-E2  ${\tt BLASTX}$ Method g4580721 NCBI GI 140 BLAST score 4.0e-09 E value Match length 68 49 % identity (AF136163) phosphoenolpyruvate carboxykinase 4 [Urochloa NCBI Description panicoides] 209330 Seq. No. Seq. ID LIB3135-028-Q1-K1-E8 Method BLASTX q464628 NCBI GI BLAST score 167 1.0e-12 E value Match length 69 % identity 57 60S RIBOSOMAL PROTEIN L22 (EPSTEIN-BARR VIRUS SMALL RNA NCBI Description ASSOCIATED PROTEIN) (EBER ASSOCIATED PROTEIN) (EAP) (HEPARIN BINDING PROTEIN HBP15) >gi 542841 pir JC2120 heparin-binding protein 15 - human >gi\_31062\_emb\_CAA42007\_(X59357) Epstein-Barr virus small RNA associated protein [Homo sapiens] >gi\_409070\_dbj\_BAA04545\_(D17652) HBp15/L22 [Homo sapiens] >gi\_4506613\_ref\_NP\_000974.1\_pRPL22\_ ribosomal protein L22 209331 Seq. No. Seq. ID LIB3135-028-Q1-K1-E9 Method BLASTX NCBI GI g100351 470 BLAST score 4.0e-47 E value Match length 137 % identity 64 pathogenesis-related protein 4A - common tobacco NCBI Description >gi 19962 emb CAA41437 (X58546) pathogenesis-related protein 4A [Nicotiana tabacum] 209332 Seq. No. Seq. ID LIB3135-028-Q1-K1-F1 Method BLASTX g4127862 NCBI GI BLAST score 325 E value 4.0e-30 78 Match length % identity (AJ010423) glyoxalase I [Glycine max] NCBI Description 209333 Seq. No.

28893

LIB3135-028-Q1-K1-F11

BLASTX

q3549691

E value

Match length

1.0e-31

89



```
BLAST score
E value
                   3.0e-10
Match length
                   30
 % identity
                   87
                   (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
NCBI Description
Seq. No.
                   209334
Seq. ID
                   LIB3135-028-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3334245
BLAST score
                   157
E value
                   4.0e-11
Match length
                   54
% identity
                   57
NCBI Description
                   LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                   (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                   MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                   >gi_2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer
                   arietinum]
Seq. No.
                   209335
Seq. ID
                   LIB3135-028-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   q1220196
BLAST score
                   739
E value
                   1.0e-78
Match length
                   158
% identity
                   91
NCBI Description
                   (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                   209336
Seq. ID
                   LIB3135-028-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g1220196
BLAST score
                   159
E value
                   6.0e-16
Match length
                   96
% identity
                   61
NCBI Description
                   (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                   209337
Seq. ID
                  LIB3135-028-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                   g3337095
BLAST score
                  215
E value
                  2.0e-17
Match length
                  107
% identity
                   30
NCBI Description
                  (AB016206) polygalacturonase inhibitor (PGIP) [Citrus iyo]
Seq. No.
                  209338
Seq. ID
                  LIB3135-028-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3108053
BLAST score
                  336
```



% identity (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea NCBI Description mays] 209339 Seq. No. LIB3135-028-Q1-K1-G4 Seq. ID BLASTX Method g3914666 NCBI GI BLAST score 365 6.0e-35 E value 82 Match length % identity 84 CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR NCBI Description >gi\_2791998\_emb\_CAA74895\_ (Y14566) ribosomal protein L4
[Arabidopsis thaliana] >gi\_2792000\_emb\_CAA74894\_ (Y14565) ribosomal protein L4 [Arabidopsis Thaliana] 209340 Seq. No. LIB3135-028-Q1-K1-G6 Seq. ID Method BLASTX NCBI GI q401189 BLAST score 469 E value 4.0e-47 Match length 111 83 % identity WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP) NCBI Description (TURGOR-RESPONSIVE PROTEIN 7A) >gi\_485511 pir S33617 trg-31 protein - garden pea >gi\_20426\_emb\_CAA79159\_ (Z18288) trg-31 [Pisum sativum] 209341 Seq. No. LIB3135-028-Q1-K1-G7 Seq. ID Method BLASTX g3158474 NCBI GI BLAST score 464 2.0e-46 E value 116 Match length 80 % identity NCBI Description (AF067184) aquaporin 1 [Samanea saman] 209342 Seq. No. Seq. ID LIB3135-028-Q1-K1-G8 BLASTX Method g3861189 NCBI GI BLAST score 137 1.0e-11 E value 83 Match length 55 % identity (AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia NCBI Description prowazekii]

209343 Seq. No.

Seq. ID LIB3135-028-Q1-K1-H1

BLASTX Method NCBI GI g2642648 BLAST score 511 4.0e-52 E value



Match length 89 % identity (AF033852) cytosolic heat shock 70 protein; HSC70-3 NCBI Description [Spinacia oleracea] >gi\_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi\_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea] Seq. No. 209344 LIB3135-028-Q1-K1-H3 Seq. ID Method BLASTX NCBI GI g1203832 BLAST score 265 E value 3.0e-23 Match length 133 % identity (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII NCBI Description [Hordeum vulgare] >gi\_1588407\_prf\_\_2208395A beta-D-glucan exohydrolase [Hordeum vulgare] 209345 Seq. No. Seq. ID LIB3135-028-Q1-K1-H5 Method BLASTX NCBI GI q4262226 BLAST score 198 2.0e-15 ¥. E value Match length 104 % identity (AC006200) putative protein kinase [Arabidopsis thaliana] NCBI Description 209346 Seq. No. LIB3135-028-Q1-K1-H9 Seq. ID Method BLASTX NCBI GI g2246380 BLAST score 281 5.0e-25 E value 72 Match length 67 % identity (Z86095) peptidyl-prolyl cis-trans isomerase [Arabidopsis NCBI Description thaliana] 209347 Seq. No. Seq. ID LIB3135-029-Q1-K1-A1 BLASTX Method g2191146 NCBI GI 362 BLAST score 1.0e-34 E value 85 Match length 80 % identity (AF007269) MAP Kinase [Arabidopsis thaliana] NCBI Description

209348 Seq. No.

LIB3135-029-Q1-K1-A2 Seq. ID

BLASTX Method g231574 NCBI GI BLAST score 379 1.0e-36 E value Match length 113



```
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                  >gi 81837 pir__S22523 asparaginase (EC 3.5.1.1) - tree
                  lupine (fragment) >gi_19137_emb_CAA36824_ (X52588)
                  asparaginase [Lupinus arboreus]
                  209349
Seq. No.
                  LIB3135-029-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  g231574
NCBI GI
                  322
BLAST score
                  6.0e-30
E value
                  110
Match length
                  59
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                  >gi 81837 pir S22523 asparaginase (EC 3.5.1.1) - tree
                  lupine (fragment) >gi_19137_emb_CAA36824_ (X52588)
                  asparaginase [Lupinus arboreus]
                  209350
Seq. No.
                  LIB3135-029-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q541920
                  487
BLAST score
                  3.0e-53
E value
                  143
Match length
                  77
% identity
NCBI Description Acetoacyl-CoA-thiolase - radish
                  209351
Seq. No.
                  LIB3135-029-Q1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g537404
                  198
BLAST score
                  1.0e-22
E value
                  66
Match length
% identity
                  (D26537) WSI76 protein induced by water stress [Oryza
NCBI Description
                  sativa]
                  209352
Seq. No.
Seq. ID
                  LIB3135-029-Q1-K1-A7
                  BLASTX
Method
NCBI GI
                  g3786008
BLAST score
                  202
                  9.0e-16
E value
                  100
Match length
                  53
% identity
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
                  209353
Seq. No.
Seq. ID
                  LIB3135-029-Q1-K1-B1
```

Method BLASTX NCBI GI g3695408 BLAST score 290 E value 4.0e-26 Match length 86



71

56

Match length

% identity

```
% identity
                  (AF096373) contains similarity to Solanum lycopersicum
NCBI Description
                   (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                   thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable
                  wound-induced protein [Arabidopsis thaliana]
                  209354
Seq. No.
                  LIB3135-029-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g515616
                  497
BLAST score
E value
                  2.0e-50
Match length
                  119
                   78
% identity
NCBI Description
                   (X61608) LHC II Type III chlorophyll a /b binding protein
                   [Brassica napus]
Seq. No.
                   209355
                  LIB3135-029-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4056493
BLAST score
                   408
E value
                   6.0e-40
Match length
                   126
% identity
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209356
                   LIB3135-029-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2414158
BLAST score
                   348
E value
                   7.0e-33
Match length
                   132
% identity
NCBI Description (Z72436) major allergen Bet v 1 [Betula pendula]
                   209357
Seq. No.
Seq. ID
                   LIB3135-029-Q1-K1-C10
Method
                   BLASTX
                   g4006914
NCBI GI
BLAST score
                   320
                   8.0e-30
E value
Match length
                   95
% identity
                   66
                   (Z99708) serine C-palmitoyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   209358
Seq. No.
                   LIB3135-029-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   q3183088
NCBI GI
                   209
BLAST score
                   1.0e-16
E value
```

28898

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

NCBI Description

209364

Seq. No.

(LTP) >gi\_629658\_pir\_\_S47084 lipid transfer like protein -cowpea >gi\_499034\_emb\_CAA56113\_ (X79604) lipid transfer like protein [Vigna unguiculata]

```
Seq. No.
                  209359
Seq. ID
                  LIB3135-029-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  g167318
BLAST score
                  47
                  2.0e-17
E value
                  127
Match length
% identity
                  84
                  Cotton legumin A D-genome alloallele gene, complete cds
NCBI Description
Seq. No.
                  209360
                  LIB3135-029-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739371
                  320
BLAST score
E value
                  1.0e-29
Match length
                  68
% identity
                  90
NCBI Description
                  (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                  209361
                  LIB3135-029-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82130
                  230
BLAST score
                  8.0e-28
E value
Match length
                  94
                  71
% identity
NCBI Description
                  beta-1,3-glucanase (EC 3.2.1.-) precursor - curled-leaved
                   tobacco >gi 170243 (M63634) beta(1,3)-glucanase regulator
                   [Nicotiana plumbaginifolia]
                  209362
Seq. No.
                  LIB3135-029-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3641868
BLAST score
                  383
E value
                  5.0e-37
Match length
                  105
                  70
% identity
                  (AJ011012) hypothetical protein [Cicer arietinum]
NCBI Description
                  209363
Seq. No.
Seq. ID
                  LIB3135-029-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3702332
BLAST score
                   232
E value
                  1.0e-19
Match length
                  87
% identity
                   54
```

28899

(AC005397) unknown protein [Arabidopsis thaliana]



```
Seq. ID
                   LIB3135-029-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                   q3033386
BLAST score
                   168
E value
                   6.0e-15
Match length
                   90
                   57
% identity
NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]
                  209365
Seq. No.
Seq. ID
                  LIB3135-029-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1420938
BLAST score
                  286
E value
                  1.0e-25
                  77
Match length
% identity
                   71
NCBI Description
                   (U61379) Vigna unguiculata ascorbate peroxidase mRNA,
                  complete cds [Vigna unguiculata]
Seq. No.
                  209366
Seq. ID
                  LIB3135-029-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1170745
BLAST score
                  338
E value
                  1.0e-31
Match length
                  94
% identity
                   68
NCBI Description
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >qi 167326
                   (M88321) Group 4 late embryogenesis-abundant protein
                   [Gossypium hirsutum] >gi 167328 (M88322) Group 4 late
                   embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  209367
Seq. ID
                  LIB3135-029-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2511574
BLAST score
                  724
E value
                  6.0e-77
Match length
                  151
% identity
                  95
NCBI Description
                  (Y13176) multicatalytic endopeptidase [Arabidopsis
                  thaliana] >gi 3421075 (AF043520) 20S proteasome subunit
                  PAB1 [Arabidopsis thaliana]
Seq. No.
                  209368
Seq. ID
                  LIB3135-029-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g116923
BLAST score
                  157
E value
                  3.0e-18
Match length
                  71
% identity
                  59
NCBI Description
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
```

>gi\_111414\_pir\_\_S13520 beta-COP protein - rat

>gi\_55819 emb CAA40505 (X57228) beta COP [Rattus

norvegicus]

28900

. 50



```
Seq. No.
                  209369
Seq. ID
                  LIB3135-029-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1871577
BLAST score
                  244
E value
                  9.0e-21
                  125
Match length
% identity
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                  209370
Seq. No.
Seq. ID
                  LIB3135-029-Q1-K1-E8
Method
                  BLASTN
                  q4544435
NCBI GI
                  35
BLAST score
                  4.0e-10
E value
Match length
                  96
% identity
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
NCBI Description
                  sequence, complete sequence
                  209371
Seq. No.
Seq. ID
                  LIB3135-029-Q1-K1-E9
Method
                  BLASTX
                  q710626
NCBI GI
                  153
BLAST score
                   4.0e-10
E value
Match length
                   43
                   60
% identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
                   209372
Seq. No.
                   LIB3135-029-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3790252
BLAST score
                   178
                   4.0e-13
E value
Match length
                   94
% identity
                   41
                  (AL031966) putative Zn-protease [Schizosaccharomyces pombe]
NCBI Description
                   209373
Seq. No.
                   LIB3135-029-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   q2493052
NCBI GI
BLAST score
                   319
                   1.0e-29
E value
                   69
Match length
                   83
% identity
                  ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL
NCBI Description
```

mitochondrial F1-ATPase [Arabidopsis thaliana]

>gi 1655486 dbj BAA13602\_ (D88377) epsilon subunit of

Seq. ID



```
Seq. No.
                  209374
                  LIB3135-029-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760330
BLAST score
                  396
                  1.0e-38
E value
Match length
                  102
                  74
% identity
NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana]
Seq. No.
                  209375
Seq. ID
                  LIB3135-029-Q1-K1-G11
Method
                  BLASTX
                  q3201613
NCBI GI
                  218
BLAST score
                  8.0e-18
E value
                  97
Match length
% identity
                  49
NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]
                  209376
Seq. No.
                  LIB3135-029-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2118319
                  242
BLAST score
                   2.0e-20
E value
                   72
Match length
                   65
% identity
                  1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
NCBI Description
                   LE-ACS3 - tomato (strain VFNT) >gi_508609 (L34171)
                   1-aminocyclopropane-1-carboxylate synthase [Lycopersicon
                   esculentum] >gi 1561696 (U18055) ACC synthase [Lycopersicon
                   esculentum]
Seq. No.
                   209377
                   LIB3135-029-Q1-K1-G6
Seq. ID
Method
                   BLASTN
                   g4455229
NCBI GI
BLAST score
                   46
                   7.0e-17
E value
Match length
                   74
                   91
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
NCBI Description
                   (ESSAII project)
                   209378
Seq. No.
                   LIB3135-029-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244855
                   235
BLAST score
                   1.0e-19
E value
                   106
Match length
                   50
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   209379
Seq. No.
```

28902

LIB3135-029-Q1-K1-G8

```
BLASTX
Method
                  q1431629
NCBI GI
                  180
BLAST score
                  3.0e-13
E value
                  56
Match length
                  57
% identity
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                  209380
Seq. No.
                  LIB3135-029-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  604
                   6.0e-63
E value
Match length
                  120
                   57
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   209381
                  LIB3135-029-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g730456
BLAST score
                   164
                   8.0e-12
E value
Match length
                   61
                   54
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   209382
Seq. No.
                   LIB3135-029-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   g4165861
NCBI GI
```

BLAST score 233 1.0e-19 E value Match length 99 % identity 24

NCBI Description (AF006603) histone deacetylase mHDA2 [Mus musculus]

209383 Seq. No. LIB3135-029-Q1-K1-H6 Seq. ID BLASTX Method g4432859 NCBI GI BLAST score 184

1.0e-13 E value 77 Match length 49 % identity

NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

209384 Seq. No.

Seq. ID LIB3135-031-Q1-K1-A2

BLASTX Method g2398679 NCBI GI BLAST score 709 3.0e-75 E value 139 Match length 97 % identity

NCBI Description (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate



## synthase [Morinda citrifolia]

```
209385
Seq. No.
Seq. ID
                   LIB3135-031-Q1-K1-A6
Method
                   BLASTX
                   q1709498
NCBI GI
BLAST score
                   569
                   9.0e-59
E value
                   143
Match length
                   73
% identity
NCBI Description
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                    [Arabidopsis thaliana]
                   209386
Seq. No.
Seq. ID
                   LIB3135-031-Q1-K1-B1
Method
                   BLASTX
                   g289920
NCBI GI
BLAST score
                    451
                    4.0e-45
E value
Match length
                   108
                    80
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                    209387
Seq. No.
                   LIB3135-031-Q1-K1-B2
Seq. ID
Method
                   BLASTN
                    q3821780
NCBI GI
BLAST score
                    36
                    9.0e-11
E value
                    36
Match length
% identity
                    100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                    209388
                    LIB3135-031-Q1-K1-B5
Seq. ID
Method
                    BLASTN
NCBI GI
                    q407800
BLAST score
                    391
                    0.0e + 00
E value
                    424
Match length
                    99
% identity
                    G.hirsutum mRNA for ribosomal protein 41, large subunit
NCBI Description
                    (RL41)
Seq. No.
                    209389
                    LIB3135-031-Q1-K1-B6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1085827
BLAST score
                    410
                    4.0e-40
E value
                    126
Match length
% identity
                    69
                    H-protein - Flaveria cronquistii >gi_547519_emb_CAA85755_
NCBI Description
                    (Z37518) H-protein [Flaveria cronquistii]
```



```
Seq. No.
                  209390
Seq. ID
                  LIB3135-031-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1730109
BLAST score
                  527
E value
                  8.0e-54
                  124
Match length
% identity
                  LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                  HYDROXYLASE) >gi_499022_emb_CAA53580_ (X75966)
                  leucoanthocyanidin dioxygenase [Vitis vinifera]
                  209391
Seq. No.
                  LIB3135-031-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  g1778370
NCBI GI
BLAST score
                  150
                  8.0e-10
E value
Match length
% identity
NCBI Description (U77678) asparagine synthetase 2 [Glycine max]
Seq. No.
                  209392
                  LIB3135-031-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g3063396
NCBI GI
                  607
BLAST score
E value
                  3.0e-63
                  132
Match length
% identity
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  209393
Seq. ID
                  LIB3135-031-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                 g167367
BLAST score
                  550
E value
                  2.0e-56
Match length
                  141
% identity
                  78
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  209394
                  LIB3135-031-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707939
BLAST score
                  583
E value
                  1.0e-60
Match length
                  113
                  96
% identity
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
NCBI Description
                  PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
```

PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi\_1076256\_pir\_\_S51943

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small

chain B1 precursor - beet (fragment)





>gi\_556622\_emb\_CAA55515\_ (X78899) glucose-1-phosphate adenylyltransferase [Beta vulgaris]

209395 Seq. No. Seq. ID LIB3135-031-Q1-K1-C3 Method BLASTX NCBI GI q4249402 BLAST score 452 E value 5.0e-45 Match length 141 % identity NCBI Description (AC006072) unknown protein [Arabidopsis thaliana] 209396 Seq. No. Seq. ID LIB3135-031-Q1-K1-C6 Method BLASTX NCBI GI g1362055 BLAST score 304 E value 8.0e-28 Match length 65 92 % identity phosphogluconate dehydrogenase (decarboxylating) (EC NCBI Description 1.1.1.44) - alfalfa >gi\_603221 (U18239) 6-phosphogluconate dehydrogenase [Medicago sativa subsp. sativa] Seq. No. 209397 LIB3135-031-Q1-K1-C7 Seq. ID Method BLASTX NCBI GI q1076746 437 BLAST score E value 3.0e-43 Match length 107 % identity 81 NCBI Description

heat shock protein 70 - rice (fragment)

>gi\_763160\_emb\_CAA47948\_ (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 209398

Seq. ID LIB3135-031-Q1-K1-C8

Method BLASTX NCBI GI g464840 BLAST score 372 E value 9.0e-36 72 Match length % identity

TUBULIN ALPHA-1 CHAIN >gi 421781 pir S32666 tubulin NCBI Description

alpha-1 chain - fern (Anemia phyllitidis)

>gi\_296494\_emb CAA48927 (X69183) alpha tubulin [Anemia

phyllitidis]

209399 Seq. No.

Seq. ID LIB3135-031-Q1-K1-C9

Method BLASTX NCBI GI g1477428 BLAST score 646 E value 9.0e-68 Match length 123



% identity NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare] 209400 Seq. No. LIB3135-031-Q1-K1-D12 Seq. ID Method BLASTX NCBI GI g4455246 394 BLAST score 2.0e-40 E value Match length 120

% identity NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 209401 LIB3135-031-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI g3461884

BLAST score 358 4.0e-34 E value Match length 118 % identity 62

(AB006082) phosphoribosyl-ATP pyrophosphohydrolase NCBI Description

[Arabidopsis thaliana] >gi\_3461886\_dbj\_BAA32529\_ (AB006083)

- ريانيور

phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis

thaliana]

Seq. No. 209402

LIB3135-031-Q1-K1-D3 Seq. ID

Method BLASTX NCBI GI g119350 BLAST score 653 E value 1.0e-68 Match length 138 % identity

ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description

> (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_81608\_pir\_\_JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi\_16271\_emb\_CAA41114\_ (X58107) enolase

[Arabidopsis thaliana]

Seq. No. 209403

LIB3135-031-Q1-K1-D7 Seq. ID

Method BLASTX NCBI GI g3928089 BLAST score 460 E value 5.0e-46 Match length 150 % identity 60

(AC005770) putative osr40 [Arabidopsis thaliana] NCBI Description

209404 Seq. No.

LIB3135-031-Q1-K1-E10 Seq. ID

BLASTX Method NCBI GI g3282505 BLAST score 390 9.0e-38 E value 138 Match length



% identity

(AF020786) polyphenol oxidase precursor [Prunus armeniaca] NCBI Description

Seq. No.

209405

Seq. ID

LIB3135-031-Q1-K1-E11

Method

BLASTX g1694976

NCBI GI BLAST score 464

E value Match length 2.0e-46129

% identity

NCBI Description

(Y09482) HMG1 [Arabidopsis thaliana]

>qi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis

thalianal

Seq. No.

209406

Seq. ID

LIB3135-031-Q1-K1-E12

Method NCBI GI BLASTN g13906

BLAST score

84

E value Match length 2.0e-39 134

% identity

NCBI Description Maize mitochondrial DNA for integrated cms S-1 element

Seq. No.

209407

Seq. ID

LIB3135-031-Q1-K1-E2

Method NCBI GI BLAST score BLASTX g730645 535

E value Match length

8.0e-55 115

% identity

90

NCBI Description

40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal protein S15 - Arabidopsis thaliana >gi\_313152 emb CAA80679

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi 313188 emb CAA80681 (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi 1903366 gb AAB70449 (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788, gb\_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.

209408

Seq. ID

LIB3135-031-Q1-K1-E3

Method

BLASTX g2429280

NCBI GI

770

BLAST score E value

3.0e-82

Match length

159

% identity NCBI Description

89 (AF014055) asparagine synthetase [Triphysaria versicolor] >gi 2429282 (AF014056) asparagine synthetase [Triphysaria

versicolor] >gi\_2429284 (AF014057) asparagine synthetase

[Triphysaria versicolor]

Seq. No.

209409

Seq. ID

LIB3135-031-Q1-K1-E5

Method

NCBI GI

BLASTX

g2827143



```
Method
NCBI GI
                   q2500376
BLAST score
                   472
                   2.0e-47
E value
                   95
Match length
                   95
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494
                    (AC005508) 23552 [Arabidopsis thaliana]
                   209410
Seq. No.
Seq. ID
                   LIB3135-031-Q1-K1-E6
Method
                   BLASTX
                   g600855
NCBI GI
                   396
BLAST score
                   2.0e-38
E value
                   127
Match length
% identity
                   62
                   (U17887) bZIP protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209411
                   LIB3135-031-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4193388
BLAST score
                   468
E value
                   6.0e-47
Match length
                   117
% identity
                   (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                   brasiliensis]
                   209412
Seq. No.
Seq. ID
                   LIB3135-031-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   g133829
BLAST score
                    193
E value
                   9.0e-15
Match length
                   59
                    66
% identity
NCBI Description
                   30S RIBOSOMAL PROTEIN S17, CHLOROPLAST PRECURSOR (CS17)
                   >gi_81948_pir__B35542 ribosomal protein S17 - garden pea
(fragment) >gi_169068 (M31025) ribosomal protein S17 [Pisum
                    sativum]
Seq. No.
                    209413
                   LIB3135-031-Q1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                    g3337361
BLAST score
                    236
                    1.0e-19
E value
Match length
                    66
% identity
                   (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                    209414
Seq. No.
                   LIB3135-031-Q1-K1-F3
Seq. ID
```

% identity

69



```
BLAST score
E value
                  4.0e-53
Match length
                  135
                  73
% identity
NCBI Description (AF027174) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
Seq. No.
                  209415
                  LIB3135-031-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g167367
                  762
BLAST score
E value
                  2.0e-81
Match length
                  143
                  99
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  209416
Seq. No.
                  LIB3135-031-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  g2982303
NCBI GI
                  190
BLAST score
                  1.0e-21
E value
Match length
                  84
% identity
                   67
NCBI Description (AF051236) hypothetical protein [Picea mariana]
                  209417
Seq. No.
                  LIB3135-031-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                   g3269288
NCBI GI
                   304
BLAST score
                   1.0e-27
E value
Match length
                   64
% identity
                   89
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                   209418
Seq. No.
                   LIB3135-031-Q1-K1-G2
Seq. ID
Method
                   BLASTN
                   q434990
NCBI GI
                   33
BLAST score
                   5.0e-09
E value
Match length
                   45
                   93
% identity
NCBI Description O.berteriana mitochondrial trnI gene
                   209419
Seq. No.
Seq. ID
                   LIB3135-031-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   q3033384
BLAST score
                   393
E value
                   4.0e-38
Match length
                   104
```

NCBI Description (AC004238) putative CTP synthase [Arabidopsis thaliana]

NCBI Description



```
209420
Seq. No.
Seq. ID
                  LIB3135-031-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3236259
BLAST score
                  368
                  3.0e-35
E value
Match length
                  84
% identity
                  80
                  (AC004684) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  209421
Seq. No.
Seq. ID
                  LIB3135-031-Q1-K1-G9
Method
                  BLASTX
                  g3874214
NCBI GI
BLAST score
                  247
                  6.0e-21
E value
                  155
Match length
% identity
                  40
                   (Z83217) Similarity to Yeast E1-E2 ATPase YEL031W
NCBI Description
                   (SW:YED1 YEAST); cDNA EST EMBL:D27574 comes from this gene;
                  cDNA EST EMBL: D33757 comes from this gene; cDNA EST
                  EMBL: D34256 comes from this gene; cDNA EST EMBL: D37288
                  comes from
Seq. No.
                  209422
Seq. ID
                  LIB3135-031-Q1-K1-H1
Method
                  BLASTX
                  g3790587
NCBI GI
BLAST score
                   327
                   2.0e-30
E value
Match length
                   156
% identity
NCBI Description
                   (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                   thaliana]
Seq. No.
                   209423
Seq. ID
                   LIB3135-031-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   q2739004
BLAST score
                   155
E value
                   2.0e-10
Match length
                   52
% identity
                   63
NCBI Description (AF022461) CYP82Clp [Glycine max]
Seq. No.
                   209424
Seq. ID
                   LIB3135-031-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   g2497752
BLAST score
                   274
                   4.0e-24
E value
                   87
Match length
                   59
% identity
```

28911

[Prunus dulcis]

NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)

>gi\_1321911\_emb\_CAA65475\_ (X96714) lipid transfer protein



```
209425
Seq. No.
                   LIB3135-031-Q1-K1-H5
Seq. ID
Method
                   BLASTX
                   g2055384
NCBI GI
BLAST score
                   224
                   3.0e-18
E value
                   84
Match length
% identity
                   26
                   (U69633) cold-stress inducible protein [Solanum tuberosum]
NCBI Description
                   209426
Seq. No.
                   LIB3135-031-Q1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244750
                   604
BLAST score
                   6.0e-63
E value
                   117
Match length
                   97
% identity
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                   >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                 209427
Seq. No.
                   LIB3135-031-Q1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3157924
                   383
BLAST score
                   6.0e-37
E value
                   125
Match length
% identity
                   60
                   (AC002131) Contains homology to extensin-like protein
NCBI Description
                   gb_D83227 from Populus nigra. ESTs gb H76425, gb T13883,
                   gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951
                   come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like
                   protein [Arabidopsis thaliana]
                   209428
Seq. No.
Seq. ID
                   LIB3135-031-Q1-K1-H8
Method
                   BLASTX
                   q1352681
NCBI GI
                   436
BLAST score
                   3.0e-43
E value
Match length
                   138
% identity
                   63
                   PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457
NCBI Description
                   phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
                   thaliana >gi_633028_dbj_BAA07287_ (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
```

Seq. No. 209429

Seq. ID LIB3135-031-Q1-K1-H9

Method BLASTX
NCBI GI g633890
BLAST score 199
E value 2.0e-15

% identity

80



```
Match length
% identity
                   69
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
                   209430
Seq. No.
                   LIB3135-032-Q1-K1-A10
Seq. ID
Method
                   BLASTX
                   g2564237
NCBI GI
BLAST score
                   558
                   1.0e-57
E value
                   108
Match length
                   88
% identity
                   (Y10112) omega-6 desaturase [Gossypium hirsutum]
NCBI Description
                   209431
Seq. No.
                   LIB3135-032-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g629483
NCBI GI
                   193
BLAST score
                   9.0e-17
E value
                   86
Match length
                   57
% identity
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                   >gi 158432\overline{2}pr\overline{f} 212237\overline{4}C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   209432
Seq. No.
                   LIB3135-032-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g4512667
NCBI GI
BLAST score
                   209
                   1.0e-16
E value
Match length
                   74
                   55
% identity
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                   209433
Seq. No.
                   LIB3135-032-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   q4545262
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
Match length
                   43
                   65
% identity
                    (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                   hirsutum]
                    209434
Seq. No.
                   LIB3135-032-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                    q1709690
                    231
BLAST score
E value
                    2.0e-19
Match length
                    55
```





PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) NCBI Description REDUCTASE) >qi 1076454 pir S55365 probable peptide methionine sulfoxide reductase - rape >qi 853739 emb CAA88538\_ (Z48619) peptide methionine sulfoxide reductase [Brassica napus] >gi 1143406\_emb\_CAA63919\_ (X94225) methionine sulfoxide reductase [Brassica napus] 209435 Seq. No. LIB3135-032-Q1-K1-A7 Seq. ID Method BLASTN NCBI GI q3821780 BLAST score 32 E value 2.0e-09 36 Match length 97 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 209436 Seq. No. LIB3135-032-Q1-K1-B1 Seq. ID Method BLASTX q3176715 NCBI GI BLAST score 400 E value 5.0e-39 Match length 119 % identity 63 (AC002392) putative receptor-like protein kinase NCBI Description [Arabidopsis thaliana] 209437 Seq. No. LIB3135-032-Q1-K1-B10 Seq. ID Method BLASTX q4455363 NCBI GI BLAST score 148 8.0e-10 E value Match length 84 % identity (AL035524) Medicago nodulin N21-like protein [Arabidopsis NCBI Description thaliana] 209438 Seq. No. LIB3135-032-Q1-K1-B12 Seq. ID Method BLASTN NCBI GI g434989 BLAST score 245 1.0e-135 E value Match length 322 94 % identity NCBI Description O.berteriana mitochondrial trnC and trnN genes 209439 Seq. No. LIB3135-032-Q1-K1-B7 Seq. ID

BLASTX Method g1352347 NCBI GI 248 BLAST score 3.0e-21 E value 57 Match length



```
% identity
                  ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
NCBI Description
                  >gi 480620_pir__S37103 translation elongation factor eEF-1
                  beta-A1 chain - Arabidopsis thaliana (cv. Colombia)
                  >gi 398608 emb_CAA52751_ (X74733) elongation factor-1 beta
                  Al [Arabidopsis thaliana]
                  209440
Seq. No.
                  LIB3135-032-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4049342
BLAST score
                  165
E value
                  2.0e-11
                  112
Match length
% identity
                  (AL034567) adenylate translocator (brittle-1)-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  209441
Seq. No.
                  LIB3135-032-Q1-K1-C10
Seq. ID
                  BLASTN
Method
                  q1204097
NCBI GI
BLAST score
                  71
E value
                  8.0e-32
                  83
Match length
                  96
% identity
NCBI Description H.annuus mitochodrial trnG gene
Seq. No.
                   209442
                  LIB3135-032-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4056488
BLAST score
                   307
                   4.0e-28
E value
Match length
                   79
                   71
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   209443
                   LIB3135-032-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g1743354
NCBI GI
                   207
BLAST score
                   1.0e-16
E value
                   61
Match length
                   66
% identity
NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
```

209444 Seq. No.

Seq. ID LIB3135-032-Q1-K1-C8

BLASTX Method g1171035 NCBI GI BLAST score 181 2.0e-13 E value 43 Match length 74 % identity

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504

>gi\_1086021\_pir\_\_S48038 metallothionein-like protein - kiwi fruit >gi\_450245 (L27813) metallothionein-like protein [Actinidia deliciosa]

Seq. No. 209445 LIB3135-032-Q1-K1-C9 Seq. ID BLASTN Method NCBI GI g1204097 BLAST score 103 1.0e-50 E value 298 Match length 93 % identity NCBI Description H.annuus mitochodrial trnG gene

Seq. No. 209446 Seq. ID LIB3135-032-Q1-K1-D1

Seq. ID LIB3135Method BLASTX
NCBI GI g3860272
BLAST score 603
E value 7.0e-63
Match length 126
% identity 91

NCBI Description (AC005824) putative suppressor protein [Arabidopsis

thaliana] >gi\_4314399\_gb\_AAD15609\_ (AC006232) putative skd1

protein [Arabidopsis thaliana]

Seq. No. 209447

Seq. ID LIB3135-032-Q1-K1-D11

Method BLASTX
NCBI GI g2832898
BLAST score 677
E value 2.0e-71
Match length 148
% identity 87

NCBI Description (AJ000886) Tetrafunctional protein of glyoxysomal fatty

acid beta-oxidation [Brassica napus]

Seq. No. 209448

Seq. ID LIB3135-032-Q1-K1-D12

Method BLASTX
NCBI GI 93402758
BLAST score 429
E value 1.0e-42
Match length 94
% identity 89

NCBI Description (AL031187) serine/threonine kinase - like protein

[Arabidopsis thaliana]

Seq. No. 209449

Seq. ID LIB3135-032-Q1-K1-D2

Method BLASTX
NCBI GI g2065531
BLAST score 485
E value 3.0e-50
Match length 121
% identity 74

NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. ID

Method



```
209450
Seq. No.
                  LIB3135-032-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3334659
NCBI GI
                  355
BLAST score
                  9.0e - 34
E value
Match length
                  128
% identity
                  51
                  (Y10489) putative cytochrome P450 [Glycine max]
NCBI Description
                  209451
Seq. No.
                  LIB3135-032-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g4510361
NCBI GI
                  315
BLAST score
                   4.0e-29
E value
                   69
Match length
                  83
% identity
                   (AC007017) putative DNA-binding protein RAV2 [Arabidopsis
NCBI Description
                  thaliana]
                   209452
Seq. No.
                  LIB3135-032-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3426049
                   336
BLAST score
                   1.0e-31
E value
                   94
Match length
                   71
% identity
                   (ACO05168) unknown protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   209453
Seq. No.
                   LIB3135-032-Q1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3757521
                   326
BLAST score
                   3.0e-30
E value
Match length
                   132
% identity
                   (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                   209454
Seq. No.
                   LIB3135-032-Q1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2275196
BLAST score
                   307
                   3.0e-28
E value
Match length
                   79
% identity
                   72
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   209455
Seq. No.
```

28917

LIB3135-032-Q1-K1-F2

BLASTX

```
q4432845
NCBI GI
BLAST score
                  209
E value
                  5.0e-18
                  119
Match length
                   47
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  209456
Seq. No.
                  LIB3135-032-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3850821
BLAST score
                   582
E value
                  2.0e-60
Match length
                   122
                   93
% identity
                  (Y18350) U2 snRNP auxiliary factor, large subunit
NCBI Description
                   [Nicotiana plumbaginifolia]
Seq. No.
                   209457
                   LIB3135-032-Q1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g170920
BLAST score
                   153
E value
                   4.0e-10
Match length
                   28
% identity
                   96
NCBI Description (M62396) ribosomal protein L41 [Candida maltosa]
                   209458
Seq. No.
                   LIB3135-032-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g3236242
NCBI GI
                   228
BLAST score
E value
                   8.0e-19
                   57
Match length
% identity
                   81
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   209459
                   LIB3135-032-Q1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245394
                   203
BLAST score
E value
                   5.0e-16
Match length
                   120
% identity
                   (U89771) ARF1-binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209460
                   LIB3135-032-Q1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g136739
BLAST score
                   145
E value
                   2.0e-09
Match length
                   49
```

28918

65

% identity



UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE NCBI Description

PYROPHOSPHORYLASE) (UDPGP) >gi\_67061\_pir\_XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi\_218001\_dbj BAA00570 (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

209461 Seq. No.

LIB3135-032-Q1-K1-G9 Seq. ID

BLASTX Method g4512685 NCBI GI 253 BLAST score 7.0e-22 E value 117 Match length

% identity

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 4559325 gb AAD22987.1\_AC007087\_6 (AC007087)

hypothetical protein [Arabidopsis thaliana]

209462 Seq. No.

LIB3135-032-Q1-K1-H1 Seq. ID

BLASTX Method g464986 NCBI GI 243 BLAST score 6.0e-21 E value Match length 46 98 % identity

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana

>gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391\_emb\_CAA51201\_ (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

209463 Seq. No.

LIB3135-032-Q1-K1-H3 Seq. ID

BLASTX Method g1705463 NCBI GI 459 BLAST score 4.0e-46 E value Match length 101

% identity NCBI Description

BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi\_2129547 pir\_\_S71201 biotin sythase - Arabidopsis thaliana >gi\_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi 1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi 1769457 (L34413)

biotin synthase [Arabidopsis thaliana] >gi\_2288983

(AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >qi 1589016 prf 2209438A biotin synthase [Arabidopsis

thaliana]

209464 Seg. No.

LIB3135-032-Q1-K1-H7 Seq. ID



Method BLASTX
NCBI GI g1705463
BLAST score 212
E value 1.0e-17
Match length 63
% identity 67

NCBI Description
BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi\_2129547\_pir\_\_S71201
biotin sythase - Arabidopsis thaliana >gi\_1045316 (U24147)
biotin sythase [Arabidopsis thaliana] >gi\_1403662 (U31806)
BIO2 protein [Arabidopsis thaliana] >gi\_1769457 (L34413)
biotin synthase [Arabidopsis thaliana] >gi\_2288983

(AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi 1589016 prf 2209438A biotin synthase [Arabidopsis

thaliana]

Seq. No. 209465

Seq. ID LIB3135-033-Q1-K1-A12

Method BLASTX
NCBI GI g2492530
BLAST score 245
E value 7.0e-21
Match length 52
% identity 87

NCBI Description CHLOROPLAST AMINOPEPTIDASE 1 PRECURSOR (LEUCINE

AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE

AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi\_924630 (U20594)

leucine aminopeptidase [Solanum lycopersicum]

Seq. No. 209466

Seq. ID LIB3135-033-Q1-K1-A3

Method BLASTX
NCBI GI g4006872
BLAST score 307
E value 5.0e-28
Match length 79
% identity 76

NCBI Description (Z99707) methionyl aminopeptidase-like protein [Arabidopsis

thaliana]

Seq. No. 209467

Seq. ID LIB3135-033-Q1-K1-A4

Method BLASTX
NCBI GI g2146740
BLAST score 204
E value 5.0e-16
Match length 80
% identity 47

NCBI Description inner mitochondrial membrane protein - Arabidopsis thaliana

>gi\_603056 (U18126) inner mitochondrial membrane protein

[Arabidopsis thaliana]

Seq. No. 209468

Seq. ID LIB3135-033-Q1-K1-A6

Method BLASTX
NCBI GI g2708532
BLAST score 439
E value 1.0e-43



Match length 26 % identity (AF029351) putative RNA binding protein [Nicotiana tabacum] NCBI Description 209469 Seq. No. LIB3135-033-Q1-K1-A7 Seq. ID BLASTX Method NCBI GI g746510 343 BLAST score 3.0e-32 E value 109 Match length 54 % identity NCBI Description (U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans] 209470 Seq. No. LIB3135-033-Q1-K1-A9 Seq. ID BLASTX Method g3426048 NCBI GI 243 BLAST score 1.0e-20 E value 60 Match length 78 % identity (AC005168) putative hydroxymethylglutaryl-CoA lyase NCBI Description precursor [Arabidopsis thaliana] 209471 Seq. No. LIB3135-033-Q1-K1-B10 Seq. ID BLASTX Method g1076758 NCBI GI 137 BLAST score 1.0e-08 E value 52 Match length 50 % identity heat-shock protein precursor - rye >gi\_2130093\_pir\_\_S65776 NCBI Description heat-shock protein, 82K, precursor - rye >gi 556673\_emb\_CAA82945\_ (Z30243) heat-shock protein [Secale cereale] Seq. No. 209472 Seq. ID LIB3135-033-Q1-K1-C11 Method BLASTX g2499115 NCBI GI 482 BLAST score E value 1.0e-48 138 Match length 67 % identity VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi\_1835788 NCBI Description (U86662) VPS41 [Lycopersicon esculentum]

Seq. No. 209473

Seq. ID LIB3135-033-Q1-K1-C2

Method BLASTX
NCBI GI g4467096
BLAST score 316
E value 2.0e-29
Match length 103



% identity NCBI Description (AL035538) putative protein [Arabidopsis thaliana] 209474 Seq. No. LIB3135-033-Q1-K1-C3 Seq. ID Method BLASTX NCBI GI g2565275 BLAST score 184 1.0e-13 E value Match length -52 % identity 79 NCBI Description (AF023611) Dimlp homolog [Homo sapiens] 209475 Seq. No. LIB3135-033-Q1-K1-C7 Seq. ID BLASTX Method q2388575 NCBI GI BLAST score 141 1.0e-08 E value 126 Match length % identity (AC000098) YUP8H12.18 [Arabidopsis thaliana] NCBI Description Seq. No. 209476 LIB3135-033-Q1-K1-D1 Seq. ID BLASTX Method g475048 NCBI GI 638 BLAST score E value 7.0e-67 136 Match length % identity 64 (X72581) tonoplast intrinsic protein gamma (gamma-TIP) NCBI Description [Arabidopsis thaliana] Seq. No. 209477 LIB3135-033-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI g3319882 BLAST score 220 E value 3.0e-18 Match length 90 53 % identity (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer NCBI Description arietinum] 209478 Seq. No. Seq. ID LIB3135-033-Q1-K1-D7

Method BLASTX q4038044 NCBI GI 300 BLAST score 3.0e-27 E value

90 Match length 60 % identity

(AC005936) unknown protein [Arabidopsis thaliana] NCBI Description >gi\_4406788\_gb\_AAD20098\_ (AC006532) unknown protein

[Arabidopsis thaliana]



```
209479
Seq. No.
Seq. ID
                  LIB3135-033-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4038044
BLAST score
                  382
                  8.0e-37
E value
Match length
                  102
% identity
                   (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4406788 gb_AAD20098_ (AC006532) unknown protein
                   [Arabidopsis thaliana]
Seq. No.
                  209480
                  LIB3135-033-Q1-K1-E2
Seq. ID
Method
                  BLASTX
                  q2935300
NCBI GI
                  570
BLAST score
E value
                  5.0e-59
Match length
                  117
                  96
% identity
                   (AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                  2 [Gossypium hirsutum]
Seq. No.
                  209481
                  LIB3135-033-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g4107037
NCBI GI
                   154
BLAST score
E value
                   3.0e-10
Match length
% identity
                   (AB021862) HMG-CoA reductase [Cucumis melo]
NCBI Description
Seq. No.
                   209482
Seq. ID
                   LIB3135-033-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   q4038044
BLAST score
                   119
E value
                   3.0e-13
Match length
                   62
% identity
                   (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4406788_gb_AAD20098_ (AC006532) unknown protein
                   [Arabidopsis thaliana]
                   209483
Seq. No.
Seq. ID
                   LIB3135-033-Q1-K1-E6
Method
                   BLASTX
                   g2935300
NCBI GI
                   576
BLAST score
                   1.0e-59
E value
                   126
Match length
                   90
% identity
```

NCBI Description (AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase

2 [Gossypium hirsutum]

Seq. No. 209484



```
LIB3135-033-Q1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q464987
                   760
BLAST score
                   4.0e-81
E value
                   144
Match length
                   96
% identity
NCBI Description
```

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi\_421858\_pir\_\_S32672 ubiquitin--protein ligase (EC

6.3.2.19) UBC10 - Arabidopsis thaliana

>gi\_297878\_emb\_CAA78715\_ (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi\_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

```
209485
Seq. No.
                  LIB3135-033-Q1-K1-E9
Seq. ID
                  BLASTX
Method
                  g1402900
NCBI GI
                  292
BLAST score
                  2.0e-26
E value
```

Match length 103 53 % identity

(X98322) peroxidase [Arabidopsis thaliana] NCBI Description

>gi 1429219 emb CAA67312\_ (X98776) peroxidase ATP13a

[Arabidopsis thaliana]

209486 Seq. No. LIB3135-033-Q1-K1-F1 Seq. ID Method BLASTX NCBI GI q464987 BLAST score 421 1.0e-41 E value

Match length 109 % identity 76

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi\_421858\_pir\_\_S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana

>gi 297878 emb CAA78715 (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

209487 Seq. No.

Seq. ID LIB3135-033-Q1-K1-F11

Method BLASTX q986969 NCBI GI 331 BLAST score E value 7.0e-31 120 Match length % identity 56

NCBI Description (L28005) TGACG-motif-binding protein [Glycine max]

209488 Seq. No.

Seq. ID LIB3135-033-Q1-K1-F12

Method BLASTX g3064039 NCBI GI



```
BLAST score
                     3.0e-24
  E value
  Match length
                     131
  % identity
                     42
                     (AF054445) major latex protein homolog [Mesembryanthemum
  NCBI Description
                     crystallinum]
                     209489
  Seq. No.
                     LIB3135-033-Q1-K1-F4
  Seq. ID
  Method
                     BLASTX
                     g487046
  NCBI GI
  BLAST score
                     447
                     2.0e-44
  E value
  Match length
                     148
  % identity
                     64
                     photosystem I chain II precursor - wood tobacco
  NCBI Description
                     >gi 407769 dbj BAA02871_ (D13718) PSI-D1 precursor
                     [Nicotiana sylvestris]
  Seq. No.
                     209490
                     LIB3135-033-Q1-K1-F9
  Seq. ID
  Method
                     BLASTX
                     g1723242
  NCBI GI
                     145
  BLAST score
                     4.0e-09
  E value
  Match length
                     51
                     57
  % identity
                     HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I
  NCBI Description
                     >qi 1177363 emb CAA93239 (Z69240) yeast dsk2 homolog,
                     ubiquitin-like protein [Schizosaccharomyces pombe]
                     209491
  Seq. No.
                     LIB3135-033-Q1-K1-G3
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g1350720
                     405
  BLAST score
                     2.0e-39
  E value
  Match length
                     85
                     88
   % identity
                     60S RIBOSOMAL PROTEIN L32
  NCBI Description
                     209492
  Seq. No.
                     LIB3135-033-Q1-K1-G5
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g1350720
                     405
  BLAST score
                     1.0e-39
  E value
  Match length
                     85
                     88
   % identity
                     60S RIBOSOMAL PROTEIN L32
  NCBI Description
```

Seq. No. 209493

Seq. ID LIB3135-033-Q1-K1-G7

Method BLASTX
NCBI GI g1350720
BLAST score 404
E value 2.0e-39



```
Match length
                   88
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
                   209494
Seq. No.
                   LIB3135-033-Q1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539405
                   480
BLAST score
                   6.0e-52
E value
                   140
Match length
                   79
% identity
                  (AL049524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
                   209495
Seq. No.
                   LIB3135-033-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g1174171
NCBI GI
                   349
BLAST score
                   5.0e-33
E value
                   122
Match length
                   54
% identity
NCBI Description (U44947) NTH1 [Pisum sativum]
                   209496
Seq. No.
                   LIB3135-033-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g218157
NCBI GI
                   483
BLAST score
                   6.0e-49
E value
                   106
Match length
                   90
% identity
                   (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
Seq. No.
                   209497
                   LIB3135-033-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                    q1082403
NCBI GI
BLAST score
                    276
                    1.0e-24
E value
Match length
                    118
                    47
% identity
                   glutamine--phenylpyruvate transaminase (EC 2.6.1.64) -
NCBI Description
                    human >gi 2146953 pir S69001 glutamine--phenylpyruvate aminotransferase (EC 2.6.1.64) - human
                    >gi 758591 emb_CAA57702_ (X82224) glutamine--phenylpyruvate
                    aminotransferase [Homo sapiens]
                    209498
 Seq. No.
                    LIB3135-033-Q1-K1-H4
 Seq. ID
                    BLASTX
Method
```

Method BLASTX
NCBI GI g4539296
BLAST score 220
E value 8.0e-18
Match length 42
% identity 83

Seq. ID

```
(AL049480) putative pathogenesis-related protein
NCBI Description
                   [Arabidopsis thaliana]
                   209499
 Seq. No.
                   LIB3135-033-Q1-K1-H8
 Seq. ID
                   BLASTX
 Method
                   g4539296
 NCBI GI
                   211
 BLAST score
                   6.0e-17
 E value
                   42
 Match length
                   81
 % identity
                    (AL049480) putative pathogenesis-related protein
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                   209500
                   LIB3135-034-Q1-K1-A1
 Seq. ID
                   BLASTX
 Method
                   g2341039
 NCBI GI
 BLAST score
                   147
                    6.0e-10
 E value
 Match length
                   50
                   58
 % identity
                   (AC000104) Similar to Nicotiana lesion-inducing ORF
 NCBI Description
                    (gb U66269). [Arabidopsis thaliana]
                   209501
 Seq. No.
                   LIB3135-034-Q1-K1-A11
 Seq. ID
                   BLASTX
 Method
                   g2996124
 NCBI GI
                    184
 BLAST score
                    6.0e-14
 E value
                    40
 Match length
                    78
 % identity
                    (AF051735) hypothetical protein [Picea mariana]
NCBI Description
                    209502
 Seq. No.
                    LIB3135-034-Q1-K1-A2
 Seq. ID
                    BLASTX
 Method
                    q3805853
 NCBI GI
 BLAST score
                    355
                    4.0e-34
 E value
                    76
 Match length
 % identity
                    (AL031986) putative protein [Arabidopsis thaliana]
 NCBI Description
                    209503
 Seq. No.
                    LIB3135-034-Q1-K1-A4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3327222
 BLAST score
                    217
                    9.0e-18
 E value
                    95
 Match length
 % identity
                    47
                    (AB014604) KIAA0704 protein [Homo sapiens]
 NCBI Description
                    209504
 Seq. No.
```

LIB3135-034-Q1-K1-A5

```
BLASTX
Method
NCBI GI
                  g131773
BLAST score
                  190
                  5.0e-15
E value
                  43
Match length
                  88
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >gi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
Seq. No.
                  209505
Seq. ID
                  LIB3135-034-Q1-K1-B1
Method
                  BLASTX
                  q1177047
NCBI GI
                   205
BLAST score
                   1.0e-16
E value
                   52
Match length
                   81
% identity
                   14 KD ZINC-BINDING PROTEIN (PROTEIN KINASE C INHIBITOR)
NCBI Description
                   (PKCI) >gi_629857_pir__S44158 protein kinase C inhibitor -
                   maize >gi_473187_emb_CAA82751_ (Z29643) protein kinase C
                   inhibitor [Zea mays]
Seq. No.
                   209506
                   LIB3135-034-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   g3395441
NCBI GI
                   318
BLAST score
                   1.0e-29
E value
                   86
Match length
                   72
% identity
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   209507
Seq. No.
                   LIB3135-034-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g126156
                   231
BLAST score
E value
                   1.0e-19
Match length
                   75
% identity
                   68
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                   [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
 Seq. No.
                   209508
 Seq. ID
                   LIB3135-034-Q1-K1-B12
 Method
                   BLASTX
                   q586053
 NCBI GI
 BLAST score
                   172
                   1.0e-12
 E value
                   59
 Match length
 % identity
                   51
 NCBI Description SULFITE OXIDASE PRECURSOR >gi_1083807_pir__A53107 sulfite
```



oxidase (EC 1.8.3.1) precursor, mitochondrial - rat
>gi 294639 (L05084) sulfite oxidase [Rattus norvegicus]

209509 Seq. No. LIB3135-034-Q1-K1-B5 Seq. ID BLASTX Method q3122659 NCBI GI 376 BLAST score 2.0e-36 E value Match length 91 74 % identity PEROXIREDOXIN (REHYDRIN HOMOLOG) >gi\_1926269\_emb\_CAA72804\_ NCBI Description (Y12089) peroxiredoxin [Arabidopsis thaliana] Seq. No. 209510 LIB3135-034-Q1-K1-B7 Seq. ID Method BLASTX q3914239 NCBI GI BLAST score 154 2.0e-12 E value Match length 63 % identity 63 PROTEIN PHOSPHATASE 2C ABI2 (PP2C) NCBI Description >gi\_1945140\_emb\_CAA70163\_ (Y08966) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi\_1945142\_emb\_CAA70162 (Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi 2564213 emb CAA72538 (Y11840) ABI2 [Arabidopsis thaliana] 209511 Seq. No. LIB3135-034-Q1-K1-C1 Seq. ID Method BLASTX q1184077 NCBI GI 287 BLAST score 8.0e-26 E value 128 Match length % identity 2 (U42445) Cf-2.2 [Lycopersicon pimpinellifolium] NCBI Description 209512 Seq. No. LIB3135-034-Q1-K1-C11 Seq. ID BLASTX Method g2598599 NCBI GI 315 BLAST score 5.0e-29 E value 88 Match length % identity 67 (Y15372) MtN4 [Medicago truncatula] NCBI Description 209513 Seq. No. LIB3135-034-Q1-K1-C4 Seq. ID Method BLASTX q1173187 NCBI GI 176 BLAST score

28929

3.0e-13

48

69

E value Match length

% identity



71

% identity

```
40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
Seq. No.
                  209514
Seq. ID
                  LIB3135-034-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2467088
BLAST score
                  257
E value
                  1.0e-22
Match length
                  80
% identity
                  64
NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana]
                  209515
Seq. No.
Seq. ID
                  LIB3135-034-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1173218
BLAST score
                  284
E value
                  5.0e-26
Match length
                  62
% identity
                  90
NCBI Description
                  40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  209516
Seq. ID
                  LIB3135-034-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  293
E value
                  2.0e-26
Match length
                  79
% identity
                  71
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  209517
Seq. ID
                  LIB3135-034-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g470373
BLAST score
                  152
E value
                  7.0e-10
Match length
                  76
% identity
                  43
NCBI Description
                  (U00047) ZK418.5 gene product [Caenorhabditis elegans]
Seq. No.
                  209518
Seq. ID
                  LIB3135-034-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q4406808
BLAST score
                  197
E value
                  2.0e-15
Match length
                  56
```

28930

NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]



```
209519
Seq. No.
                  LIB3135-034-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g4006894
NCBI GI
                  159
BLAST score
                  5.0e-11
E value
                  68
Match length
                  43
% identity
                  (Z99708) homeodomain protein [Arabidopsis thaliana]
NCBI Description
                  209520
Seq. No.
                  LIB3135-034-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g2088651
NCBI GI
BLAST score
                  505
                  2.0e-51
E value
Match length
                  123
                  72
% identity
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   209521
Seq. No.
                  LIB3135-034-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                   g1403138
NCBI GI
BLAST score
                   406
                   7.0e-40
E value
Match length
                   99
% identity
                   73
                   (X98190) peroxidase ATP2a [Arabidopsis thaliana]
NCBI Description
                   >qi 4371288 gb AAD18146 (AC006260) putative peroxidase
                   ATPZa [Arabidopsis thaliana]
                   209522
Seq. No.
                   LIB3135-034-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g2385344
NCBI GI
                   404
BLAST score
                   8.0e-40
E value
                   86
Match length
                   93
% identity
                   (Y14567) sigma factorB [Arabidopsis thaliana]
NCBI Description
                   209523
Seq. No.
                   LIB3135-034-Q1-K1-E12
Seq. ID
                   BLASTN
Method
                   g2829205
NCBI GI
                   81
BLAST score
                   8.0e-38
E value
                   232
Match length
                   15
% identity
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
```

Seq. No. 209524

Seq. ID LIB3135-034-Q1-K1-E5

Method BLASTX



```
q399052
  NCBI GI
BLAST score
                    199
  E value
                    1.0e-15
  Match length
                     67
  % identity
                     51
                    ACETYLGLUTAMATE KINASE (NAG KINASE) (AGK)
  NCBI Description
                     (N-ACETYLGLUTAMATE 5-PHOSPHOTRANSFERASE)
                    >gi_485454_pir__S28959 acetylglutamate kinase (EC 2.7.2.8)
                     - red alga (Porphyra umbilicalis) chloroplast
                    >gi_2147073_pir__S73249 acetylglutamate kinase (EC 2.7.2.8)
                    argB - Porphyra purpurea chloroplast >gi_343131 (M94625)
                    N-acetylglutamate kinase [Porphyra umbilīcalis] >gi_1276794
                     (U38804) acetylglutamate kinase [Porphyra purpurea]
  Seq. No.
                    209525
                    LIB3135-034-Q1-K1-E8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g4539346
                    107
  BLAST score
                     1.0e-08
  E value
  Match length
                     82
                     46
  % identity
  NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
  Seq. No.
                     209526
                    LIB3135-034-Q1-K1-E9
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                     g642244
  BLAST score
                     253
  E value
                     6.0e-22
  Match length
                     52
                     87
  % identity
                    (X84055) mammalian acyl CoA oxidase homologous [Hordeum
  NCBI Description
                     vulgare]
                     209527
  Seq. No.
                     LIB3135-034-Q1-K1-F10
  Seq. ID
  Method
                     BLASTX
                     g3551838
  NCBI GI
  BLAST score
                     396
                     8.0e-39
  E value
  Match length
                     98
                     80
  % identity
                    (AF070967) SKP1-like protein [Nicotiana clevelandii]
  NCBI Description
  Seq. No.
                     209528
                     LIB3135-034-Q1-K1-F9
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g2129898
                     321
  BLAST score
  E value
                     1.0e-29
                     74
  Match length
                     78
  % identity
                     UDPqlucose--starch glucosyltransferase (EC 2.4.1.11)
  NCBI Description
                     isoform II precursor - garden pea >gi_385412_bbs_131619
                     granule-bound starch synthase isoform II, GBSSII [Pisum
```

sativum=peas, BC1/9RR, Peptide, 752 aa]

NCBI GI

BLAST score

g3821280

473



```
209529
Seq. No.
                  LIB3135-034-Q1-K1-G1
Seq. ID
Method
                  BLASTN
                  g19212
NCBI GI
                  36
BLAST score
                  9.0e-11
E value
Match length
                  190
% identity
                  34
NCBI Description Tomato extensin mRNA (clone w17-1)
                  209530
Seq. No.
                  LIB3135-034-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  g3288883
NCBI GI
                  225
BLAST score
                   1.0e-18
E value
                   85
Match length
                   56
% identity
                  (AB015431) SAR DNA binding protein [Oryza sativa]
NCBI Description
                   209531
Seq. No.
                  LIB3135-034-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                   g3327222
NCBI GI
BLAST score
                   223
                   3.0e-18
E value
Match length
                   122
% identity
                   40
NCBI Description
                  (AB014604) KIAA0704 protein [Homo sapiens]
                   209532
Seq. No.
                   LIB3135-034-Q1-K1-G2
Seq. ID
Method
                   BLASTX
                   g1361983
NCBI GI
BLAST score
                   485
                   7.0e-49
E value
Match length
                   153
% identity
                   67
                   ARP protein - Arabidopsis thaliana >gi 886434_emb_CAA89858_
NCBI Description
                   (Z49776) ARP protein [Arabidopsis thaliana]
                   209533
Seq. No.
                   LIB3135-034-Q1-K1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3925703
BLAST score
                   485
                   4.0e-49
E value
                   117
Match length
% identity
                   79
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
                   209534
Seq. No.
                   LIB3135-034-Q1-K1-G5
Seq. ID
Method
                   BLASTX
```

85

% identity

```
9.0e-48
E value
Match length
                  101
% identity
                  (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                  vulgaris]
                  209535
Seq. No.
                  LIB3135-034-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2462762
BLAST score
                  224
                  1.0e-18
E value
Match length
                  67
% identity
                  64
NCBI Description (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  209536
Seq. No.
                  LIB3135-034-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g1402912
NCBI GI
                   336
BLAST score
                  8.0e-32
E value
Match length
                   86
% identity
                  78
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]
                  209537
Seq. No.
                  LIB3135-034-Q1-K1-G9
Seq. ID
Method
                  BLASTX
                  g2129496
NCBI GI
                   310
BLAST score
                   3.0e-31
E value
Match length
                   90
                   79
% identity
                  acetolactate synthase (EC 4.1.3.18) precursor (clone A19) -
NCBI Description
                   upland cotton
                   209538
Seq. No.
Seq. ID
                   LIB3135-034-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   g927577
BLAST score
                   331
E value
                   3.0e-31
Match length
                   75
                   76
% identity
NCBI Description (U12927) alpha-galactosidase [Phaseolus vulgaris]
                   209539
Seq. No.
                   LIB3135-034-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g2252860
NCBI GI
BLAST score
                   196
                   2.0e-15
E value
                   48
Match length
```

NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]

Seq. ID

Method



```
Seq. No.
                  209540
                  LIB3135-034-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                  q1050918
NCBI GI
                  178
BLAST score
E value
                  3.0e-13
                   54
Match length
% identity
                  (X92648) lipid transfer protein [Helianthus annuus]
NCBI Description
                  209541
Seq. No.
Seq. ID
                  LIB3135-035-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  q1871193
BLAST score
                  136
                  1.0e-08
E value
Match length
                   59
% identity
                   47
                  (U90439) receptor-like protein kinase isolog [Arabidopsis
NCBI Description
                   thaliana] >gi_2335090 (AC002339) putative receptor-like
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                   209542
                  LIB3135-035-Q1-K1-A5
Seq. ID
Method
                   BLASTX
                   g294845
NCBI GI
                   146
BLAST score
E value
                   3.0e-09
                   51
Match length
                   49
% identity
                   (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                   H65-7052]
Seq. No.
                   209543
Seq. ID
                   LIB3135-035-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q3549691
BLAST score
                   388
E value
                   1.0e-37
                   96
Match length
                   69
% identity
                   (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
NCBI Description
                   209544
Seq. No.
                   LIB3135-035-Q1-K1-A9
Seq. ID
Method
                   BLASTX
                   q2618721
NCBI GI
BLAST score
                   147
                   2.0e-09
E value
Match length
                   45
                   67
% identity
                  (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                   209545
Seq. No.
```

28935

LIB3135-035-Q1-K1-B1

BLASTX



NCBI GI g1345642 BLAST score 306 E value 4.0e-28 Match length 110 % identity 55 FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450 NCBI Description 75A1) (CYPLXXVA1) >gi\_629710\_pir\_\_\$38985 flavonoid 3',5'-hydroxylase Hf1 - garden petunia >gi\_311656\_emb\_CAA80266\_ (Z22545) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi\_1853972\_dbj\_BAA03438 (D14588) flavonoid-3,5,-hydroxylase [Petunia x hybrida] >gi\_3426337 (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi\_738772 prf 2001426B flavonoid 3',5'-hydroxylase [Petunia x hybrida] Seq. No. 209546 Seq. ID LIB3135-035-Q1-K1-B11 Method BLASTX NCBI GI g1173223 BLAST score 144 E value 3.0e-09 Match length 72 % identity 49 NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi\_454848 (L28831) ribosomal protein S11 [Glycine max] Seq. No. 209547 Seq. ID LIB3135-035-Q1-K1-B5 Method BLASTX NCBI GI g1843525 BLAST score 548 E value 2.0e-56 Match length 107 % identity NCBI Description (U73746) annexin [Gossypium hirsutum] Seq. No. 209548 Seq. ID LIB3135-035-Q1-K1-B6 Method BLASTX NCBI GI g1166450 BLAST score 257 E value 2.0e-22 Match length 55 % identity NCBI Description (X95262) Tfm5 [Lycopersicon esculentum] Seq. No. 209549 Seq. ID LIB3135-035-Q1-K1-C1 Method BLASTX g3763927 283

NCBI GI BLAST score E value 9.0e-26 Match length 77 % identity 75

(AC004450) putative carboxyphosphoenolpyruvate mutase NCBI Description

[Arabidopsis thaliana]

Seq. ID Method

NCBI GI



```
Seq. No.
                  209550
Seq. ID
                  LIB3135-035-Q1-K1-C10
                  BLASTX
Method
NCBI GI
                   g4204306
BLAST score
                   217
E value
                   1.0e-17
Match length
                   76
% identity
                   59
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   209551
Seq. ID
                  LIB3135-035-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q2982466
BLAST score
                  201
E value
                  1.0e-15
Match length
                  86
                   45
% identity
NCBI Description
                  (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                  209552
Seq. ID
                  LIB3135-035-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                   q4406775
BLAST score
                   161
E value
                   5.0e-11
Match length
                   130
% identity
                   35
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                   209553
Seq. ID
                  LIB3135-035-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                   g1354849
BLAST score
                   294
                  2.0e-37
E value
Match length
                  135
% identity
                   61
NCBI Description
                  (U57350) epoxide hydrolase [Nicotiana tabacum]
Seq. No.
                  209554
Seq. ID
                  LIB3135-035-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2500354
BLAST score
                   513
E value
                  2.0e~53
Match length
                  120
                  88
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                  209555
Seq. No.
```

28937

LIB3135-035-Q1-K1-D1

BLASTX

g4006957



```
BLAST score
E value
                   3.0e-25
                   109
Match length
% identity
                   52
                   (AJ006910) pollen allergen Betv1, isoform at45 [Betula
NCBI Description
                   209556
Seq. No.
Seq. ID
                   LIB3135-035-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g475048
BLAST score
                   166
E value
                   4.0e-12
Match length
                    46
% identity
                   74
NCBI Description
                    (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
                    [Arabidopsis thaliana]
Seq. No.
                   209557
Seq. ID
                   LIB3135-035-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   g643469
BLAST score
                   243
E value
                    9.0e-21
Match length
                    65
% identity
                   71
NCBI Description
                   (U19886) unknown [Lycopersicon esculentum]
Seq. No.
                   209558
Seq. ID
                   LIB3135-035-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   q3183088
BLAST score
                   209
                   1.0e-16
E value
Match length
                   71
                   56
% identity
                   PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                   like protein [Vigna unguiculata]
                   209559
Seq. No.
Seq. ID
                   LIB3135-035-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g2507421
BLAST score
                   169
                   6.0e-12
E value
Match length
                   52
% identity
                   63
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
```

(U81042) translation initiation factor [Arabidopsis thaliana] >gi 4490709 emb CAB38843.1 (AL035680) translation initiation factor [Arabidopsis thaliana]

209560 Seq. No.

LIB3135-035-Q1-K1-D6 Seq. ID

Method BLASTX



```
NCBI GI
                  q1350720
BLAST score
                  440
E value
                  1.0e-43
                  110
Match length
                  75
% identity
                  60S RIBOSOMAL PROTEIN L32
NCBI Description
                  209561
Seq. No.
                  LIB3135-035-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3522950
BLAST score
                  167
E value
                  1.0e-11
                  49
Match length
                  63
% identity
                  (AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  209562
Seq. No.
                  LIB3135-035-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4103635
BLAST score
                  227
E value
                  9.0e-19
Match length
                  111
                  39
% identity
NCBI Description
                  (AF026538) ABA-responsive protein [Hordeum vulgare]
Seq. No.
                  209563
Seq. ID
                  LIB3135-035-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3122673
                   355
BLAST score
                  7.0e-34
E value
Match length
                  99
                  73
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   209564
Seq. ID
                  LIB3135-035-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   g3549691
BLAST score
                   438
E value
                   2.0e-43
Match length
                  104
                   71
% identity
NCBI Description
                  (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
                   209565
Seq. No.
Seq. ID
                  LIB3135-035-Q1-K1-E6
Method
                  BLASTX
                   q1169534
NCBI GI
BLAST score
                   603
                   8.0e-63
E value
Match length
                  130
                  90
% identity
```

28939

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)





(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_542019\_pir\_\_S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi\_433609\_emb\_CAA82232\_ (Z28386) enolase [Ricinus communis]

Seq. No. 209566

Seq. ID LIB3135-035-Q1-K1-F11

Method BLASTX
NCBI GI g2191138
BLAST score 199
E value 2.0e-15
Match length 104
% identity 48

NCBI Description (AF007269) A IG002N01.18 gene product [Arabidopsis

thaliana]

Seq. No. 209567

Seq. ID LIB3135-035-Q1-K1-F2

Method BLASTX
NCBI GI g1172977
BLAST score 158
E value 8.0e-11
Match length 38
% identity 84

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi\_606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 209568

Seq. ID LIB3135-035-Q1-K1-G2

Method BLASTX
NCBI GI g2388575
BLAST score 259
E value 2.0e-22
Match length 129
% identity 42

NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 209569

Seq. ID LIB3135-035-Q1-K1-G4

Method BLASTX
NCBI GI g2662341
BLAST score 573
E value 2.0e-59
Match length 111
% identity 99

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 209570

Seq. ID LIB3135-035-Q1-K1-G7

Method BLASTX
NCBI GI g2497752
BLAST score 279
E value 8.0e-25
Match length 96



```
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1321911 emb CAA65475 (X96714) lipid transfer protein
                  [Prunus dulcis]
                  209571
Seq. No.
                  LIB3135-035-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760844
                  459
BLAST score
                  4.0e-46
E value
                  110
Match length
                  76
% identity
NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  209572
                  LIB3135-035-Q1-K1-H10
Seq. ID
                  BLASTX
Method
                  g806310
NCBI GI
                  159
BLAST score
E value
                  1.0e-10
                  116
Match length
% identity
                  9
NCBI Description (J02746) proline-rich protein [Glycine max]
Seq. No.
                  209573
                  LIB3135-035-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982318
BLAST score
                  282
                  2.0e-25
E value
                  57
Match length
                  88
% identity
                  (AF051244) probable 60S ribosomal protein L15 [Picea
NCBI Description
                  mariana]
                  209574
Seq. No.
                  LIB3135-035-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832620
BLAST score
                  162
E value
                   5.0e-11
Match length
                   61
                   54
% identity
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
                   209575
Seq. No.
                  LIB3135-035-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1166450
BLAST score
                   199
                   1.0e-15
E value
                   46
Match length
                   78
% identity
```

Seq. No. 209576

NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]



```
Seq. ID
                   LIB3135-035-Q1-K1-H8
Method
                   BLASTN
NCBI GI
                   g12614
BLAST score
                   211
E value
                   1.0e-115
Match length
                   389
% identity
                   89
NCBI Description L.esculentum genes for tRNA Asn and tRNA Tyr
Seq. No.
                   209577
Seq. ID
                   LIB3135-036-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2655098
BLAST score
                   249
E value
                   3.0e-21
Match length
                   145
% identity
                   37
NCBI Description
                  (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                   209578
Seq. ID
                   LIB3135-036-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   q531829
BLAST score
                   142
E value
                   6.0e-09
Match length
                   46
% identity
                   65
NCBI Description
                   (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                  209579
Seq. ID
                  LIB3135-036-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q729618
BLAST score
                  374
E value
                  6.0e-36
Match length
                  89
% identity
                  82
NCBI Description
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2)
                   (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP
                  2) >gi_82172_pir__PQ0262 luminal binding protein BLP-2 -
                  common tobacco (fragment) >gi_100338_pir__S21878 heat shock
                  protein BiP homolog blp2 - common tobacco (fragment)
                  >gi_19807_emb_CAA42661 (X60059) luminal binding protein
                  (BiP) [Nicotiana tabacum]
Seq. No.
                  209580
Seq. ID
                  LIB3135-036-Q1-K1-A7
Method
                  BLASTX
                  g166949
                  432
                  1.0e-42
```

NCBI GI BLAST score E value Match length 145 % identity 58

NCBI Description (M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea

americana]



209581 Seq. No. Seq. ID LIB3135-036-Q1-K1-B10 Method BLASTX g1173234 NCBI GI BLAST score 327 2.0e-30 E value 72 Match length 89 % identity 40S RIBOSOMAL PROTEIN S25 >gi\_481909\_pir\_\_S40089 ribosomal NCBI Description protein S25 - tomato >gi 435679 emb\_CAA54132\_ (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi\_1584836\_prf\_\_2123431A ribosomal protein S25 [Lycopersicon esculentum] Seq. No. 209582 LIB3135-036-Q1-K1-B3 Seq. ID BLASTX Method NCBI GI q1709498 BLAST score 527 7.0e-54 E value Match length 125 76 % identity OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR NCBI Description >gi 1362001\_pir \_\_S57524 osmotin precursor - Arabidopsis thaliana >gi 887390\_emb\_CAA61411\_ (X89008) osmotin [Arabidopsis thaliana] Seq. No. 209583 LIB3135-036-Q1-K1-B7 Seq. ID Method BLASTX NCBI GI g2501599 BLAST score 168 6.0e-12 E value 102 Match length 37 % identity HYPOTHETICAL 29.1 KD PROTEIN W06E11.4 IN CHROMOSOME III NCBI Description >gi\_669022 (U20862) W06E11.4 gene product [Caenorhabditis elegans] 209584 Seq. No. Seq. ID LIB3135-036-Q1-K1-C2 Method BLASTX NCBI GI g3128209 BLAST score 552 E value 8.0e-57 Match length 143 37 % identity (AC004077) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 209585 Seq. ID LIB3135-036-Q1-K1-C4

Method BLASTX g2982268 NCBI GI BLAST score 448 E value 1.0e-44 Match length 96 % identity 92

Seq. ID

```
(AF051217) probable 40S ribosomal protein S15 [Picea
NCBI Description
                  mariana]
Seq. No.
                  209586
                  LIB3135-036-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  q2688824
NCBI GI
BLAST score
                  316
                  4.0e-29
E value
Match length
                  107
% identity
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
Seq. No.
                  209587
                  LIB3135-036-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  g3341697
NCBI GI
BLAST score
                  475
                  4.0e-55
E value
Match length
                  135
% identity
                  81
                  (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  209588
Seq. No.
                  LIB3135-036-Q1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2232147
BLAST score
                  39
                  1.0e-12
E value
                  75
Match length
% identity
                  88
                  Arabidopsis thaliana 14-3-3-like protein GF14 upsilon
NCBI Description
                   (GRF5) gene, complete cds
                  209589
Seq. No.
                  LIB3135-036-Q1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3757522
BLAST score
                   557
                   2.0e-57
E value
                  148
Match length
                   75
% identity
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
                   209590
Seq. No.
                  LIB3135-036-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                   g3096939
NCBI GI
BLAST score
                   184
                   1.0e-13
E value
Match length
                   51
                   65
% identity
                  (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209591
```

28944

LIB3135-036-Q1-K1-D8



```
BLASTX
Method
                  g4406810
NCBI GI
BLAST score
                  368
E value
                  9.0e-48
Match length
                  140
% identity
                  61
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                  209592
Seq. No.
                  LIB3135-036-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g3193297
NCBI GI
BLAST score
                  395
                  2.0e-38
E value
                  120
Match length
% identity
                  54
                  (AF069298) similar to epoxide hydrolases [Arabidopsis
NCBI Description
                  thaliana]
                  209593
Seq. No.
                  LIB3135-036-Q1-K1-E10
Seq. ID .
Method
                  BLASTX
NCBI GI
                  g2213608
BLAST score
                   163
                   2.0e-11
E value
                   74
Match length
% identity
                  (AC000103) F21J9.2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   209594
                   LIB3135-036-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g2665890
NCBI GI
BLAST score
                   710
                   3.0e-75
E value
                   154
Match length
% identity
                   87
                   (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                   ananassa]
                   209595
Seq. No.
                   LIB3135-036-Q1-K1-E3
Seq. ID
                   BLASTN
Method
                   g2351064
NCBI GI
                   41
BLAST score
                   1.0e-13
E value
Match length
                   73
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MDJ22, complete sequence [Arabidopsis thaliana]
                   209596
Seq. No.
                   LIB3135-036-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g1170897
NCBI GI
BLAST score
                   116
```

28945

3.0e-09

E value



Match length 79 % identity 45

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi\_1076276\_pir\_\_S52039 NAD-malate dehydrogenase - cucumber

>gi 695311 (L31900) glyoxysomal malate dehydrogenase

[Cucumis sativus]

Seq. No.

Seq. ID

209597 LIB3135-036-Q1-K1-E5

Method BLASTX
NCBI GI g1304227
BLAST score 456
E value 2.0e-45
Match length 139

Match length 3 sidentity 5

NCBI Description (D63781) Epoxide hydrolase [Glycine max]

>qi 2764804 emb\_CAA55293\_ (X78547) epoxide hydrolase

[Glycine max]

Seq. No.

Seq. ID

209598 LIB3135-036-Q1-K1-E6

Method BLASTX
NCBI GI g2492519
BLAST score 197
E value 1.0e-16
Match length 60

Match length 60 % identity 85

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT

7) >gi\_1395191\_dbj\_BAA13021\_ (D86121) 26S proteasome ATPase

subunit [Spinacia oleracea]

Seq. No. 209599

Seq. ID

LIB3135-036-Q1-K1-E8

Method BLASTX
NCBI GI g1730109
BLAST score 558
E value 2.0e-57
Match length 146
% identity 77

NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN

HYDROXYLASE) >gi\_499022\_emb\_CAA53580\_ (X75966) leucoanthocyanidin dioxygenase [Vitis vinifera]

Seq. No. 209600

Seq. ID LIB3135-036-Q1-K1-F10

Method BLASTX
NCBI GI g1402912
BLAST score 636
E value 1.0e-66
Match length 155
% identity 79

NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 209601

Seq. ID LIB3135-036-Q1-K1-F3

Method BLASTX NCBI GI g4263721



```
BLAST score
                  2.0e-51
E value
                  104
Match length
% identity
                  95
                 (AC006223) putative DNA repair protein RAD50 [Arabidopsis
NCBI Description
                  thaliana]
                  209602
Seq. No.
                  LIB3135-036-Q1-K1-F8
Seq. ID
Method
                 BLASTX
                  g3123745
NCBI GI
                  488
BLAST score
                  6.0e-65
E value
                  146
Match length
% identity
                  86
NCBI Description (AB013447) aluminum-induced [Brassica napus]
                  209603
Seq. No.
                  LIB3135-036-Q1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3510538
BLAST score
                  149
                  1.0e-09
E value
Match length
                  30
                  90
% identity
NCBI Description (U93167) expansin [Prunus armeniaca]
Seq. No.
                  209604
                  LIB3135-036-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                  q2826884
NCBI GI
BLAST score
                   385
                   3.0e-37
E value
                   116
Match length
                   68
% identity
                   (AJ223635) transcription factor IIA large subunit
NCBI Description
                   [Arabidopsis thaliana]
                   209605
Seq. No.
                   LIB3135-036-Q1-K1-G12
Seq. ID
Method
                   BLASTX
                   g629483
NCBI GI
                   390
BLAST score
                   9.0e-38
E value
                   149
Match length
                   55
% identity
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                   >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   209606
```

Seq. No.

LIB3135-036-Q1-K1-G4 Seq. ID

BLASTX Method g3549691 NCBI GI BLAST score 453 3.0e-45E value



```
Match length
                   73
% identity
                   (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
NCBI Description
                   209607
Seq. No.
                   LIB3135-036-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   g2497753
NCBI GI
                   342
BLAST score
                   4.0e-32
E value
                   123
Match length
                   51
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                   >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                    [Prunus dulcis]
                    209608
Seq. No.
                   LIB3135-036-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                    g122770
NCBI GI
                    266
BLAST score
                    1.0e-23
E value
                    71
Match length
                    76
% identity
                   HEMOGLOBIN II >gi_99509_pir__S13378 hemoglobin II - swamp oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina
NCBI Description
                    glauca]
                    209609
Seq. No.
                    LIB3135-036-Q1-K1-H10
Seq. ID
                    BLASTX
Method
                    g2282584
NCBI GI
                    179
BLAST score
                    2.0e-22
E value
                    98
Match length
                    63
% identity
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]
                    209610
Seq. No.
                    LIB3135-036-Q1-K1-H6
Seq. ID
                    BLASTX
Method
                    q4539545
NCBI GI
                    615
BLAST score
                    3.0e-64
E value
                    132
Match length
                    89
 % identity
                    (Y16644) PRCI [Nicotiana tabacum]
NCBI Description
                    209611
 Seq. No.
                    LIB3135-036-Q1-K1-H8
 Seq. ID
 Method
                    BLASTX
                    q2345148
 NCBI GI
                    161
 BLAST score
                     4.0e-11
 E value
                    54
 Match length
                     61
 % identity
 NCBI Description (AF014821) developmentally regulated GTP binding protein
```

\*...



## [Pisum sativum]

209612 Seq. No. Seq. ID LIB3135-036-Q1-K1-H9 Method BLASTX NCBI GI q4150974 BLAST score 374 E value 7.0e-36 Match length 95 71 % identity

209613

NCBI Description (AJ224331) cystatin [Castanea sativa]

Seq. ID LIB3135-037-Q1-K1-A2 Method BLASTX NCBI GI g3292849 BLAST score 254 E value 7.0e-22 Match length 93 % identity 58

Seq. No.

NCBI Description (AJ007582) arginine methyltransferase [Arabidopsis

thaliana]

Seq. No. 209614

Seq. ID LIB3135-037-Q1-K1-A3

Method BLASTX
NCBI GI g3914535
BLAST score 444
E value 3.0e-44
Match length 104
% identity 80

NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi\_2791948\_emb\_CAA11283\_

(AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No. 209615

Seq. ID LIB3135-037-Q1-K1-A5

Method BLASTX
NCBI GI g3377507
BLAST score 679
E value 1.0e-71
Match length 148
% identity 90

NCBI Description (AF056026) auxin transport protein EIR1 [Arabidopsis

thaliana] >gi\_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi\_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi\_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No. 209616

Seq. ID LIB3135-037-Q1-K1-B1

Method BLASTX
NCBI GI g1519241
BLAST score 252
E value 1.0e-21
Match length 54
% identity 81

Seq. ID





```
(U65890) 10 kDa chaperonin [Brassica napus]
NCBI Description
                  209617
Seq. No.
                  LIB3135-037-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g2853097
NCBI GI
                  158
BLAST score
                  5.0e-11
E value
                  81
Match length
% identity
                  44
                  (AL021767) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  209618
Seq. No.
                  LIB3135-037-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                   g2570827
NCBI GI
                   569
BLAST score
                   9.0e-59
E value
                   148
Match length
                   71
% identity
                   (AF026058) anthocyanidin synthase [Matthiola incana]
NCBI Description
                   209619
Seq. No.
                   LIB3135-037-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g3776029
NCBI GI
                   276
BLAST score
                   3.0e-28
E value
                   127
Match length
                   56
% identity
                   (AJ010476) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   209620
Seq. No.
                   LIB3135-037-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   g2828280
NCBI GI
                   393
BLAST score
                   4.0e-38
E value
                   82
Match length
                   91
% identity
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2832633_emb_CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
                   209621
Seq. No.
                   LIB3135-037-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g683553
NCBI GI
                   203
BLAST score
                   5.0e-16
E value
                   98
Match length
                   44
% identity
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   209622
 Seq. No.
```

28950

LIB3135-037-Q1-K1-C11



```
BLASTX
Method
                   g2499115
NCBI GI
BLAST score
                   387
E value
                   1.0e-37
Match length
                   117
% identity
                   63
                  VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788
NCBI Description
                   (U86662) VPS41 [Lycopersicon esculentum]
Seq. No.
                   209623
                   LIB3135-037-Q1-K1-C12
Seq. ID
Method
                   BLASTX
                   g1709498
NCBI GI
BLAST score
                   423
                   9.0e-42
E value
Match length
                   112
% identity
                   71
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                   tha\overline{l}iana >g\overline{l} 88\overline{r}390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
                   209624
Seq. No.
                   LIB3135-037-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g3269284
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
                   49
Match length
% identity
                   84
NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]
                   209625
Seq. No.
                   LIB3135-037-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g3435196
NCBI GI
BLAST score
                   381
                   8.0e-37
E value
                   96
Match length
                   73
% identity
NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                   209626
                   LIB3135-037-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   g1653142
NCBI GI
BLAST score
                   140
                   1.0e-08
E value
                    67
Match length
                    45
 % identity
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
                    209627
 Seq. No.
                   LIB3135-037-Q1-K1-D3
 Seq. ID
```

28951

BLASTX

275

g3834309

Method

NCBI GI BLAST score



E value 3.0e-24 Match length 89 % identity 52

NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb\_L16983

Daucus carota and a member of S locus glycoprotein family PF\_00954. ESTs gb\_F13813, gb\_T21052, gb\_R30218 and gb\_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No. 209628

Seq. ID LIB3135-037-Q1-K1-D5

Method BLASTX
NCBI GI g2961378
BLAST score 247
E value 4.0e-21
Match length 126
% identity 46

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 209629

Seq. ID LIB3135-037-Q1-K1-E10

Method BLASTX
NCBI GI g1171978
BLAST score 217
E value 5.0e-26
Match length 98
% identity 65

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi\_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi 2911051\_emb\_CAA17561\_ (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 209630

Seq. ID LIB3135-037-Q1-K1-E2

Method BLASTX
NCBI GI g2194125
BLAST score 563
E value 4.0e-58
Match length 132
% identity 79

NCBI Description (AC002062) ESTs gb\_R30459,gb\_N38441 come from this gene.

[Arabidopsis thaliana]

Seq. No. 209631

Seq. ID LIB3135-037-Q1-K1-E4

Method BLASTX
NCBI GI g1130682
BLAST score 370
E value 2.0e-35
Match length 78
% identity 88

NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No. 209632

Seq. ID LIB3135-037-Q1-K1-E5

Method BLASTX NCBI GI g3121848 BLAST score 629



```
8.0e-66
 E value
                    140
 Match length
 % identity
                    58
                    CALMODULIN >gi_1835521 (U83402) calmodulin [Capsicum
 NCBI Description
                    annuum]
                    209633
 Seq. No.
                    LIB3135-037-Q1-K1-E8
 Seq. ID
                    BLASTX
 Method
                    g4457219
 NCBI GI
                    299
 BLAST score
                    4.0e-27
 E value
 Match length
                    105
  % identity
                    65
                    (AF127796) acyl carrier protein [Capsicum chinense]
  NCBI Description
                    209634
  Seq. No.
                    LIB3135-037-Q1-K1-F10
  Seq. ID
                    BLASTX
 Method
                    g3892057
  NCBI GI
  BLAST score
                    507
                    1.0e-51
  E value
                    125
  Match length
  % identity
                    42
                    (AC002330) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                    209635
  Seq. No.
                    LIB3135-037-Q1-K1-F11
  Seq. ID
  Method
                    BLASTX
                    q986969
  NCBI GI
                    254
  BLAST score
                    7.0e-22
  E value
                    101
  Match length
                    53
  % identity
                    (L28005) TGACG-motif-binding protein [Glycine max]
  NCBI Description
                    209636
  Seq. No.
                    LIB3135-037-Q1-K1-F12
  Seq. ID
                    BLASTX
  Method
                     g3935147
  NCBI GI
  BLAST score
                     363
                     1.0e-34
  E value
                     126
  Match length
                     57
% identity
                    (AC005106) T25N20.11 [Arabidopsis thaliana]
  NCBI Description
                     209637
  Seq. No.
                     LIB3135-037-Q1-K1-F2
  Seq. ID
  Method
                     BLASTX
                     g3702332
  NCBI GI
  BLAST score
                     286
                     3.0e-27
  E value
                     91
  Match length
  % identity
                     70
                    (AC005397) unknown protein [Arabidopsis thaliana]
  NCBI Description
```

28953

209638

Seq. No.

```
LIB3135-037-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3805845
BLAST score
                  366
E value
                  4.0e-35
Match length
                  94
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                  209639
Seq. No.
                  LIB3135-037-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g1931647
NCBI GI
BLAST score
                  283
                  3.0e-25
E value
Match length
                  71
% identity
                  77
                   (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
                   209640
Seq. No.
Seq. ID
                  LIB3135-037-Q1-K1-F7
                   BLASTX
Method
                   q1172873
                                                                         .3
NCBI GI
                   243
BLAST score
                   1.0e-20
E value
Match length
                   84
% identity
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir
NCBI Description
                   drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                   precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                   (D13043) thiol protease [Arabidopsis thaliana]
                   209641
Seq. No.
                   LIB3135-037-Q1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3287832
                   675
BLAST score
                   3.0e-71
E value
                   136
Match length
% identity
                   94
                   (+)-DELTA-CADINENE SYNTHASE (D-CADINENE SYNTHASE)
NCBI Description
                   >gi 1843647 (U88318) (+)-delta-cadinene synthase [Gossypium
                   hirsutum]
                   209642
Seq. No.
                   LIB3135-037-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   g1703380
NCBI GI
                   225
BLAST score
                   8.0e-19
E value
Match length
                   41
                   100
% identity
                   ADP-RIBOSYLATION FACTOR >gi 1132483 dbj_BAA04607 (D17760)
NCBI Description
                   ADP-ribosylation factor [Oryza sativa]
```

Seq. No. 209643



```
LIB3135-037-Q1-K1-G12
Seq. ID
                  BLASTX
Method
                  g1113941
NCBI GI
                  178
BLAST score
                  1.0e-13
E value
                  63
Match length
                  59
% identity
NCBI Description (U40713) Pv42p [Phaseolus vulgaris]
                  209644
Seq. No.
                  LIB3135-037-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g1350720
NCBI GI
                  372
BLAST score
E value
                  7.0e-36
Match length
                  86
% identity
                  79
NCBI Description 60S RIBOSOMAL PROTEIN L32
                  209645
Seq. No.
                  LIB3135-037-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g1928981
NCBI GI
                  653
BLAST score
                  1.0e-68
E value
                   138
Match length
% identity
                   65
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   209646
Seq. No.
                   LIB3135-037-Q1-K1-G4
Seq. ID
                   BLASTX
Method
                   g4337210
NCBI GI
BLAST score
                   189
                   3.0e-14
E value
                   85
Match length
                   45
% identity
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
                   209647
Seq. No.
                   LIB3135-037-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g2829206
NCBI GI
                   207
BLAST score
                   1.0e-16
E value
                   91
Match length
                   12
 % identity
                   (AF044205) proline-rich protein precursor [Gossypium
 NCBI Description
                   hirsutum]
                   209648
 Seq. No.
                   LIB3135-037-Q1-K1-G8
 Seq. ID
                   BLASTX
 Method
```

28955

q1805359

421 2.0e-41

NCBI GI BLAST score

E value



```
Match length
                  119
% identity
                  61
                  (AB000623) glucosyl transferase [Nicotiana tabacum]
NCBI Description
                  209649
Seq. No.
Seq. ID
                  LIB3135-037-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  q1709498
BLAST score
                  527
                  7.0e-54
E value
Match length
                  116
                  82
% identity
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                  >gi 1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi 887390 emb CAA61411 (X89008) osmotin
                  [Arabidopsis thaliana]
                  209650
Seq. No.
                  LIB3135-037-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g2829206
NCBI GI
                  177
BLAST score
                  6.0e-13
E value
                  120
Match length
% identity
                  13
                  (AF044205) proline-rich protein precursor [Gossypium
NCBI Description
                  hirsutum]
                  209651
Seq. No.
                  LIB3135-037-01-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  152
E value
                  6.0e-80
Match length
                  446
% identity
                  19
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
Seq. No.
                  209652
Seq. ID
                  LIB3135-038-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g3986695
BLAST score
                  640
                  4.0e-67
E value
                  140
Match length
% identity
                  (AF101423) ribosomal protein L12 [Cichorium intybus]
NCBI Description
Seq. No.
                  209653
Seq. ID
                  LIB3135-038-Q1-K1-A10
```

Method BLASTX NCBI GI g3426045 BLAST score 249 2.0e-21 E value Match length 130 % identity 46

Match length

NCBI Description

% identity

90



```
(AC005168) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  209654
Seq. No.
                  LIB3135-038-Q1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076511
BLAST score
                  587
E value
                  6.0e-61
                  138
Match length
                  83
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                  >gi 758250 emb_CAA59799 (X85804) H(+)-transporting ATPase
                  [Phaseolus vulgaris]
                  209655
Seq. No.
Seq. ID
                  LIB3135-038-Q1-K1-A12
Method
                  BLASTX
                  q2078298
NCBI GI
BLAST score
                  414
                  9.0e-41
E value
Match length
                  94
% identity
                  85
                  (U97257) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                  [Lycopersicon esculentum]
Seq. No.
                  209656
                  LIB3135-038-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827561
                  376
BLAST score
E value
                  2.0e-36
Match length
                  101
                  70
% identity
                  (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3292809_emb_CAA19799_ (AL031018) putative protein
                  [Arabidopsis thaliana]
                  209657
Seq. No.
                  LIB3135-038-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3986695
BLAST score
                  651
E value
                  2.0e-68
Match length
                  140
% identity
                  93
                  (AF101423) ribosomal protein L12 [Cichorium intybus]
NCBI Description
                  209658
Seq. No.
                  LIB3135-038-Q1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662375
BLAST score
                  175
                  7.0e-13
E value
```

(D89060) oligosaccharyltransferase [Homo sapiens]



```
209659
Seq. No.
                  LIB3135-038-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  q4176446
NCBI GI
                  182
BLAST score
                  1.0e-13
E value
                  107
Match length
                  33
% identity
                   (AL022238) dJ1042K10.2.1 (novel protein with probable
NCBI Description
                   rabGAP domains and Src homology domain 3) (isoform 1) [Homo
                   sapiens]
                   209660
Seq. No.
                   LIB3135-038-Q1-K1-B12
Seq. ID
Method
                   BLASTX
                   q2493046
NCBI GI
                   441
BLAST score
                   7.0e-44
E value
                   113
Match length
                   75
% identity
                   ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                   3.6.1.34) delta' chain precursor - sweet potato
                   >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                   delta subunit [Ipomoea batatas]
                   209661
Seq. No.
                   LIB3135-038-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                   q2760837
NCBI GI
                   377
BLAST score
                   3.0e-36
E value
                   144
Match length
                   49
% identity
                   (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   209662
Seq. No.
                   LIB3135-038-Q1-K1-B5
Seq. ID
                   BLASTX
Method
                   g320608
NCBI GI
                   586
BLAST score
                   9.0e-61
E value
                   118
Match length
                   27
% identity
                   ubiquitin precursor - wild oat >gi_15989 emb_CAA49200
NCBI Description
                    (X69422) tetraubiquitin [Avena fatua] >g\bar{i}_777758 (L41\overline{6}58)
                   polyubiquitin [Saccharum sp.]
                    209663
 Seq. No.
                   LIB3135-038-Q1-K1-B6
 Seq. ID
 Method
                    BLASTX
                    q2497752
 NCBI GI
```

Method BLASTX
NCBI GI g2497752
BLAST score 277
E value 1.0e-24
Match length 96
% identity 57

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)





>gi\_1321911\_emb\_CAA65475\_ (X96714) lipid transfer protein
[Prunus dulcis]

Seq. No. 209664

Seq. ID LIB3135-038-Q1-K1-B7

Method BLASTX
NCBI GI g1657948
BLAST score 638
E value 7.0e-67
Match length 144
% identity 46

NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 209665

Seq. ID LIB3135-038-Q1-K1-B8

Method BLASTX
NCBI GI g3915031
BLAST score 651
E value 2.0e-68
Match length 133
% identity 96

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi\_1217628\_emb\_CAA65232\_

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. 209666

Seq. ID LIB3135-038-Q1-K1-C10

Method BLASTX
NCBI GI g3341678
BLAST score 212
E value 4.0e-17
Match length 51
% identity 76

NCBI Description (AC003672) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 209667

Seq. ID LIB3135-038-Q1-K1-C12

Method BLASTX
NCBI GI g1888357
BLAST score 371
E value 1.0e-35
Match length 121
% identity 60

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi\_1890154\_emb\_CAA72432\_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 209668

Seq. ID LIB3135-038-Q1-K1-C3

Method BLASTX
NCBI GI g3738257
BLAST score 392
E value 1.0e-40
Match length 112
% identity 80

```
NCBI Description
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
                  nigra]
                  209669
Seq. No.
                  LIB3135-038-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q585241
BLAST score
                  186
E value
                  7.0e-14
Match length
                  98
% identity
                  47
NCBI Description
                  HISTONE H1 >gi_629668_pir__S45662 histone H1 - tomato
                  >gi 424100 (U03391) histone H1 [Lycopersicon esculentum]
Seq. No.
                  209670
Seq. ID
                  LIB3135-038-01-K1-C8
Method
                  BLASTX
NCBI GI
                  g1934730
BLAST score
                  148
E value
                  1.0e-09
                  39
Match length
                  62
% identity
NCBI Description
                  (U95036) germin-like protein [Arabidopsis thaliana]
                  209671
Seq. No.
Seq. ID
                  LIB3135-038-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  q4510345
BLAST score
                  209
E value
                  1.0e-16
Match length
                  126
                  37
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  209672
Seq. ID
                  LIB3135-038-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g4519671
BLAST score
                  153
                   4.0e-10
E value
                  74
Match length
% identity
                   47
                  (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
                  209673
Seq. No.
Seq. ID
                  LIB3135-038-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4193382
BLAST score
                  386
                  2.0e-37
E value
                  86
Match length
                  83
% identity
                  (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                  >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
```

Seq. No. 209674

thaliana]

```
LIB3135-038-Q1-K1-D6
Seq. ID
                   BLASTX
Method
                   g2586083
NCBI GI
                   295
BLAST score
                   1.0e-26
E value
                   151
Match length
% identity
                   (U72725) receptor kinase-like protein [Oryza
NCBI Description
                   longistaminata]
                   209675
Seq. No.
                   LIB3135-038-Q1-K1-D8
Seq. ID
                   BLASTN
Method
                   g3047317
NCBI GI
BLAST score
                   37
E value
                   8.0e-12
                   53
Match length
                   56
% identity
                   Magnaporthe grisea strain Guy-11 poly-ubiquitin (PUB4)
NCBI Description
                   mRNA, complete cds
                    209676
Seq. No.
                   LIB3135-038-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                    g1706547
NCBI GI
BLAST score
                    315
                    1.0e-31
E value
                    99
Match length
                    71
% identity
                    GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
NCBI Description
                    PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                    ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE)
>gi_2129912_pir__S65077 beta-1,3-glucanase class I
                    precursor - Para rubber tree >gi_1184668 (U22147)
                    beta-1,3-glucanase [Hevea brasiliensis]
                    209677
Seq. No.
                    LIB3135-038-Q1-K1-E1
Seq. ID
                    BLASTX
Method
                    g1263291
NCBI GI
                    421
 BLAST score
                    3.0e-43
 E value
                    90
Match length
                    97
 % identity
                    (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
 NCBI Description
                    209678
 Seq. No.
                    LIB3135-038-Q1-K1-E12
 Seq. ID
                    BLASTN
 Method
                    g434989
 NCBI GI
                    50
 BLAST score
                    2.0e-19
 E value
                    78
 Match length
                    91
 % identity
 NCBI Description O.berteriana mitochondrial trnC and trnN genes
```

28961

209679

Seq. No.



Seq. ID LIB3135-038-Q1-K1-E2

Method BLASTX
NCBI GI g1352821
BLAST score 230
E value 2.0e-19
Match length 92
% identity 58

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 279581 pir RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gosspium birsutum]

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 209680

Seq. ID LIB3135-038-Q1-K1-E4

Method BLASTX
NCBI GI g3135261
BLAST score 217
E value 1.0e-17
Match length 69
% identity 62

NCBI Description (AC003058) putative 18.5 KDa class I heat shock protein

[Arabidopsis thaliana]

Seq. No. 209681

Seq. ID LIB3135-038-Q1-K1-E6

Method BLASTX
NCBI GI g2829893
BLAST score 204
E value 5.0e-16
Match length 57
% identity 74

NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No. 209682

Seq. ID LIB3135-038-Q1-K1-F1

Method BLASTN
NCBI GI g12292
BLAST score 125
E value 7.0e-64
Match length 215
% identity 92

NCBI Description Spinach chloroplast DNA homologous to ARS and ARC elements

upstream of rDNA operon

Seq. No. 209683

Seq. ID LIB3135-038-Q1-K1-F3

Method BLASTX
NCBI GI g2132171
BLAST score 212
E value 4.0e-17
Match length 93
% identity 43

NCBI Description hypothetical protein YPL063w - yeast (Saccharomyces

cerevisiae) >gi\_1079679 (U39205) similar to Caenorhabditis elegans CELF45EI2\_5 F45E12.1 gene product, encoded by GenBank Accession Number U29536 [Saccharomyces cerevisiae]

NCBI Description



```
209684
Seq. No.
Seq. ID
                   LIB3135-038-Q1-K1-F4
                   BLASTX
Method
NCBI GI
                   g3212862
BLAST score
                   341
                   3.0e-32
E value
                   72
Match length
% identity
NCBI Description (AC004005) putative riboflavin synthase [Arabidopsis
                   thaliana]
                   209685
Seq. No.
                   LIB3135-038-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g3738325
NCBI GI
                   202
BLAST score
                   2.0e-16
E value
                   55
Match length
                   71
% identity
NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis
                   thaliana]
                   209686
Seq. No.
                   LIB3135-038-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g3738325
NCBI GI
                   395
BLAST score
                   2.0e-44
E value
Match length
                   135
% identity
                   (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                   thaliana]
                    209687
Seq. No.
                   LIB3135-038-Q1-K1-G1
Seq. ID
                    BLASTX
Method
                    q629483
NCBI GI
                    233
BLAST score
                    2.0e-19
E value
                    82
Match length
 % identity
                    gene 1-Sc3 protein - European white birch
NCBI Description
                    >gi 534898 emb CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                    >gi^-158432\overline{2} pr\overline{f} 212237\overline{4}C allergen Bet v 1-Sc3 [Betula
                    pendula]
                    209688
 Seq. No.
                    LIB3135-038-Q1-K1-G3
 Seq. ID
                    BLASTX
 Method
                    g3242659
 NCBI GI
 BLAST score
                    572
E value
                    2.0e-59
 Match length
                    112
 % identity
                    94
```

(AB015599) spermidine synthase [Coffea arabica]



Seq. No. 209689 Seq. ID LIB3135-038-Q1-K1-G4 Method BLASTX NCBI GI q1495366 BLAST score 183 E value 1.0e-13 Match length 44 64 % identity (Z69370) nitrite transporter [Cucumis sativus] NCBI Description Seq. No. 209690 LIB3135-038-Q1-K1-G5 Seq. ID Method BLASTX NCBI GI g1934730 BLAST score 300 E value 3.0e-27 90 Match length 59 % identity (U95036) germin-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 209691 Seq. ID LIB3135-038-Q1-K1-G8 Method BLASTX NCBI GI g3096930 BLAST score 147 E value 2.0e-09 Match length 94 % identity 46 (AL023094) Homeodomain - like protein [Arabidopsis NCBI Description thaliana] 209692 Seq. No. Seq. ID LIB3135-038-Q1-K1-H11 Method BLASTX NCBI GI q1781348 BLAST score 505 E value 3.0e-51102 Match length % identity 93 NCBI Description (Y10380) homologous to plastidic aldolases [Solanum tuberosum] 209693 Seq. No. LIB3135-038-Q1-K1-H2 Seq. ID Method BLASTX NCBI GI g2980793 BLAST score 206 2.0e-16 E value Match length 94 40 % identity

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

209694 Seq. No.

LIB3135-038-Q1-K1-H6 Seq. ID

Method BLASTX NCBI GI g1172874 BLAST score 362



E value 1.0e-34
Match length 131
% identity 57

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi\_479589\_pir\_\_S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi\_391608\_dbj\_BAA01546\_ (D10703) rd22
[Arabidopsis thaliana] >gi\_447134\_prf\_\_1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 209695

Seq. ID LIB3135-039-Q1-K1-A11

Method BLASTX
NCBI GI g4337175
BLAST score 443
E value 5.0e-44
Match length 126
% identity 67

NCBI Description (AC006416) ESTs gb\_T20589, gb\_T04648, gb\_AA597906,

gb\_T04111, gb\_R84180, gb\_R654\overline{2}8, gb\_T444\overline{3}9, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb\_AA720210, game\_from\_this\_game\_[Amabidopsis\_theliana]

gb\_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 209696

Seq. ID LIB3135-039-Q1-K1-A2

Method BLASTN
NCBI GI g3108245
BLAST score 106
E value 2.0e-52
Match length 220
% identity 87

NCBI Description Gossypium barbadense clone pXP020 repetitive DNA sequence

Seq. No. 209697

Seq. ID LIB3135-039-Q1-K1-A6

Method BLASTX
NCBI GI 94455359
BLAST score 149
E value 1.0e-09
Match length 52
% identity 63

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 209698

Seq. ID LIB3135-039-Q1-K1-A7

Method BLASTX
NCBI GI g2529665
BLAST score 229
E value 5.0e-19
Match length 60
% identity 73

NCBI Description (AC002535) putative ribosomal protein L7A [Arabidopsis

thaliana]

Seq. No. 209699

Seq. ID LIB3135-039-Q1-K1-A8

Method BLASTX NCBI GI g1362009

```
BLAST score
                   6.0e-46
E value
                   134
Match length
                   43
% identity
NCBI Description
                   ubiquitin-like protein 7 - Arabidopsis thaliana
                   209700
Seq. No.
                   LIB3135-039-Q1-K1-B10
Sea. ID
Method
                   BLASTX
NCBI GI
                   g1934730
BLAST score
                   350
E value
                   4.0e-33
Match length
                   90
 % identity
                   72
                   (U95036) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   209701
Seq. No.
                   LIB3135-039-Q1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2826786
                   292
BLAST score
                   3.0e-26
E value
                   94
Match length
                   64
 % identity
NCBI Description
                   (Y10905) RAPB protein [Oryza sativa]
                   209702
Seq. No.
                   LIB3135-039-Q1-K1-B12
 Seq. ID
Method
                   BLASTN
                   g2104680
NCBI GI
BLAST score
                   37
 E value
                   2.0e-11
Match length
                   68
 % identity
                   96
 NCBI Description V.faba mRNA for putative transciption factor (1556bp)
                   209703
 Seq. No.
 Seq. ID
                   LIB3135-039-Q1-K1-B4
Method
                   BLASTX
 NCBI GI
                   g2995953
 BLAST score
                   313
 E value
                   9.0e-29
Match length
                   105
 % identity
                   60
                   (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
 NCBI Description
 Seq. No.
                   209704
 Seq. ID
                   LIB3135-039-Q1-K1-B7
 Method
                   BLASTX
 NCBI GI
                   g2129915
 BLAST score
                   188
```

4.0e-14 E value Match length 76 50 % identity

ferredoxin precursor - sweet orange NCBI Description

>gi\_1360725\_emb\_CAA87068\_ (Z46944) non-photosynthetic

ferredoxin [Citrus sinensis]



```
209705
Seq. No.
                  LIB3135-039-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244916
BLAST score
                  259
                  2.0e-22
E value
                  141
Match length
% identity
NCBI Description
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  209706
                  LIB3135-039-Q1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656031
BLAST score
                  54
                  2.0e-21
E value
                  130
Match length
% identity
                  85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC20
                  209707
Seq. No.
                  LIB3135-039-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  q4185819
NCBI GI
BLAST score
                  192
E value
                  1.0e-14
Match length
                  47
% identity
                  68
                  (AF116845) metallothionein-like type 1 protein [Ipomoea
NCBI Description
                  batatas]
                  209708
Seq. No.
Seq. ID
                  LIB3135-039-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q2129726
BLAST score
                  625
E value
                  2.0e-65
Match length
                  149
% identity
NCBI Description
                  RNA polymerase II third largest chain RPB35.5A -
                  Arabidopsis thaliana >gi 514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >gi 4544370 gb AAD22281.1 AC006920 5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
                  209709
Seq. No.
Seq. ID
                  LIB3135-039-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3033375
BLAST score
                  354
E value
                  1.0e-33
Match length
                  143
% identity
                  47
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
```

thaliana]

Match length

% identity

143 3



```
209710
Seq. No.
                  LIB3135-039-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  g2286153
NCBI GI
                  625
BLAST score
                  2.0e-65
E value
                  127
Match length
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  209711
Seq. No.
                  LIB3135-039-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g1173256
NCBI GI
                  504
BLAST score
                  4.0e-57
E value
                  120
Match length
                  85
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                  209712
Seq. No.
                  LIB3135-039-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                   g2129578
NCBI GI
                   193
BLAST score
                   1.0e-14
E value
                   91
Match length
                   53
% identity
                   dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                   thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
                   dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                   >gi 1585435_prf__2124427B diamide resistance gene
                   [Arabidopsis thaliana]
                   209713
Seq. No.
                   LIB3135-039-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   q2440044
NCBI GI
                   582
BLAST score
                   2.0e-60
E value
                   131
Match length
                   86
 % identity
                   (AJ001293) major intrinsic protein PIPB [Craterostigma
NCBI Description
                   plantagineum]
                   209714
 Seq. No.
                   LIB3135-039-Q1-K1-D9
 Seq. ID
                   BLASTX
 Method
                   q1841966
 NCBI GI
                   202
 BLAST score
                   1.0e-15
 E value
```

BLAST score

Match length

E value

36

47

1.0e-10



```
(U65916) ankyrin [Rattus norvegicus]
NCBI Description
                   209715
Seq. No.
                   LIB3135-039-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g399213
NCBI GI
                   592
BLAST score
                   2.0e-61
E value
                   151
Match length
                   79
% identity
                   ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                   CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato
                   >gi 170435 (M32604) ATP-dependent protease (CD4B)
                    [Lycopersicon esculentum]
                   209716
Seq. No.
                   LIB3135-039-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g2501353
NCBI GI
BLAST score
                    665
                    5.0e-70
E value
                    150
Match length
% identity
                   TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum
NCBI Description
                    (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase
                    [Craterostigma plantagineum]
                    209717
Seq. No.
                    LIB3135-039-Q1-K1-F1
Seq. ID
                    BLASTX
Method
                    g2650633
NCBI GI
                    122
BLAST score
                    7.0e-10
E value
                    110
Match length
                    38
% identity
                    (AE001105) 3-hydroxyacyl-CoA dehydrogenase (hbd-1)
NCBI Description
                    [Archaeoglobus fulgidus]
                    209718
Seq. No.
                    LIB3135-039-01-K1-F10
Seq. ID
                    BLASTX
Method
                    g4262154
NCBI GI
                    546
BLAST score
E value
                    4.0e-56
                    141
Match length
                    78
% identity
                    (AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    209719
                    LIB3135-039-Q1-K1-F12
Seq. ID
                    BLASTN
Method
NCBI GI
                    g3821780
```



% identity 49 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 209720

Seq. ID LIB3135-039-Q1-K1-F4

Method BLASTX
NCBI GI g4580523
BLAST score 229
E value 3.0e-19
Match length 95
% identity 54

NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No. 209721

Seq. ID LIB3135-039-Q1-K1-F5

Method BLASTX
NCBI GI g2501353
BLAST score 387
E value 1.0e-37
Match length 110
% identity 70

NCBI Description TRANSKETOLASE, CHLOROPLAST (TK) >gi\_1084440\_pir\_\_S54300

transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi\_664901\_emb\_CAA86607\_ (Z46646) transketolase

[Craterostigma plantagineum]

Seq. No. 209722

Seq. ID LIB3135-039-Q1-K1-F7

Method BLASTX
NCBI GI g3287855
BLAST score 295
E value 9.0e-27
Match length 92
% identity 59

NCBI Description 3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA

DEHYDROGENASE) (BHBD) >gi 1667355 emb\_CAB04792\_ (Z82038)

3-hydroxybutyryl coenzyme A dehydrogenase [Thermoanaerobacterium thermosaccharolyticum]

>gi\_1903331\_emb\_CAB07499\_ (Z92974) 3-hydroxybutyryl coenzyme A dehydrogenase [Thermoanaerobacterium

thermosaccharolyticum]

Seq. No. 209723

Seq. ID LIB3135-039-Q1-K1-F8

Method BLASTX
NCBI GI g1346524
BLAST score 377
E value 3.0e-36
Match length 77
% identity 94

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi\_497900 (M73430) S-adenosyl methionine synthetase [Populus

deltoides]

Seq. No. 209724

Seq. ID LIB3135-039-Q1-K1-G9

Method BLASTX
NCBI GI g3875304
BLAST score 485
E value 7.0e-49
Match length 131
% identity 66

NCBI Description (Z74030) predicted using Genefinder; cDNA EST EMBL:C07609

comes from this gene; cDNA EST EMBL:C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com

Seq. No. 209725

Seq. ID LIB3135-039-Q1-K1-H10

Method BLASTX
NCBI GI g2911807
BLAST score 452
E value 4.0e-45
Match length 111
% identity 84

NCBI Description (AF009568) H+-pyrophosphatase [Gossypium hirsutum]

Seq. No. 209726

Seq. ID LIB3135-039-Q1-K1-H2

Method BLASTX
NCBI GI g4432835
BLAST score 390
E value 8.0e-38
Match length 125
% identity 54

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 209727

Seq. ID LIB3135-039-Q1-K1-H6

Method BLASTX
NCBI GI g629483
BLAST score 333
E value 4.0e-31
Match length 125
% identity 55

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898 emb\_CAA54696 (X77601) 1 Sc-3 [Betula pendula] >gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 209728

Seq. ID LIB3135-039-Q1-K1-H9

Method BLASTX
NCBI GI g2621324
BLAST score 200
E value 2.0e-15
Match length 127
% identity 37

NCBI Description (AE000813) conserved protein [Methanobacterium

thermoautotrophicum]

Seq. No. 209729

Seq. ID LIB3135-040-Q1-K1-A1

Seq. ID



```
BLASTX
Method
                  g3687251
NCBI GI
                  208
BLAST score
                  9.0e-17
E value
                  48
Match length
                  75
% identity
                  (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
                  209730
Seq. No.
                  LIB3135-040-Q1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q529353
                   236
BLAST score
                   1.0e-19
E value
                   120
Match length
                   43
% identity
                   (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                   209731
Seq. No.
                   LIB3135-040-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g2190992
NCBI GI
BLAST score
                   283
                   2.0e-25
E value
                   97
Match length
                   59
% identity
                   (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                   tauschii]
                   209732
Seq. No.
                   LIB3135-040-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g1865721
NCBI GI
BLAST score
                   488
                   3.0e-49
E value
Match length
                   106
 % identity
                   81
                   (Y08067) mitochondrial single-subunit DNA-dependent RNA
 NCBI Description
                   polymerase [Chenopodium album]
                    209733
 Seq. No.
                   LIB3135-040-Q1-K1-A8
 Seq. ID
                   BLASTX
 Method
                    g1706547
 NCBI GI
                    314
 BLAST score
                    5.0e-29
 E value
                    77
 Match length
                    79
 % identity
                   GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
 NCBI Description
                    PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                    ((1->3)-BETA-GLUCANASE) (BETA-1, 3-ENDOGLUCANASE)
                    >gi_2129912_pir__S65077 beta-1,3-glucanase class I
                    precursor - Para rubber tree >gi_1184668 (U22147)
                    beta-1,3-glucanase [Hevea brasiliensis]
                    209734
 Seq. No.
```

28972

LIB3135-040-Q1-K1-B3

```
Method
                   BLASTX
NCBI GI
                   q480618
BLAST score
                   527
                   7.0e-54
E value
                   106
Match length
% identity
                   92
NCBI Description
                  ATAF1 protein - Arabidopsis thaliana (fragment)
                   >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis
                   thaliana]
Seq. No.
                   209735
Seq. ID
                   LIB3135-040-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   q2244979
BLAST score
                   340
E value
                   3.0e - 32
Match length
                   102
% identity
                   66
                   (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   209736
Seq. ID
                   LIB3135-040-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   q1420887
BLAST score
                   140
E value
                   7.0e-09
                  74
Match length
                   49
% identity
                   (U34334) non-specific lipid transfer-like protein
NCBI Description
                   [Phaseolus vulgaris]
                   209737
Seq. No.
Seq. ID
                   LIB3135-040-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   g4375834
BLAST score
                   233
E value
                   2.0e-19
Match length
                   109
% identity
                   48
                  (AL021713) putative protein [Arabidopsis thaliana]
NCBI Description
                   209738
Seq. No.
                  LIB3135-040-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1173055
BLAST score
                   322
E value
                   3.0e-30
Match length
                   82
% identity
                   87
                  60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__$42497
NCBI Description
```

ribosomal protein L11.e - alfalfa >gi\_1076504\_pir\_\_S51819 RL5 ribosomal protein - alfalfa >gi 463252 emb CAA55090

(X78284) RL5 ribosomal protein [Medicago sativa]

209739 Seq. No.

Seq. ID LIB3135-040-Q1-K1-C10

BLAST score

E value

308 3.0e-28



```
Method
                  BLASTX
NCBI GI
                  q4262250
BLAST score
                  530
                  2.0e-54
E value
Match length
                  116
% identity
                  86
NCBI Description
                  (AC006200) putative aldolase [Arabidopsis thaliana]
                  209740
Seq. No.
Seq. ID
                  LIB3135-040-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q629597
BLAST score
                  273
                  3.0e-24
E value
Match length
                  63
% identity
                  76
NCBI Description
                  proline-rich protein - rape >gi 545029 bbs 142669 (S68113)
                  proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                  Peptide, 147 aa] [Brassica napus]
                  209741
Seq. No.
Seq. ID
                  LIB3135-040-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g4006957
BLAST score
                  292
E value
                  2.0e-26
Match length
                  99
                  59
% identity
                  (AJ006910) pollen allergen Betv1, isoform at45 [Betula
NCBI Description
                  pendula]
Seq. No.
                  209742
                  LIB3135-040-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4336205
                  295
BLAST score
                  1.0e-26
E value
                  136
Match length
% identity
                  46
NCBI Description
                  (AF077372) cytochrome b5 reductase [Zea mays]
                  209743
Seq. No.
Seq. ID
                  LIB3135-040-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3172025
BLAST score
                  173
E value
                  8.0e-16
Match length
                  61
                  77
% identity
                  (AB005805) aldehyde oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  209744
Seq. ID
                  LIB3135-040-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2829894
```

NCBI Description

Seq. No.

209750

```
Match length
                  72
% identity
                  (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  209745
Seq. No.
                  LIB3135-040-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  q2706544
NCBI GI
                   666
BLAST score
E value
                   4.0e-70
Match length
                   146
% identity
                   87
                   (Y15899) Sig1 [Sinapis alba]
NCBI Description
                   209746
Seq. No.
                   LIB3135-040-Q1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3560228
BLAST score
                   148
                   2.0e-09
E value
                   66
Match length
% identity
                   (AL031530) putative nadh-cytochrome b5 reductase
NCBI Description
                   [Schizosaccharomyces pombe]
                   209747
Seq. No.
                   LIB3135-040-Q1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1279654
                   459
BLAST score
                   6.0e-46
E value
                   128
Match length
                   70
% identity
                   (X97351) peroxidase [Populus balsamifera subsp.
NCBI Description
                   trichocarpa]
                   209748
Seq. No.
                   LIB3135-040-Q1-K1-D2
Seq. ID
Method
                   BLASTX
                   g3282092
NCBI GI
                   154
BLAST score
                   3.0e-10
E value
                   102
Match length
 % identity
                   37
                   (AJ007446) hypothetical protein [Thermotoga neapolitana]
 NCBI Description
                   209749
 Seq. No.
                   LIB3135-040-Q1-K1-D3
 Seq. ID
                   BLASTX
 Method
                    g2982432
 NCBI GI
                    330
 BLAST score
                    9.0e-31
 E value
                    76
 Match length
                    79
 % identity
```

28975

(AL022224) putative protein [Arabidopsis thaliana]

BLAST score

E value

319 2.0e-29



```
LIB3135-040-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g730456
NCBI GI
                  430
BLAST score
                  7.0e-49
E value
                  128
Match length
                  74
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                  209751
Seq. No.
                  LIB3135-040-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  g2570203
NCBI GI
                  278
BLAST score
                  7.0e-25
E value
                  109
Match length
                  56
% identity
NCBI Description (U59235) unknown [Synechococcus PCC7942]
                   209752
Seq. No.
                  LIB3135-040-Q1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3047117
BLAST score
                   553
                   4.0e-57
E value
                   111
Match length
% identity
                   93
                   (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                   [Arabidopsis thaliana]
                   209753
Seq. No.
                   LIB3135-040-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g2648032
NCBI GI
                   333
BLAST score
                   4.0e-31
E value
                   143
Match length
                   51
 % identity
NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]
                   209754
 Seq. No.
                   LIB3135-040-Q1-K1-E12
 Seq. ID
                   BLASTN
 Method
                   g2829205
 NCBI GI
                   40
 BLAST score
                   3.0e-13
 E value
                   203
 Match length
                   34
 % identity
NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
                   precursor (PRP) mRNA, complete cds
                   209755
 Seq. No.
                   LIB3135-040-Q1-K1-E2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2894598
```



```
Match length
% identity
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  209756
                  LIB3135-040-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q114682
                  145
BLAST score
E value
                  3.0e-09
Match length
                  36
                  81
% identity
                 ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >gi 168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
                  209757
Seq. No.
Seq. ID
                  LIB3135-040-Q1-K1-E4
Method
                  BLASTX
                                                                           25
NCBI GI
                  g3924596
BLAST score
                  172
E value
                  2.0e-12
Match length
                  68
% identity
                  56
NCBI Description
                  (AF069442) putative phospho-ser/thr phosphatase
                  [Arabidopsis thaliana]
                  209758
Seq. No.
Seq. ID
                  LIB3135-040-Q1-K1-E8
Method
                  BLASTX
                  g2501025
NCBI GI
BLAST score
                  314
                  7.0e-29
E value
                  101
Match length
                  54
% identity
                 LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)
NCBI Description
                  >gi 1147585 emb CAA64223 (X94451) Lysyl-tRNA synthetase
                  [Lycopersicon esculentum]
                  209759
Seq. No.
                  LIB3135-040-Q1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1199467
BLAST score
                  308
E value
                  2.0e-28
Match length
                  103
% identity
                  53
```

NCBI Description (D64155) possible aldehyde decarbonylase [Arabidopsis thaliana]

Seq. No. 209760

Seq. ID LIB3135-040-Q1-K1-F10

Method BLASTX NCBI GI g1710077

```
BLAST score
                   1.0e-54
E value
                   131
Match length
                   74
% identity
                   PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)
NCBI Description
                   >gi_2130029_pir__S60285 B15C protein - barley
                   >gi_471321 emb_CAA54066_ (X76605) HvB15C [Hordeum vulgare]
>gi_1694833_emb_CAA65387_ (X96551) peroxiredoxin [Hordeum
                   vulgare]
                    209761
Seq. No.
                   LIB3135-040-Q1-K1-F12
Seq. ID
                    BLASTX
Method
                    q2829863
NCBI GI
                    379
BLAST score
                    1.0e-36
E value
                    115
Match length
                    62
% identity
                   (AC002396) Putative peroxidase [Arabidopsis thaliana]
NCBI Description
                    209762
Seq. No.
                    LIB3135-040-Q1-K1-F2
Seq. ID
                    BLASTX
Method
NCBI GI
                    q548774
                    323
BLAST score
                    5.0e-30
E value
                    83
Match length
                    75
% identity
                    60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
NCBI Description
                    protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                    ribosomal protein L7A [Oryza sativa]
                    209763
Seq. No.
                    LIB3135-040-Q1-K1-F8
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3033400
BLAST score
                    589
 E value
                     3.0e-61
                     127
Match length
                     89
 % identity
                     (AC004238) putative Ser/Thr protein kinase [Arabidopsis
 NCBI Description
                     thaliana]
                     209764
 Seq. No.
                     LIB3135-040-Q1-K1-G1
 Seq. ID
                     BLASTX
 Method
                     g3927825
 NCBI GI
                     603
 BLAST score
                     6.0e-63
 E value
                     117
```

Match length 96 % identity

(AC005727) putative dTDP-glucose 4-6-dehydratase NCBI Description

[Arabidopsis thaliana]

209765 Seq. No.

LIB3135-040-Q1-K1-G10 Seq. ID

BLASTX Method

E value

Match length % identity

5.0e-35 85



```
NCBI GI
                  g4376203
BLAST score
                  339
E value
                  8.0e-32
Match length
                  140
% identity
                  45
                  (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                  plumbaginifolia]
                  209766
Seq. No.
                  LIB3135-040-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245128
BLAST score
                  421
E value
                  2.0e-41
Match length
                  113
                  68
% identity
NCBI Description
                  (Z97344) peroxidase [Arabidopsis thaliana]
Seq. No.
                  209767
Seq. ID
                  LIB3135-040-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2829863
BLAST score
                  297
E value
                  6.0e-27
Match length
                  113
% identity
                  55
                  (AC002396) Putative peroxidase [Arabidopsis thaliana]
NCBI Description
                  209768
Seq. No.
Seq. ID
                  LIB3135-040-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q2597826
                  595
BLAST score
                  8.0e-62
E value
Match length
                  144
% identity
                  76
NCBI Description
                  (Y14590) class IV chitinase [Arabidopsis thaliana]
                  209769
Seq. No.
Seq. ID
                  LIB3135-040-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2511578
BLAST score
                  160
                  4.0e-14
E value
                  99
Match length
% identity
                  49
                  (Y13178) multicatalytic endopeptidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  209770
                  LIB3135-040-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2493494
BLAST score
                  366
```



NCBI Description

SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)

>gi\_619351\_bbs\_153537 CP-MII.2=serine carboxypeptidase
[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
aa]

Seq. No.

209771

 Seq. No.
 2097/1

 Seq. ID
 LIB3135-040-Q1-K1-H10

 Method
 BLASTX

NCBI GI g1171577
BLAST score 600
E value 2.0e-62
Match length 140
% identity 77

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 209772

Seq. ID LIB3135-040-Q1-K1-H11

Method BLASTX
NCBI GI g2267567
BLAST score 389
E value 7.0e-38
Match length 87
% identity 85

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium

x hortorum] >gi\_2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

Seq. No. 209773

Seq. ID LIB3135-040-Q1-K1-H12

Method BLASTX
NCBI GI g2642638
BLAST score 394
E value 2.0e-38
Match length 94
% identity 81

NCBI Description (AF032472) ADP-glucose pyrophosphorylase large subunit 1

[Citrullus lanatus]

Seq. No. 209774

Seq. ID LIB3135-040-Q1-K1-H4

Method BLASTX
NCBI GI g3176681
BLAST score 161
E value 4.0e-11
Match length 96
% identity 42

NCBI Description (AC003671) F1707.11 [Arabidopsis thaliana]

Seq. No. 209775

Seq. ID LIB3135-040-Q1-K1-H5

Method BLASTX
NCBI GI g4539292
BLAST score 409
E value 3.0e-40
Match length 87
% identity 85

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis



## thaliana]

```
209776
Seq. No.
                  LIB3135-040-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  q3915847
NCBI GI
                  259
BLAST score
                  1.0e-22
E value
                  64
Match length
                  75
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  209777
Seq. No.
                  LIB3135-040-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                  q2935450
NCBI GI
                  186
BLAST score
                  5.0e-14
E value
                  38
Match length
                  97
% identity
NCBI Description (AF048824) histone H2B [Malus domestica]
                  209778
Seq. No.
                  LIB3135-040-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g2760334
NCBI GI
                   403
BLAST score
                   2.0e-39
E value
                   91
Match length
                   78
% identity
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
                   209779
Seq. No.
                   LIB3135-041-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3882211
                   154
BLAST score
                   2.0e-20
E value
Match length
                   123
                   50
% identity
NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]
                   209780
Seq. No.
                   LIB3135-041-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g421929
NCBI GI
                   507
BLAST score
                   1.0e-51
E value
Match length
                   109
 % identity
                   14
                   ubiquitin - tomato >gi_312160_emb CAA51679 (X73156)
 NCBI Description
                   ubiquitin [Lycopersicon esculentum]
                   209781
 Seq. No.
                   LIB3135-041-Q1-K1-A4
 Seq. ID
```

28981

BLASTX

Method



```
a602076
NCBI GI
BLAST score
                  582
                  2.0e-60
E value
                  129
Match length
% identity
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                  209782
Seq. No.
                  LIB3135-041-Q1-K1-A5
Seq. ID
                  BLASTN
Method
NCBI GI
                  q12614
BLAST score
                   165
                   9.0e-88
E value
                   243
Match length
% identity
NCBI Description L.esculentum genes for tRNA Asn and tRNA Tyr
                   209783
Seq. No.
                   LIB3135-041-Q1-K1-A8
Seq. ID
                   BLASTX
Method
                   q3885328
NCBI GI
                   160
BLAST score
                   4.0e-11
E value
                   48
Match length
% identity
                   60
                   (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   209784
Seq. No.
                   LIB3135-041-Q1-K1-B1
Seq. ID
                   BLASTX
Method
                   q124226
NCBI GI
                   160
BLAST score
E value
                   3.0e-11
                   35
Match length
% identity
                   91
                   INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi 100278_pir___S21059 translation initiation factor
                   eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (\overline{2}) [Nicotiana]
                   plumbaginifolia]
                   209785
 Seq. No.
                   LIB3135-041-Q1-K1-B12
 Seq. ID
Method
                   BLASTX
                   g3152660
NCBI GI
BLAST score
                   188
                   4.0e-14
E value
                   106
Match length
                   34
 % identity
 NCBI Description (AF064603) GA17 protein [Homo sapiens]
                   209786
 Seq. No.
                   LIB3135-041-Q1-K1-B3
 Seq. ID
                   BLASTX
 Method
```

28982

g4567215

400

NCBI GI

BLAST score



5.0e-39 E value Match length 124 % identity

NCBI Description (AC007113) putative presenilin [Arabidopsis thaliana]

209787 Seq. No.

LIB3135-041-Q1-K1-B5 Seq. ID

Method BLASTX NCBI GI g3493172 BLAST score 587 4.0e-61 E value Match length 118 % identity 65

NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

209788 Seq. No.

LIB3135-041-Q1-K1-B6 Seq. ID

Method BLASTX NCBI GI q2827143 BLAST score 439 E value 1.0e-43 Match length 86 % identity 91

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 209789

Seq. ID LIB3135-041-Q1-K1-C10

Method BLASTX NCBI GI g2492860 BLAST score 321 5.0e-30 E value Match length 86 74 % identity

GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2 PRECURSOR (GSA NCBI Description

2) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 2) (GSA-AT 2)

>gi 498914 (U10278) glutamate-1-semialdehyde aminotransferase [Arabidopsis thaliana]

Seq. No. 209790

LIB3135-041-Q1-K1-C11 Seq. ID

Method BLASTX NCBI GI g1172817 BLAST score 486 E value 5.0e-49 Match length 113 84 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L11B (L16B) >gi 550547 emb\_CAA57396\_

> (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi\_4539392\_emb\_CAB37458.1\_ (AL035526) ribosomal protein
> L11, cytosolic [Arabidopsis thaliana]

Seq. No. 209791

Seq. ID LIB3135-041-Q1-K1-C12

Method BLASTX NCBI GI g3342798 BLAST score 469

```
4.0e-47
E value
                  128
Match length
% identity
                  (AF061240) glutamine cyclotransferase precursor [Carica
NCBI Description
                  papaya]
                  209792
Seq. No.
                  LIB3135-041-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  g4335751
NCBI GI
BLAST score
                  541
E value
                  1.0e-55
Match length
                  122
% identity
                   (AC006284) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                   209793
Seq. No.
                   LIB3135-041-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g2832359
NCBI GI
                   161
BLAST score
E value
                   4.0e-11
Match length
                   94
% identity
NCBI Description (Y14072) HMG protein [Arabidopsis thaliana]
                   209794
Seq. No.
                   LIB3135-041-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g1632822
NCBI GI
                   342
BLAST score
                   3.0e-32
E value
Match length
                   107
                   67
% identity
                   (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
NCBI Description
                   (U77297) transmembrane protein [Oryza sativa]
                   209795
Seq. No.
                   LIB3135-041-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   g2970051
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   106
Match length
 % identity
                   64
NCBI Description (AB012110) ARG10 [Vigna radiata]
                   209796
 Seq. No.
                   LIB3135-041-Q1-K1-D1
 Seq. ID
                   BLASTX
 Method
                   g4530585
 NCBI GI
                   354
 BLAST score
                   1.0e-33
 E value
                   85
 Match length
                   73
 % identity
 NCBI Description (AF130978) B12D protein [Ipomoea batatas]
```



```
209797
Seq. No.
                  LIB3135-041-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  q3885334
NCBI GI
                  539
BLAST score
                  3.0e-55
E value
                  141
Match length
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  209798
Seq. No.
                  LIB3135-041-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g2213558
NCBI GI
                  244
BLAST score
                  1.0e-20
E value
                  115
Match length
                   44
% identity
NCBI Description (Z97052) hypothetical protein [Schizosaccharomyces pombe]
                   209799
Seq. No.
                  LIB3135-041-Q1-K1-D5
Seq. ID
Method
                   BLASTX
                   g3043428
NCBI GI
                   524
BLAST score
                   2.0e-53
E value
                   111
Match length
% identity
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                   209800
Seq. No.
                   LIB3135-041-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   q2459417
NCBI GI
BLAST score
                   246
                   3.0e - 34
E value
                   112
Match length
% identity
                   (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                   [Arabidopsis thaliana]
                   209801
Seq. No.
                   LIB3135-041-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   q99583
NCBI GI
                   155
BLAST score
E value
                   2.0e-10
                   100
Match length
 % identity
                   42
                   seed-specific protein - prince's feather
NCBI Description
                   >gi_423770_pir__A47185 storage protein isoform AmA1, 35K -
                   prince's feather >gi_15999_emb_CAA77664_ (Z11577) seed
                   specific protein of balanced nutritional quality
```

[Amaranthus hypochondriacus]

```
209802
Seq. No.
                  LIB3135-041-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  g4006848
NCBI GI
                  272
BLAST score
                  3.0e-24
E value
                  97
Match length
                  54
% identity
                   (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                  bisulcatus]
                  209803
Seq. No.
                  LIB3135-041-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g4522004
NCBI GI
                   Ī57
BLAST score
                   1.0e-10
E value
                   42
Match length
                   69
% identity
                   (AC007069) putative histidine kinase, sensory transduction
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   209804
                   LIB3135-041-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   g4545261
NCBI GI
BLAST score
                   41
                   1.0e-13
E value
                   143
Match length
                   86
% identity
                   Gossypium hirsutum metallothionein-like protein mRNA,
NCBI Description
                   complete cds
                   209805
Seq. No.
                   LIB3135-041-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g3776021
NCBI GI
                   588
BLAST score
                   4.0e-61
E value
                   119
Match length
                   97
% identity
                   (AJ010472) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   209806
Seq. No.
Seq. ID
                   LIB3135-041-Q1-K1-E7
                   BLASTX
Method
                   g404467
NCBI GI
                   207
BLAST score
                   7.0e-20
E value
                   77
```

Match length

NCBI Description

% identity

Seq. No.

Seq. ID LIB3135-041-Q1-K1-E8

73

aa] [Styela plicata]

BLASTX Method

(S64499) H4 histone [Styela plicata, sperm, Peptide, 103

```
g3068704
NCBI GI
                  228
BLAST score
                  4.0e-19
E value
                  84
Match length
                  29
% identity
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                  209808
Seq. No.
                  LIB3135-041-Q1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244847
BLAST score
                  610
E value
                  1.0e-63
                  133
Match length
% identity
                   (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   209809
Seq. No.
                   LIB3135-041-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   q2499328
NCBI GI
BLAST score
                   400
                   5.0e-39
E value
                   80
Match length
                   93
% identity
                   NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-20KD) (CI-20KD) >gi_1235607_emb_CAA65451.1_
                   (X96671) NADH-ubiquinone oxidoreductase [Solanum tuberosum]
                   209810
Seq. No.
                   LIB3135-041-Q1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076531
                   524
BLAST score
E value
                   1.0e-53
Match length
                   102
                   88
% identity
                   hypothetical protein, pollen allergen homolog - garden pea
NCBI Description
                   >gi_2129891_pir__S65056 pollen allergen homolog precursor
                   (clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)
                   homology with pollen allergens [Pisum sativum]
                   209811
Seq. No.
                   LIB3135-041-Q1-K1-F4
 Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1353352
BLAST score 375
E value 4.0e-36
Match length 103
% identity 70

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

Seq. No. 209812

Seq. ID LIB3135-041-Q1-K1-F5

Method BLASTX

```
NCBI GI
                  q3123745
BLAST score
                  350
E value
                  3.0e - 33
Match length
                  112
% identity
                  54
NCBI Description
                  (AB013447) aluminum-induced [Brassica napus]
                  209813
Seq. No.
Seq. ID
                  LIB3135-041-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q3089553
BLAST score
                  155
                  1.0e-10
E value
                  68
Match length
                  49
% identity
                  (AF059505) exopolygalacturonase [Yersinia enterocolitica]
NCBI Description
Seq. No.
                  209814
Seq. ID
                  LIB3135-041-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3548818
BLAST score
                  551
                  8.0e-57
E value
Match length
                  121
% identity
                  86
NCBI Description
                  (AC005313) unknown protein [Arabidopsis thaliana]
                  209815
Seq. No.
                  LIB3135-041-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170747
BLAST score
                  291
                  2.0e-26
E value
Match length
                  59
                  100
% identity
```

LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345 NCBI Description (M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

209816 Seq. No.

Seq. ID LIB3135-041-Q1-K1-G2

Method BLASTX NCBI GI q3023857 BLAST score 459 E value 6.0e-46 Match length 100 % identity 87

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi\_629591 pir \_S48839 guanine nucleotide

regulatory protein - rape >qi 563335 emb CAA83924 (Z33643)

guanine nucleotide regulatory protein [Brassica napus]

Seq. No. 209817

Seq. ID LIB3135-041-Q1-K1-G3

Method BLASTX NCBI GI g20683

```
BLAST score
                  4.0e-10
E value
                  65
Match length
                  57
% identity
NCBI Description (X54357) 289 aa peptide [Pisum sativum]
                  209818
Seq. No.
                  LIB3135-041-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  q1928981
NCBI GI
                  639
BLAST score
E value
                   5.0e-67
Match length
                   144
                   88
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   209819
Seq. No.
                   LIB3135-041-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   q1297359
NCBI GI
                   413
BLAST score
                   2.0e-40
E value
Match length
                   79
                   99
% identity
NCBI Description (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]
                   209820
Seq. No.
                   LIB3135-041-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g4456760
NCBI GI
                   403
BLAST score
                   2.0e-39
E value
Match length
                   89
                   73
 % identity
                   (AJ000692) osmotin-like protein [Quercus suber]
NCBI Description
                   209821
 Seq. No.
                   LIB3135-041-Q1-K1-H3
 Seq. ID
                   BLASTX
Method
                   g2924776
 NCBI GI
                   254
 BLAST score
                   5.0e-22
 E value
 Match length
                   61
                   80
 % identity
                   (AC002334) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   209822
 Seq. No.
                   LIB3135-042-Q1-K1-A11
 Seq. ID
                   BLASTX
 Method
                   g2781357
 NCBI GI
```

Method BLASTX
NCBI GI g2781357
BLAST score 283
E value 2.0e-25
Match length 103
% identity 55

NCBI Description (AC003113) F2401.13 [Arabidopsis thaliana]

```
209823
Seq. No.
                  LIB3135-042-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g1370180
NCBI GI
BLAST score
                   481
                  1.0e-48
E value
Match length
                  113
                  88
% identity
                  (Z73939) RAB5B [Lotus japonicus]
NCBI Description
```

 Seq. No.
 209824

 Seq. ID
 LIB3135-042-Q1-K1-A8

 Method
 BLASTX

 NCBI GI
 g1199772

 PLAST score
 239

NCBI GI g1199772
BLAST score 239
E value 4.0e-20
Match length 122
% identity 46

NCBI Description (D83226) extensin like protein [Populus nigra]

>gi\_1199774\_dbj\_BAA11855\_ (D83227) extensin like protein

[Populus nigra]

 Seq. No.
 209825

 Seq. ID
 LIB3135-042-Q1-K1-A9

 Method
 BLASTX

 NCBI GI
 g2130521

NCBI GI g2130521 BLAST score 263 E value 4.0e-23 Match length 63 % identity 75

NCBI Description (U31565) reversibly glycosylatable polypeptide [Pisum

sativum]

Seq. No. 209826

Seq. ID LIB3135-042-Q1-K1-B1

Method BLASTX
NCBI GI g2352931
BLAST score 182
E value 3.0e-16
Match length 114
% identity 46

NCBI Description (AF012867) cytosolic chorismate mutase 2 [Petroselinum

crispum]

Seq. No. 209827

Seq. ID LIB3135-042-Q1-K1-B12

Method BLASTX
NCBI GI g2497953
BLAST score 365
E value 7.0e-35
Match length 119
% identity 64

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi\_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis

thaliana] >gi 4469123 emb CAB38312 (AJ236870) molybdenum

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. ID



```
209828
Seq. No.
                  LIB3135-042-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g3434975
NCBI GI
                  241
BLAST score
                  2.0e-20
E value
                  83
Match length
                  52
% identity
                   (AB008107) ethylene responsive element binding factor 5
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  209829
                  LIB3135-042-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                  q1841870
NCBI GI
                   329
BLAST score
E value
                   1.0e-30
                   87
Match length
% identity
                   75
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
Seq. No.
                   209830
                   LIB3135-042-Q1-K1-B9
Seq. ID
                   BLASTX
Method
                   g232031
NCBI GI
                   168
BLAST score
                   3.0e-12
E value
Match length
                   78
                   49
% identity
                   ELONGATION FACTOR 1 BETA' >gi 322851_pir__$29224
NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >gi 218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                   209831
Seq. No.
                   LIB3135-042-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1110502
                   237
BLAST score
                   6.0e-29
E value
                   131
Match length
                   49
% identity
                   (U40387) coil protein [Medicago sativa]
NCBI Description
                   209832
Seq. No.
                   LIB3135-042-Q1-K1-C3
Seq. ID
                   BLASTX
Method
                   g2388575
NCBI GI
                   236
BLAST score
                   9.0e-20
E value
                   126
Match length
                   40
 % identity
                   (AC000098) YUP8H12.18 [Arabidopsis thaliana]
NCBI Description
                   209833
 Seq. No.
```

28991

LIB3135-042-Q1-K1-C4

```
BLASTX
Method
                  g3157920
NCBI GI
                  207
BLAST score
                  2.0e-16
E value
                  87
Match length
                  47
% identity
                  (AC002131) F12F1.6 [Arabidopsis thaliana]
NCBI Description
                  209834
Seq. No.
                  LIB3135-042-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g2894599
NCBI GI
                  394
BLAST score
                  3.0e-38
E value
                  143
Match length
                  64
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                  209835
Seq. No.
                  LIB3135-042-Q1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1346155
BLAST score
                  446
                  9.0e-65
E value
                  131
Match length
                  94
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481942 pir S40212 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                   >gi 437995 emb CAA81078_ (Z25859) glycine
                  hydroxymethyltransferase [Flaveria pringlei]
                   209836
Seq. No.
                  LIB3135-042-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                   q3128220
NCBI GI
BLAST score
                   187
                   5.0e-14
E value
                   87
Match length
                   47
% identity
                   (AC004077) putative urease accessory protein [Arabidopsis
NCBI Description
                   thaliana] >gi 3337375 (AC004481) putative urease accessory
                   protein [Arabidopsis thaliana]
                   209837
Seq. No.
Seq. ID
                   LIB3135-042-Q1-K1-D11
                   BLASTX
Method
                   g2213783
NCBI GI
                   228
BLAST score
                   6.0e-19
E value
```

103 Match length 49 % identity

(U89256) Pti5 [Lycopersicon esculentum] NCBI Description

209838 Seq. No.

LIB3135-042-Q1-K1-D4 Seq. ID

```
BĒASTX
Method
NCBI GI
                  q4455207
                  428
BLAST score
                  3.0e-42
E value
                  91
Match length
                  90
% identity
                  (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
                  209839
Seq. No.
                  LIB3135-042-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g2497953
NCBI GI
BLAST score
                   408
                   7.0e-57
E value
                   137
Match length
                   82
% identity
                  MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM
NCBI Description
                   COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323)
                   molybdenum cofactor biosynthesis enzyme [Arabidopsis
                   thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum
                   cofactor biosynthesis enzyme [Arabidopsis thaliana]
                   209840
Seq. No.
                   LIB3135-042-Q1-K1-E1
Seq. ID
                   BLASTX
Method
                   g3860277
NCBI GI
                   503
BLAST score
                   4.0e-53
E value
                   140
Match length
                   81
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi 4314394 gb AAD15604 (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   209841
Seq. No.
                   LIB3135-042-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4205741
                   582
BLAST score
                   3.0e-60
E value
                   136
Match length
                   78
 % identity
                   (AF034566) class I chitinase [Gossypium hirsutum]
 NCBI Description
                    209842
 Seq. No.
                    LIB3135-042-Q1-K1-E2
 Seq. ID
                    BLASTX
 Method
                    g687677
 NCBI GI
 BLAST score
                    216
                    2.0e-17
 E value
 Match length
                    65
                    56
 % identity
                   (U19925) unknown [Arabidopsis thaliana]
 NCBI Description
```

209843

BLASTX

LIB3135-042-Q1-K1-E3

Seq. No.

Seq. ID

Method

```
g480618
NCBI GI
                   221
BLAST score
                   2.0e-18
E value
                   69
Match length
                   65
% identity
                  ATAF1 protein - Arabidopsis thaliana (fragment)
NCBI Description
                   >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis
                   thaliana]
                   209844
Seq. No.
                   LIB3135-042-Q1-K1-E4
Seq. ID
Method
                   BLASTX
                   q3287681
NCBI GI
                   465
BLAST score
                   1.0e-46
E value
                   146
Match length
                   66
% identity
                   (AC003979) ESTs gb_Z34075, gb_Z34835 and gb_AA404888 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
                   209845
 Seq. No.
 Seq. ID
                   LIB3135-042-Q1-K1-E5
Method
                   BLASTN
                   q4205740
 NCBI GI
 BLAST score
                   46
                   4.0e-17
 E value
                   110
 Match length
                   87
 % identity
 NCBI Description Gossypium hirsutum class I chitinase mRNA, partial cds
                   209846
 Seq. No.
                   LIB3135-042-Q1-K1-E6
 Seq. ID
 Method
                   BLASTX
                   g2130052
 NCBI GI
                    309
 BLAST score
                    2.0e-34
 E value
                    107
 Match length
                    67
 % identity
                   xylose isomerase (EC 5.3.1.5) - barley
 NCBI Description
                    >gi 1296809_emb_CAA64545 (X95257) xylose isomerase
                    [Hordeum vulgare]
                    209847
 Seq. No.
                    LIB3135-042-Q1-K1-E8
 Seq. ID
                    BLASTN
 Method
                    g2924651
 NCBI GI
                    42
 BLAST score
                    2.0e-14
 E value
                    62
 Match length
                    92
 % identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 NCBI Description
                    K2A18, complete sequence [Arabidopsis thaliana]
```

Seq. No. 209848

Seq. ID LIB3135-042-Q1-K1-F1

Method BLASTX NCBI GI g2129915

28994

. .

```
BLAST score
                  5.0e-37
E value
                  115
Match length
% identity
                  ferredoxin precursor - sweet orange
NCBI Description
                  >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
                   ferredoxin [Citrus sinensis]
                   209849
Seq. No.
                  LIB3135-042-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q1173187
NCBI GI
BLAST score
                   278
                   7.0e-25
E value
                   56
Match length
                   98
% identity
                   40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi_643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
                   209850
Seq. No.
                   LIB3135-042-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g629483
                   323
BLAST score
                   5.0e-30
E value
                   116
Match length
```

% identity 54 NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula] >gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 209851

Seq. ID LIB3135-042-Q1-K1-F5

Method BLASTX
NCBI GI g130840
BLAST score 498
E value 2.0e-50
Match length 123
% identity 73

NCBI Description PATHOGENESIS-RELATED PROTEIN PR-4B PRECURSOR

>gi 19968\_emb\_CAA42821\_ (X60282) PR-4b protein [Nicotiana

tabacum]

Seq. No. 209852

Seq. ID LIB3135-042-Q1-K1-F6

Method BLASTX
NCBI GI 94415931
BLAST score 421
E value 1.0e-41
Match length 110
% identity 67

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi\_4559393\_gb\_AAD23053.1\_AC006526\_18 (AC006526) unknown

protein [Arabidopsis thaliana]



```
209853
Seq. No.
                  LIB3135-042-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  g4220541
NCBI GI
                  333
BLAST score
                   4.0e-31
E value
                   132
Match length
                   59
% identity
                   (AL035356) Rab geranylgeranyl transferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   209854
Seq. No.
                   LIB3135-042-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   q478673
NCBI GI
                   259
BLAST score
                   2.0e-22
E value
                   92
Match length
                   54
% identity
                   proline-rich protein precursor - kidney bean
NCBI Description
                   >gi 21046 emb CAA42942 (X60391) proline-rich protein
                   [Phaseolus vulgaris]
                   209855
Seq. No.
                   LIB3135-042-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   q2832304
NCBI GI
BLAST score
                   231
                   3.0e-29
E value
                   104
Match length
                   62
% identity
                   (AF044489) receptor-like protein kinase [Oryza sativa]
NCBI Description
                   209856
Seq. No.
                   LIB3135-042-Q1-K1-H1
Seq. ID
Method
                   BLASTX
                   q2894612
NCBI GI
BLAST score
                   583
                   2.0e-60
E value
                   140
Match length
                   76
 % identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   209857
Seq. No.
                   LIB3135-043-P1-K1-A1
 Seq. ID
Method
                   BLASTN
                   g3334857
 NCBI GI
                   221
 BLAST score
                   1.0e-121
 E value
                   294
Match length
                   94
 % identity
                   Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2
 NCBI Description
                   genes
```

Seq. No. 209858

Seq. ID LIB3135-043-P1-K1-A10



Method BLASTX
NCBI GI g1710840
BLAST score 508
E value 1.0e-51
Match length 128
% identity 75

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57) >gi\_441217\_dbj\_BAA03709\_ (D16138) S-adenosyl-L-homocystein hydrolase [Nicotiana sylvestris] >gi\_1857024\_dbj\_BAA08142\_ (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana

tabacum] >gi\_2588781\_dbj\_BAA23164\_ (D49804)

S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No. 209859

Seq. ID LIB3135-043-P1-K1-A11

Method BLASTN
NCBI GI g2642323
BLAST score 176
E value 1.0e-94
Match length 184
% identity 99

NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 209860

Seq. ID LIB3135-043-P1-K1-A2

Method BLASTX
NCBI GI 9464986
BLAST score 592
E value 2.0e-61
Match length 113
% identity 97

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi 421857 pir S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi 4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 209861

Seq. ID LIB3135-043-P1-K1-A9

Method BLASTX
NCBI GI g1561774
BLAST score 334
E value 1.0e-31
Match length 84
% identity 79

NCBI Description (U67426) malate dehydrogenase [Vitis vinifera]

Seq. No. 209862

Seq. ID LIB3135-043-P1-K1-B11

Method BLASTX

```
NCBI GI
                  a4104931
BLAST score
                  406
E value
                  1.0e-39
                  105
Match length
                  74
% identity
                  (AF042196) auxin response factor 8 [Arabidopsis thaliana]
NCBI Description
                  209863
Seq. No.
                  LIB3135-043-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1905876
BLAST score
                  141
E value
                  2.0e-14
Match length
                  118
% identity
                  52
NCBI Description
                  (U90879) biotin carboxylase subunit [Arabidopsis thaliana]
                  >gi 1916300 (U91414) heteromeric acetyl-CoA carboxylase
                  biotin carboxylase subunit [Arabidopsis thaliana]
                  >gi 3047099 (AF058826) Arabidopsis thaliana biotin
                  carboxylase subunit (GB:U90879) [Arabidopsis thaliana]
Seq. No.
                  209864
Seq. ID
                  LIB3135-043-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2668744
BLAST score
                  146
E value
                  3.0e-09
Match length
                  32
                  75
% identity
NCBI Description
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                  209865
Seq. ID
                  LIB3135-043-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q3334857
BLAST score
                  218
E value
                  1.0e-119
Match length
                  349
% identity
                  91
NCBI Description
                  Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2
                  genes
                  209866
Seq. No.
Seq. ID
                  LIB3135-043-P1-K1-C5
                  BLASTX
Method
NCBI GI
                  q3334113
```

Method BLASTX
NCBI GI g3334113
BLAST score 455
E value 2.0e-45
Match length 89
% identity 97

NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >qi 1006831 (U35015)

acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No. 209867

Seq. ID LIB3135-043-P1-K1-C7

Method BLASTX NCBI GI g2443348



```
BLAST score 300
E value 2.0e-27
Match length 112
% identity 49
```

NCBI Description (AB001379) cytochrome P450 [Glycyrrhiza echinata]

Seq. No. 209868

Seq. ID LIB3135-043-P1-K1-C8

Method BLASTN
NCBI GI g12614
BLAST score 34
E value 6.0e-10
Match length 70
% identity 87

NCBI Description L.esculentum genes for tRNA Asn and tRNA Tyr

Seq. No. 209869

Seq. ID LIB3135-043-P1-K1-D1

Method BLASTN
NCBI GI 94106514
BLAST score 65
E value 4.0e-28
Match length 149
% identity 86

NCBI Description Populus tremula x Populus tremuloides CAK associated

cyclinH homolog (cycH) mRNA, complete cds

Seq. No. 209870

Seq. ID LIB3135-043-P1-K1-D2

Method BLASTN
NCBI GI g2829205
BLAST score 158
E value 2.0e-83
Match length 421
% identity 18

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 209871

Seq. ID LIB3135-043-P1-K1-D4

Method BLASTX
NCBI GI g401322
BLAST score 564
E value 3.0e-58
Match length 122
% identity 93

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi\_167313 (L03186) vacuolar H+-ATPase catalytic

subunit [Gossypium hirsutum]

Seq. No. 209872

Seq. ID LIB3135-043-P1-K1-D9

Method BLASTX
NCBI GI g480450
BLAST score 204
E value 3.0e-32
Match length 100



₹ identity 76

ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 209873

NCBI Description

Seq. ID LIB3135-043-P1-K1-E3

Method BLASTX
NCBI GI g1402912
BLAST score 236
E value 4.0e-20
Match length 57
% identity 74

NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 209874

Seq. ID LIB3135-043-P1-K1-E6

Method BLASTX
NCBI GI 94567232
BLAST score 327
E value 2.0e-30
Match length 71
% identity 92

NCBI Description (AC007119) putative 40S ribosomal protein S25 [Arabidopsis

thaliana)

Seq. No. 209875

Seq. ID LIB3135-043-P1-K1-F1

Method BLASTX
NCBI GI g2997591
BLAST score 505
E value 3.0e-51
Match length 123
% identity 76

NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator

precursor [Pisum sativum]

Seq. No. 209876

Seq. ID LIB3135-043-P1-K1-F2

Method BLASTX
NCBI GI g3695408
BLAST score 230
E value 5.0e-19
Match length 80
% identity 65

NCBI Description (AF096373) contains similarity to Solanum lycopersicum

(tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi\_4538956\_emb\_CAB39780.1\_ (AL049488) probable

wound-induced protein [Arabidopsis thaliana]

Seq. No. 209877

Seq. ID LIB3135-043-P1-K1-F6

Method BLASTX
NCBI GI g2738949
BLAST score 595
E value 7.0e-62
Match length 122

```
% identity
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                  ananassa]
                  209878
Seq. No.
                  LIB3135-043-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g1419370
NCBI GI
                  401
BLAST score
                  3.0e-39
E value
                  76
Match length
% identity
                  100
                  (X97726) actin depolymerizing factor [Zea mays]
NCBI Description
                   209879
Seq. No.
                  LIB3135-043-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3892052
BLAST score
                   555
E value
                   4.0e-57
Match length
                   136
                   71
% identity
                   (AC002330) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   209880
Seq. No.
                   LIB3135-043-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2529229
BLAST score
                   396
                   8.0e-39
E value
Match length
                   82
% identity
                   89
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                   209881
Seq. No.
                   LIB3135-043-P1-K1-G7
Seq. ID
                   BLASTX
Method
                   g2894599
NCBI GI
                   331
BLAST score
                   7.0e-31
E value
                   88
Match length
                   68
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   209882
Seq. No.
                   LIB3135-043-P1-K1-H1
Seq. ID
                   BLASTX
Method
                   g2909522
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
                   103
Match length
                   35
% identity
                   (AL021932) ufaA1 [Mycobacterium tuberculosis]
NCBI Description
                   209883
Seq. No.
                   LIB3135-043-P1-K1-H11
Seq. ID
```

NCBI GI

BLAST score

```
BLASTX
   Method
                      q902525
   NCBI GI
                      310
   BLAST score
                      2.0e-28
   E value
                      59
   Match length
   % identity
                      97
                      (U29160) ubiquitin fusion protein [Zea mays]
   NCBI Description
                      >gi 1589387_prf__2211240A ubiquitin fusion protein [Zea
                      mays]
                      209884
   Seq. No.
   Seq. ID
                      LIB3135-043-P1-K1-H5
   Method
                      BLASTX
                      g286001
   NCBI GI
                      153
   BLAST score
                      5.0e-10
   E value
   Match length
                      119
   % identity
                      30
   NCBI Description (D13630) KIAA0005 [Homo sapiens]
                      209885
   Seq. No.
                      LIB3135-043-P1-K1-H9
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g3204108
   BLAST score
                      236
                      7.0e-20
   E value
                      70
   Match length
                      67
    % identity
                      (AJ006764) putative deoxycytidylate deaminase [Cicer
   NCBI Description
                      arietinum]
                      209886
    Seq. No.
    Seq. ID
                      LIB3135-044-Q1-K1-A10
                      BLASTX
    Method
                      g3738329
    NCBI GI
                      506
    BLAST score
                      2.0e-51
    E value
Match length
                      120
    % identity
                      84
                      (AC005170) unknown protein [Arabidopsis thaliana]
    NCBI Description
                      209887
    Seq. No.
                      LIB3135-044-Q1-K1-A2
    Seq. ID
                      BLASTX
    Method
                      g4559342
    NCBI GI
                      556
    BLAST score
                      3.0e-57
    E value
                      132
    Match length
                      75
    % identity
                       (AC007087) putative copper methylamine oxidase [Arabidopsis
    NCBI Description
                      thaliana]
                       209888
    Seq. No.
                      LIB3135-044-Q1-K1-A3
    Seq. ID
                       BLASTX
    Method
```

29002

g1769887 345

```
0e-32
E value
                  79
Match length
                  80
% identity
                  (X95736) amino acid permease 6 [Arabidopsis thaliana]
NCBI Description
                  209889
Seq. No.
                  LIB3135-044-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g1871577
NCBI GI
BLAST score
                  225
                  2.0e-18
E value
Match length
                  105
% identity
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                   209890
Seq. No.
                  LIB3135-044-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4469024
                   307
BLAST score
                   1.0e-29
E value
                   110
Match length
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   209891
Seq. No.
                   LIB3135-044-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006890
BLAST score
                   436
                   3.0e-43
E value
Match length
                   87
                   90
% identity
                   (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   209892
Seq. No.
                   LIB3135-044-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   g122770
NCBI GI
                   321
BLAST score
                   1.0e-29
E value
                   79
Match length
                   80
% identity
                   HEMOGLOBIN II >gi 99509 pir S13378 hemoglobin II - swamp
NCBI Description
                   oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina
                   glauca]
                   209893
Seq. No.
                   LIB3135-044-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g131026
NCBI GI
BLAST score
                   340
                   6.0e-32
E value
                   127
Match length
                   54
 % identity
NCBI Description PATHOGENESIS-RELATED PROTEIN STH-2 >gi_479691_pir__S35161
```

```
H-2 protein - potato >gi_169551 (Mz5155) pSTH-2 protein
                   [Solanum tuberosum] >gi 16\overline{9}576 (M29041) STH-2 protein
                   [Solanum tuberosum]
                  209894
Seq. No.
                  LIB3135-044-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g1173218
NCBI GI
                  518
BLAST score
                   7.0e-53
E value
                   130
Match length
% identity
                   81
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                   protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                   cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                   209895
Seq. No.
                   LIB3135-044-Q1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2558655
BLAST score
                   286
                   1.0e-25
E value
Match length
                   135
                   47
% identity
                   (AC002354) No definition line found [Arabidopsis thaliana]
NCBI Description
                   209896
Seq. No.
                   LIB3135-044-Q1-K1-D12
Seq. ID
                   BLASTX
Method
                   q3334261
NCBI GI
                   207
BLAST score
                   1.0e-16
E value
Match length
                   77
                   53
% identity
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
NCBI Description
                   metallothionein-like protein [Malus domestica]
                   209897
Seq. No.
                   LIB3135-044-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   g1480012
NCBI GI
                   331
BLAST score
                   6.0e-31
E value
                   65
Match length
                   95
% identity
                   (D78492) putative ubiquitin extension protein [Brassica
NCBI Description
                   rapa]
                   209898
Seq. No.
                   LIB3135-044-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g4456760
NCBI GI
```

NCBI Description (AJ000692) osmotin-like protein [Quercus suber]

356

80

71

8.0e-34

BLAST score

Match length

% identity

E value



```
209899
Seq. No.
                  LIB3135-044-Q1-K1-D7
Seq. ID
                  BLASTX
Method
                  g3549691
NCBI GI
BLAST score
                  399
                  8.0e-39
E value
                  111
Match length
                  63
% identity
NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
Seq. No.
                  209900
                  LIB3135-044-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                  q4567281
NCBI GI
                  333
BLAST score
                  4.0e-31
E value
Match length
                  130
% identity
NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]
                   209901
Seq. No.
Seq. ID
                  LIB3135-044-Q1-K1-E12
Method
                  BLASTX
                  q3785987
NCBI GI
                   214
BLAST score
                   3.0e-17
E value
                   103
Match length
% identity
                   45
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
                   209902
Seq. No.
                   LIB3135-044-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g1707640
NCBI GI
                   155
BLAST score
                   2.0e-10
E value
                   90
Match length
% identity
                   40
                  (X98355) transcription factor GAMyb [Oryza sativa]
NCBI Description
                   209903
Seq. No.
                   LIB3135-044-Q1-K1-E3
Seq. ID
Method
                   BLASTX
                   g3193336
NCBI GI
                   167
BLAST score
                   1.0e-11
E value
                   78
Match length
                   42
 % identity
                  (AF069301) DBI-related protein [Homo sapiens]
NCBI Description
                   209904
 Seq. No.
                   LIB3135-044-Q1-K1-E7
 Seq. ID
                   BLASTX
Method
                   g4038043
NCBI GI
                   160
BLAST score
```

8.0e-11

E value



Match length 96 % identity 33

NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 209905

Seq. ID LIB3135-044-Q1-K1-F1

Method BLASTX
NCBI GI g129233
BLAST score 320
E value 1.0e-29
Match length 61
% identity 90

NCBI Description ORYZAIN GAMMA CHAIN PRECURSOR >gi\_67646\_pir\_\_KHRZOG oryzain

(EC 3.4.22.-) gamma precursor - rice

>gi 218185 dbj BAA14404\_ (D90408) oryzain gamma precursor

[Oryza sativa]

Seq. No. 209906

Seq. ID LIB3135-044-Q1-K1-F11

Method BLASTX
NCBI GI g3395432
BLAST score 539
E value 2.0e-55
Match length 130
% identity 78

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 209907

Seq. ID LIB3135-044-Q1-K1-F12

Method BLASTX
NCBI GI g2947063
BLAST score 189
E value 3.0e-14
Match length 136
% identity 44

NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 209908

Seq. ID LIB3135-044-Q1-K1-F3

Method BLASTX
NCBI GI g134101
BLAST score 683
E value 4.0e-72
Match length 144
% identity 96

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD

CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi 72958 pir HHCSBA ribulose-bisphosphate carboxylase

subunit-binding protein alpha chain - castor bean

(fragment)

Seq. No. 209909

Seq. ID LIB3135-044-Q1-K1-F8

Method BLASTX NCBI GI g1777386

```
BLAST score
                  1.0e-10
E value
Match length
                  87
                  51
% identity
                  (U39301) caffeic acid O-methyltransferase [Pinus taeda]
NCBI Description
                  209910
Seq. No.
                  LIB3135-044-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g135860
NCBI GI
                  239
BLAST score
                  4.0e-20
E value
                  65
Match length
                  66
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi 166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >qi 445129 prf 1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
                  209911
Seq. No.
                  LIB3135-044-Q1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2982303
                  144
BLAST score
                  4.0e-09
E value
                  42
Match length
                  69
% identity
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
                  209912
Seq. No.
                  LIB3135-044-Q1-K1-G2
Seq. ID
                  BLASTX
```

Method BLASTX
NCBI GI g643469
BLAST score 419
E value 2.0e-41
Match length 119
% identity 69

NCBI Description (U19886) unknown [Lycopersicon esculentum]

Seq. No. 209913

Seq. ID LIB3135-044-Q1-K1-G4

Method BLASTX
NCBI GI g976174
BLAST score 175
E value 6.0e-22
Match length 103
% identity 47

NCBI Description (L47181) reverse transcriptase [Arabidopsis thaliana]

Seq. No. 209914

Seq. ID LIB3135-044-Q1-K1-G6

Method BLASTX NCBI GI g464707

```
BLAST score
                  5.0e-63
E value
                  126
Match length
                  93
% identity
                  40S RIBOSOMAL PROTEIN S18 >gi 480908 pir_S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                  >qi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 434343 emb_CAA82273_ (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >qi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] > \overline{g}i_3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                  thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
                  gb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
```

 Seq. No.
 209915

 Seq. ID
 LIB3135-044-Q1-K1-G8

 Method
 BLASTX

 NCBI GI
 g3152583

 BLAST score
 212

 E value
 5.0e-17

 Match length
 112

 % identity
 47

thaliana]

Seq. No. 209916

Seq. ID LIB3135-044-Q1-K1-G9

Method BLASTX
NCBI GI g984756
BLAST score 335
E value 2.0e-31
Match length 88
% identity 69

NCBI Description (Z54153) chilling-inducible protein [Oryza sativa]

Seq. No. 209917

Seq. ID LIB3135-044-Q1-K1-H1

Method BLASTX
NCBI GI g418507
BLAST score 243
E value 1.0e-20
Match length 110
% identity 44

NCBI Description S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE

METHYLTRANSFERASE >gi\_541097\_pir\_\_S40872 hypothetical protein f161 - Escherichia coli >gi\_305032 (L19201) ORF f161 [Escherichia coli] >gi\_1336002 (U56082)

S-adenosylmethionine: 2-demethylmenaquinone

methyltransferase [Escherichia coli] >gi\_1790364 (AE000467)

menaquinone biosynthesis, unknown [Escherichia coli]



```
209918
Seq. No.
                  LIB3135-044-Q1-K1-H10
Seq. ID
                  BLASTX
Method
                  g4567229
NCBI GI
                  161
BLAST score
                  5.0e-11
E value
                  54
Match length
% identity
                  (AC007119) putative pectin methylesterase [Arabidopsis
NCBI Description
                  thaliana]
                  209919
Seq. No.
                  LIB3135-044-Q1-K1-H11
Seq. ID
Method
                  BLASTX
                  q2961300
NCBI GI
BLAST score
                  348
E value
                  3.0e-33
                  90
Match length
                  77
% identity
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
Seq. No.
                  209920
                  LIB3135-044-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                   q1076288
NCBI GI
BLAST score
                   347
                   5.0e-33
E value
Match length
                   95
                   64
% identity
NCBI Description amino acid permease AAP3 - Arabidopsis thaliana
Seq. No.
                   209921
                   LIB3135-044-Q1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629483
                   340
BLAST score
                   6.0e-32
E value
Match length
                   134
                   54
% identity
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                   >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   209922
Seq. No.
                   LIB3135-044-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   g2493852
NCBI GI
                   297
BLAST score
                   7.0e-27
E value
                   63
Match length
                   86
% identity
                   CYTOCHROME C OXIDASE POLYPEPTIDE VC
NCBI Description
```

subunit [Hordeum vulgare]

>gi\_1070356\_emb\_CAA92107\_ (Z68091) cytochrome c oxidase, Vc

Method

BLASTX

```
9923
9
Seq. No.
                  LIB3135-044-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g135860
NCBI GI
                  115
BLAST score
                  7.0e-10
E value
                  52
Match length
                  62
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_99761 pir S22202 tonoplast intrinsic
                  protein gamma - Arabidopsīs thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi 445129 prf 1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
Seq. No.
                  209924
                  LIB3135-045-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  q122781
NCBI GI
                  401
BLAST score
E value
                  1.0e-52
Match length
                  131
% identity
                  POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229)
NCBI Description
                  >gi 82210 pir_A05198 hypothetical protein 229 - common
                  tobacco chloroplast >gi_11844_emb_CAA77364 (Z00044)
                  hypothetical protein [Nicotiana tabacum]
                  >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]
                  209925
Seq. No.
Seq. ID
                  LIB3135-045-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1685003
                  158
BLAST score
                  1.0e-10
E value
                   124
Match length
% identity
                   38
                   (U32643) immediate-early salicylate-induced
NCBI Description
                   glucosyltransferase [Nicotiana tabacum]
                   209926
Seq. No.
                   LIB3135-045-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                   g122770
NCBI GI
                   577
BLAST score
                   1.0e-59
E value
                   134
Match length
                   84
% identity
                  HEMOGLOBIN II >gi 99509 pir S13378 hemoglobin II - swamp
NCBI Description
                   oak >gi 18015 emb CAA37898 (X53950) hemoglobin [Casuarina
                   glauca]
                   209927
Seq. No.
Seq. ID
                   LIB3135-045-Q1-K1-A6
```



```
g2764941
NCBI GI
                  408
BLAST score
                  6.0e-40
E value
                  101
Match length
                  69
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  209928
Seq. No.
                  LIB3135-045-Q1-K1-B1
Seq. ID
                  BLASTX
```

Method BLASTX
NCBI GI g3080439
BLAST score 231
E value 4.0e-19
Match length 140
% identity 39

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 209929

Seq. ID LIB3135-045-Q1-K1-B11

Method BLASTX
NCBI GI g2462761
BLAST score 176
E value 3.0e-13
Match length 51
% identity 67

NCBI Description (AC002292) Highly similar to auxin-induced protein

(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 209930

Seq. ID LIB3135-045-Q1-K1-B4

Method BLASTX
NCBI GI g2129825
BLAST score 331
E value 6.0e-31
Match length 105
% identity 84

NCBI Description dynamin-like protein phragmoplastin 12 - soybean

>gi\_1217994 (U25547) SDL [Glycine max]

Seq. No. 209931

Seq. ID LIB3135-045-Q1-K1-B5

Method BLASTX
NCBI GI g3367594
BLAST score 228
E value 5.0e-19
Match length 78
% identity 55

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 209932

Seq. ID LIB3135-045-Q1-K1-B7

Method BLASTX
NCBI GI g3451075
BLAST score 574
E value 2.0e-59



```
Match length
                  80
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                  209933
Seq. No.
                  LIB3135-045-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g4038035
NCBI GI
                   323
BLAST score
                  5.0e-30
E value
                  107
Match length
                   59
% identity
                   (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   209934
Seq. No.
                  LIB3135-045-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                   g629483
NCBI GI
                   319
BLAST score
                   2.0e-29
E value
Match length
                   112
% identity
                   57
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >qi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                   >gi_1584322prf__2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   209935
Seq. No.
Seq. ID
                   LIB3135-045-Q1-K1-D1
                   BLASTX
Method
NCBI GI
                   g218157
                   580
BLAST score
                   4.0e-60
E value
                   133
Match length
                   86
% identity
                  (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
                   209936
Seq. No.
Seq. ID
                   LIB3135-045-Q1-K1-D2
                   BLASTX
Method
NCBI GI
                   q122770
BLAST score
                   442
                   5.0e-44
E value
Match length
                   106
                   83
% identity
                   HEMOGLOBIN II >qi 99509 pir S13378 hemoglobin II - swamp
NCBI Description
```

oak >qi 18015 emb CAA37898 (X53950) hemoglobin [Casuarina

glauca]

209937 Seq. No.

Seq. ID LIB3135-045-Q1-K1-D5

BLASTX Method NCBI GI q1076670 BLAST score 150 E value 9.0e-10 Match length 44

```
% identity
NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato
                  >gi 668985_emb_CAA59062_ (X84319) NADH dehydrogenase
                  [Solanum tuberosum]
                  209938
Seq. No.
                  LIB3135-045-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g4432823
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
                  62
Match length
% identity
                  58
                  (AC006593) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  209939
Seq. No.
                  LIB3135-045-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g4090533
NCBI GI
                  540
BLAST score
                  2.0e-55
E value
Match length
                  141
% identity
                  74
                 (U68215) ACC oxidase [Carica papaya]
NCBI Description
                  209940
Seq. No.
                  LIB3135-045-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                  g1220196
NCBI GI
BLAST score
                  162
                  3.0e-11
E value
Match length
                   38
% identity
                   84
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                   209941
Seq. No.
                  LIB3135-045-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                   g3935167
NCBI GI
                   324
BLAST score
                   3.0e-30
E value
                   67
Match length
                   93
% identity
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
NCBI Description
                   209942
Seq. No.
                   LIB3135-045-Q1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1709498
BLAST score
                   226
                   4.0e-19
E value
                   52
Match length
                   79
% identity
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi 1362001 pir S57524 osmotin precursor - Arabidopsis
                   thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
```



```
209943
Seq. No.
                  LIB3135-045-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                  g3746071
NCBI GI
                  559
BLAST score
                  1.0e-57
E value
                  129
Match length
% identity
                  82
                  (AC005311) putative GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  209944
Seq. No.
                  LIB3135-045-Q1-K1-F3
Seq. ID
                  BLASTX
Method
                  g3522961
NCBI GI
BLAST score
                   485
                   4.0e-49
E value
                  109
Match length
% identity
                  83
                  (AC004411) putative pto kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  209945
                  LIB3135-045-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                   q4006856
NCBI GI
                   459
BLAST score
                   7.0e-46
E value
                   145
Match length
                   68
% identity
                   (Z99707) receptor kinase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   209946
Seq. No.
                   LIB3135-045-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g1922964
NCBI GI
                   159
BLAST score
                   1.0e-10
E value
                   77
Match length
                   52
% identity
                   (AC000106) Similar to Schizosaccharomyces CCAAT-binding
NCBI Description
                   factor (gb_U88525). EST gb_T04310 comes from this gene.
                   [Arabidopsis thaliana]
                   209947
Seq. No.
                   LIB3135-045-Q1-K1-G6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2708532
BLAST score
                   330
                   9.0e-31
E value
Match length
                   93
% identity
                   28
                  (AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
```

209948

LIB3135-045-Q1-K1-H1

Seq. No.

Seq. ID

```
Method
                  g3046815
NCBI GI
                  517
BLAST score
                  1.0e-52
E value
                  135
Match length
                  73
% identity
                  (AL021687) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  209949
Seq. No.
                  LIB3135-045-Q1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3193297
                  277
BLAST score
                   6.0e-25
E value
                  77
Match length
                   69
% identity
                   (AF069298) similar to epoxide hydrolases [Arabidopsis
NCBI Description
                   thaliana]
                   209950
Seq. No.
                  LIB3135-045-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                   g167367
NCBI GI
                   499
BLAST score
                   8.0e-51
E value
                   97
Match length
                   95
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   209951
Seq. No.
                   LIB3135-045-Q1-K1-H8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g19229
                   33
BLAST score
                   4.0e-09
E value
                   121
Match length
                   21
% identity
                   Tomato extensin mRNA (clone uG-18)
NCBI Description
                   209952
Seq. No.
                   LIB3135-045-Q1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3334245
BLAST score
                   500
                   1.0e-50
E value
                   136
Match length
                   68
% identity
                   LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
NCBI Description
                   (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                   MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                   >gi 2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer
                   arietinum]
                   209953
Seq. No.
Seq. ID
                   LIB3135-046-Q1-K1-A1
                   BLASTX
Method
```

q3901014

NCBI GI



BLAST score 228
E value 7.0e-19
Match length 55
% identity 75

NCBI Description (AJ130886) metallothionein-like protein class II [Fagus

sylvatica]

Seq. No. 209954

Seq. ID LIB3135-046-Q1-K1-A3

Method BLASTX
NCBI GI 94455223
BLAST score 132
E value 4.0e-16
Match length 78
% identity 52

NCBI Description (AL035440) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 209955

Seq. ID LIB3135-046-Q1-K1-A4

Method BLASTX
NCBI GI g2244835
BLAST score 226
E value 8.0e-19
Match length 83
% identity 60

NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 209956

Seq. ID LIB3135-046-Q1-K1-A5

Method BLASTX
NCBI GI g3914685
BLAST score 296
E value 6.0e-27
Match length 101
% identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi\_2668748 (AF034948) ribosomal

protein L17 [Zea mays]

Seq. No. 209957

Seq. ID LIB3135-046-Q1-K1-A7

Method BLASTX
NCBI GI g2801536
BLAST score 480
E value 2.0e-48
Match length 136
% identity 65

NCBI Description (AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No. 209958

Seq. ID LIB3135-046-Q1-K1-A8

Method BLASTX
NCBI GI g2244835
BLAST score 170
E value 3.0e-12
Match length 68
% identity 57

```
(Z97337) protein kinase homolog [Arabidopsis thaliana]
NCBI Description
                  209959
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2245066
BLAST score
                  418
                  4.0e-41
E value
Match length
                  141
                  56
% identity
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
NCBI Description
                  209960
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g478673
                  146
BLAST score
                  2.0e-09
E value
                  71
Match length
                  45
% identity
                  proline-rich protein precursor - kidney bean
NCBI Description
                  >gi 21046 emb CAA42942 (X60391) proline-rich protein
                  [Phaseolus vulgaris]
                  209961
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1352664
BLAST score
                  759
                  4.0e-81
E value
                  140
Match length
                  98
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
NCBI Description
                  SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase
                   (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana
                  >gi 473259 (U08047) Ser/Thr protein phosphatase
                   [Arabidopsis thaliana] >qi 4204949 (U60136)
                  serine/threonine protein phosphatase 2A-4 catalytic subunit
                   [Arabidopsis thaliana]
                  209962
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-B2
                  BLASTX
Method
NCBI GI
                  g1703275
                  232
BLAST score
E value
                  2.0e-19
                  45
Match length
% identity
                  89
                  METHIONINE AMINOPEPTIDASE 2 (METAP 2) (PEPTIDASE M 2)
NCBI Description
                  (INITIATION FACTOR 2 ASSOCIATED 67 KD GLYCOPROTEIN) (P67)
```

Seq. No. 209963

Seq. ID LIB3135-046-Q1-K1-B5

Method BLASTX
NCBI GI g2130073
BLAST score 498
E value 2.0e-50



Match length % identity

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase

C-1 [Oryza sativa] >gi\_790970\_dbj\_BAA08830\_ (D50301)

aldolase C-1 [Oryza sativa]

209964 Seq. No.

Seq. ID LIB3135-046-Q1-K1-B6

Method BLASTX NCBI GI g2498706 BLAST score 175 1.0e-12 E value 59 Match length

47 % identity

ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi 1113103 NCBI Description

(U40269) atOrc2p [Arabidopsis thaliana] >gi 3236239

(AC004684) origin recognition complex protein [Arabidopsis

thaliana]

Seq. No. 209965

LIB3135-046-Q1-K1-B7 Seq. ID

BLASTX Method g2213867 NCBI GI BLAST score 216 1.0e-18 E value Match length 85 % identity 64

(AF003124) fructose-biphosphate aldolase [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 209966

Seq. ID LIB3135-046-Q1-K1-B9

Method BLASTX NCBI GI q4049341 BLAST score 271 E value 6.0e-24 108 Match length % identity 49

(AL034567) putative protein [Arabidopsis thaliana] NCBI Description

209967 Seq. No.

Seq. ID LIB3135-046-Q1-K1-C1

Method BLASTX NCBI GI q3650033 BLAST score 390 E value 8.0e-38 127 Match length % identity

(AC005396) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 209968

Seq. ID LIB3135-046-Q1-K1-C11

Method BLASTX NCBI GI q2498565 BLAST score 188 E value 4.0e-14

```
Match length
                  40
% identity
                  C-MYC BINDING PROTEIN MM-1 >gi 1731809 dbj BAA14006
NCBI Description
                  (D89667) c-myc binding protein [Homo sapiens]
                  >gi 4505743 ref_NP_002615.1_pPFDN5_ prefoldin
                  209969
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-C2
                  BLASTX
Method
                  q3650033
NCBI GI
                  372
BLAST score
                  8.0e-36
E value
                  105
Match length
                  75
% identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  209970
                  LIB3135-046-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1765899
BLAST score
                  307
E value
                  2.0e-28
Match length
                  95
% identity
                  62
                  (Y07917) Spot 3 protein [Arabidopsis thaliana] >gi_1839244
NCBI Description
                   (U86700) EGF receptor like protein [Arabidopsis thaliana]
Seq. No.
                  209971
                  LIB3135-046-Q1-K1-C4
Seq. ID
Method
                  BLASTX
                  g4056455
NCBI GI
BLAST score
                  308
E value
                  3.0e-28
                  83
Match length
% identity
                  65
                  (AC005990) Similar to gb L19255 carbonic anhydrase from
NCBI Description
                  Nicotiana tabacum and a member of the prokaryotic-type
                  carbonic anhydrase family PF_00484. EST gb_Z235745 comes
                  from this gene. [Arabidopsis thaliana]
                  209972
Seq. No.
                  LIB3135-046-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g1710078
NCBI GI
BLAST score
                  524
                  1.0e-53
E value
                  129
Match length
                  75
% identity
                  RAB24 PROTEIN >gi 971280 dbj BAA09947 (D63917) RAB24
NCBI Description
                  protein [Oryza sativa]
                   209973
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-C6
```

BLASTX

445 2.0e-44

g1710078

Method NCBI GI

E value

BLAST score

Match length

% identity

49 94

```
Match length
                     75
  % identity
                    RAB24 PROTEIN >qi 971280 dbj BAA09947 (D63917) RAB24
  NCBI Description
                    protein [Oryza sativa]
                     209974
  Seq. No.
                    LIB3135-046-Q1-K1-C7
  Seq. ID
                    BLASTX
  Method
                    q1710076
  NCBI GI
                     199
  BLAST score
                     3.0e-22
  E value
                     104
  Match length
                     59
  % identity
                    REHYDRIN HOMOLOG (DORMANCY-ASSOCIATED PROTEIN PBS128)
  NCBI Description
                     >gi_82340_pir__S22499 hypothetical protein - chess
                     bromegrass (fragment) >gi_17932_emb_CAA44884_ (X63202) ORF
                     [Bromus secalinus]
                     209975
  Seq. No.
                     LIB3135-046-Q1-K1-C8
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g3860315
                     183
  BLAST score
                     1.0e-13
  E value
                     48
  Match length
                     75
  % identity
                    (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
NCBI Description
                     209976
  Seq. No.
                     LIB3135-046-Q1-K1-D10
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q1769887
                     110
  BLAST score
                     1.0e-08
  E value
                     86
  Match length
                     47
   % identity
  NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]
                     209977
   Seq. No.
                     LIB3135-046-Q1-K1-D11
   Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g1169014
  BLAST score
                     163
                     4.0e-24
  E value
  Match length
                     123
                     56
   % identity
                     COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
   NCBI Description
                     >gi 472343 (L31852) bcop [Drosophila melanogaster]
                     209978
   Seq. No.
   Seq. ID
                     LIB3135-046-Q1-K1-D7
                     BLASTX
  Method
                     q3094012
   NCBI GI
                     276
   BLAST score
   E value
                     2.0e-24
```

```
AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
NCBI Description
                  209979
Seq. No.
                  LIB3135-046-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g4567210
NCBI GI
                  309
BLAST score
                  3.0e-28
E value
                  108
Match length
                  52
% identity
                  (ACO07168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  209980
Seq. No.
                  LIB3135-046-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                   1.0e-10
E value
Match length
                   36
                   100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                   209981
                   LIB3135-046-Q1-K1-E3
Seq. ID
                   BLASTN
Method
                   q3046851
NCBI GI
                   35
BLAST score
E value
                   4.0e-10
                   120
Match length
                   36
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MIJ24, complete sequence [Arabidopsis thaliana]
                   209982
Seq. No.
                   LIB3135-046-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g2832683
NCBI GI
                   328
BLAST score
                   1.0e-30
E value
                   74
Match length
                   74
% identity
                   (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                   209983
Seq. No.
                   LIB3135-046-Q1-K1-E6
Seq. ID
                   BLASTX
Method
                   g132864
NCBI GI
BLAST score
                   248
                   2.0e-28
E value
                   91
Match length
                   75
% identity
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi 81823 pir S00718
NCBI Description
                   ribosomal protein L2 - soybean chloroplast (fragment)
                   >gi_669076_emb_CAA29735_ (X06429) exon 2 [Glycine max]
                   209984
Seq. No.
                   LIB3135-046-Q1-K1-E8
Seq. ID
```

NCBI Description

```
Method
                  q2832683
NCBI GI
BLAST score
                  200
                  9.0e-16
E value
Match length
                  58
                  59
% identity
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                  209985
Seq. No.
                  LIB3135-046-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464444
BLAST score
                  620
                  8.0e-65
E value
Match length
                  129
                  91
% identity
                  PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX 30 KD SUBUNIT) >qi 541889 pir S39900 proteasome -
                  Arabidopsis thaliana >gi 166830 (M98495) proteasome
                   [Arabidopsis thaliana]
                  209986
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q4006957
BLAST score
                  270
                  9.0e-24
E value
                  92
Match length
                  57
% identity
                  (AJ006910) pollen allergen Betv1, isoform at45 [Betula
NCBI Description
                  pendula]
                  209987
Seq. No.
                  LIB3135-046-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1708777
BLAST score
                  216
                  2.0e-17
E value
                  84
Match length
                   56
% identity
NCBI Description
                  (Z83202) potassium channel [Arabidopsis thaliana]
                  >gi_3063705_emb_CAA18596.1_ (AL022537) potassium channel
                  protein [Arabidopsis thaliana] >gi 4090537 (U73325) K+
                   inward rectifying channel protein [Arabidopsis thaliana]
                  >gi 4098949 (U81239) K+ inward rectifying channel
                   [Arabidopsis thaliana]
Seq. No.
                  209988
Seq. ID
                  LIB3135-046-Q1-K1-F4
                  BLASTX
Method
NCBI GI
                  g1871182
BLAST score
                   217
                   1.0e-34
E value
Match length
                  120
% identity
                   66
                   (U90439) phospholipase D isolog [Arabidopsis thaliana]
```

```
209989
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-F5
                  BLASTX
Method
NCBI GI
                  g2431769
BLAST score
                  265
                  3.0e-23
E value
Match length
                  111
                  54
% identity
                  (U62752) acidic ribosomal protein Pla [Zea mays]
NCBI Description
                  209990
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-F9
                  BLASTN
Method
NCBI GI
                  q167366
BLAST score
                  35
                  3.0e-10
E value
                  234
Match length
                  82
% identity
NCBI Description Gossypium hirsutum peroxidase mRNA, complete cds
                  209991
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2832672
BLAST score
                  457
                  9.0e-46
E value
Match length
                  107
% identity
                  83
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                  209992
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g99684
BLAST score
                  373
                  7.0e-36
E value
Match length
                  95
                  39
% identity
NCBI Description DNA-binding protein - Arabidopsis thaliana
                  209993
Seq. No.
Seq. ID
                  LIB3135-046-Q1-K1-G5
                  BLASTX
Method
NCBI GI
                  g1723515
BLAST score
                  171
                  3.0e-12
E value
Match length
                  94
                  35
% identity
                  HYPOTHETICAL PROTEIN C22E12.01 IN CHROMOSOME I
NCBI Description
                  >gi 1220276 emb CAA93888 (Z70043) unknown
```

[Schizosaccharomyces pombe]

Seq. No. 209994

Seq. ID LIB3135-046-Q1-K1-G9

Method BLASTX NCBI GI g3201613 BLAST score 298



E value 2.0e-27
Match length 81
% identity 72

NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 209995

Seq. ID LIB3135-046-Q1-K1-H10

Method BLASTX
NCBI GI g1709498
BLAST score 526
E value 1.0e-57
Match length 143
% identity 74

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis
thaliana >gi\_887390 emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 209996

Seq. ID LIB3135-046-Q1-K1-H2

Method BLASTX
NCBI GI g1076675
BLAST score 521
E value 2.0e-53
Match length 113
% identity 90

NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur

protein - potato

Seq. No. 209997

Seq. ID LIB3135-046-Q1-K1-H3

Method BLASTX
NCBI GI g4263715
BLAST score 204
E value 4.0e-16
Match length 124
% identity 35

NCBI Description (AC006223) putative alanine acetyl transferase [Arabidopsis

thaliana]

Seq. No. 209998

Seq. ID LIB3135-046-Q1-K1-H5

Method BLASTX
NCBI GI g133940
BLAST score 500
E value 1.0e-50
Match length 134
% identity 78

NCBI Description 40S RIBOSOMAL PROTEIN S3A (S1A) >gi 70851 pir R3XL3A

ribosomal protein S3a - African clawed frog

>gi\_65091\_emb\_CAA40592\_ (X57322) ribosomal protein S1a

[Xenopus laevis]

Seq. No. 209999

Seq. ID LIB3135-047-Q1-K1-A1

Method BLASTX NCBI GI g461530



BLAST score 180
E value 3.0e-13
Match length 64
% identity 62
NCBI Description N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
>gi\_159365 (L11348) ARD1 protein homologue [Leishmania donovani]

Seq. No. 210000
Seq. ID LIB3135-047-Q1-K1-A12

Method BLASTX
NCBI GI g1762933
BLAST score 492
E value 9.0e-50
Match length 141
% identity 72

NCBI Description (U66263) tumor-related protein [Nicotiana tabacum]

Seq. No. 210001

Seq. ID LIB3135-047-Q1-K1-A3

Method BLASTX
NCBI GI g421836
BLAST score 601
E value 1.0e-62
Match length 135
% identity 86

NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi\_553040

(M96855) GF14 [Arabidopsis thaliana]

Seq. No. 210002

Seq. ID LIB3135-047-Q1-K1-A4

Method BLASTX
NCBI GI g126075
BLAST score 193
E value 1.0e-14
Match length 97
% identity 45

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-113 (LEA D-113)

>gi\_81550\_pir\_\_S04044 embryonic abundant protein D-113 upland cotton >gi\_18492\_emb\_CAA31590\_ (X13202) D-113 Lea
protein [Gossypium hirsutum] >gi\_226553 prf\_1601521C Lea

D-113 gene [Saguinus oedipus]

Seq. No. 210003

Seq. ID LIB3135-047-Q1-K1-A7

Method BLASTX
NCBI GI g3687251
BLAST score 391
E value 5.0e-38
Match length 97
% identity 75

NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 210004

Seq. ID LIB3135-047-Q1-K1-B1

Method BLASTN NCBI GI q167386



BLAST score 302 E value 1.0e-169 Match length 346 % identity 97 NCBI Description G.hirsut

NCBI Description G.hirsutum (cotton) storage protein (late embryogenesis

abundant) mRNA, partial cds, clone D113

Seq. No. 210005

Seq. ID LIB3135-047-Q1-K1-B10

Method BLASTX
NCBI GI 94490302
BLAST score 494
E value 2.0e-51
Match length 132
% identity 84

NCBI Description (AL035678) Tic22-like protein [Arabidopsis thaliana]

Seq. No. 210006

Seq. ID LIB3135-047-Q1-K1-B4

Method BLASTX
NCBI GI g3334157
BLAST score 487
E value 4.0e-49
Match length 100
% identity 93

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >qi 1220142 emb CAA59468 (X85185) cyclophilin

[Catharanthus roseus]

Seq. No. 210007

Seq. ID LIB3135-047-Q1-K1-B7

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 210008

Seq. ID LIB3135-047-Q1-K1-B8

Method BLASTX
NCBI GI g3738325
BLAST score 669
E value 2.0e-70
Match length 139
% identity 89

NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis

thaliana]

Seq. No. 210009

Seq. ID LIB3135-047-Q1-K1-C1

Method BLASTX
NCBI GI g167387
BLAST score 142
E value 4.0e-09

```
Match length
% identity
                  (M19406) storage protein [Gossypium hirsutum]
NCBI Description
                  210010
Seq. No.
Seq. ID
                  LIB3135-047-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2342727
BLAST score
                  420
                  2.0e-41
E value
Match length
                  113
% identity
                  64
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  LIB3135-047-Q1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3510540
BLAST score
                  416
                  5.0e-41
E value
                  93
Match length
                  77
% identity
NCBI Description
                  (AF038815) expansin [Prunus armeniaca]
                  210012
Seq. No.
                  LIB3135-047-Q1-K1-C12
Seq. ID
                  BLASTX
Method
                   q2388710
NCBI GI
BLAST score
                   285
E value
                   1.0e-25
Match length
                   70
                   69
% identity
                   (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                  hypochondriacus]
                   210013
Seq. No.
                   LIB3135-047-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832300
                   400
BLAST score
                   5.0e-39
E value
                   117
Match length
% identity
                   68
                   (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
NCBI Description
                   roseus]
Seq. No.
                   210014
                   LIB3135-047-Q1-K1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q464849
BLAST score
                   639
                   5.0e-67
E value
Match length
                   132
                   92
% identity
                   TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 20413 emb CAA47635_ (X67162)
```

29027

alpha-tubulin [Prunus dulcis]



```
210015
Seq. No.
                   LIB3135-047-Q1-K1-C5
Seq. ID
Method
                   BLASTX
                   g1354849
NCBI GI
                   460
BLAST score
                   5.0e-46
E value
                   141
Match length
                   60
% identity
                   (U57350) epoxide hydrolase [Nicotiana tabacum]
NCBI Description
                   210016
Seq. No.
Seq. ID
                   LIB3135-047-Q1-K1-D1
                   BLASTX
Method
NCBI GI
                   g124224
BLAST score
                   631
                   5.0e-66
E value
Match length
                   124
                   95
% identity
                   INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_100345_pir__S21060 translation initiation factor eIF-5A
                   - common tobacco >gi_19887_emb_CAA45105_ (X63543)
                   eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
                   210017
Seq. No.
Seq. ID
                   LIB3135-047-Q1-K1-D12
Method
                   BLASTX
                   g2764941
NCBI GI
                   248
BLAST score
                   2.0e-21
E value
Match length
                   72
% identity
                   64
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                   thaliana]
Seq. No.
                   210018
Seq. ID
                   LIB3135-047-Q1-K1-D3
                   BLASTX
Method
NCBI GI
                   g3183247
BLAST score
                   365
                   7.0e-35
E value
                   112
Match length
                   62
% identity
                   PUTATIVE GTP-BINDING PROTEIN W08E3.3
NCBI Description
                   >gi_3880615_emb_CAB07131_ (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD
                   protein, putative GTP-binding protein (SW:P38219); cDNA EST
                   EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777
                   comes from this gene; cDNA EST EMB
Seq. No.
                   210019
                   LIB3135-047-Q1-K1-D4
```

Seq. ID

Method BLASTX NCBI GI g1172704 BLAST score 460 5.0e-46 E value

10 Mary 100



Match length 61 % identity

PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN) NCBI Description

>gi 633940 (L39082) transport protein [Arabidopsis thaliana] >gi 4406786 gb AAD20096\_ (AC006532) histidine

transport protein PTR2-B [Arabidopsis thaliana]

210020 Seq. No.

Seq. ID LIB3135-047-Q1-K1-D5

Method BLASTX g3033380 NCBI GI BLAST score 503 3.0e-51 E value Match length 116 % identity 83

(AC004238) putative coatomer epsilon subunit [Arabidopsis NCBI Description

thaliana]

210021 Seq. No.

LIB3135-047-Q1-K1-D9 Seq. ID

Method BLASTX NCBI GI g625547 BLAST score 431 8.0e-43 E value 100 Match length % identity 82

chlorophyll a/b-binding protein type I - common tobacco NCBI Description

>qi 493723 emb CAA45523 (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

210022 Seq. No.

Seq. ID LIB3135-047-Q1-K1-E10

Method BLASTX g940288 NCBI GI 251 BLAST score 9.0e-22 E value 84 Match length 30 % identity

(L43510) protein localized in the nucleoli of pea nuclei; NCBI Description

ORF; putative [Pisum sativum]

Seq. No. 210023

Seq. ID LIB3135-047-Q1-K1-E4

Method BLASTX NCBI GI q974782 BLAST score 733 E value 5.0e-78 143 Match length 96 % identity

(Z49150) cobalamine-independent methionine synthase NCBI Description

[Solenostemon scutellarioides]

Seq. No. 210024

Seq. ID LIB3135-047-Q1-K1-E5

Method BLASTX NCBI GI q1350977

```
BLAST score
                  6.0e-13
E value
Match length
                  58
                  64
% identity
NCBI Description PROBABLE 40S RIBOSOMAL PROTEIN S30
                  210025
Seq. No.
Seq. ID
                  LIB3135-047-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q2760320
                  305
BLAST score
                  8.0e-28
E value
                  145
Match length
                  42
% identity
                  (AC002130) F1N21.4 [Arabidopsis thaliana]
NCBI Description
                  210026
Seq. No.
Seq. ID
                  LIB3135-047-Q1-K1-E8
Method
                  BLASTX
                  g4220512
NCBI GI
                  256
BLAST score
E value
                  3.0e-22
Match length
                  87
% identity
                  63
                  (AL035356) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
                  210027
Seq. No.
Seq. ID
                  LIB3135-047-Q1-K1-E9
Method
                  BLASTX
                  g1762933
NCBI GI
BLAST score
                  232
                  1.0e-19
E value
                  59
Match length
                  78
% identity
NCBI Description (U66263) tumor-related protein [Nicotiana tabacum]
Seq. No.
                  210028
Seq. ID
                  LIB3135-047-Q1-K1-F11
                  BLASTX
Method
NCBI GI
                  g3335354
BLAST score
                  152
E value
                  2.0e-11
Match length
                  81
                  57
% identity
                  (AC004512) This gene is continued from gene F5I14.1 from
NCBI Description
                  BAC sequence gb AC001229 from A. thaliana. EST gb AA585814
                  comes from this gene. [Arabidopsis thaliana]
```

Seq. No. 210029

Seq. ID LIB3135-047-Q1-K1-F3

Method BLASTX
NCBI GI g3786008
BLAST score 185
E value 9.0e-14
Match length 67
% identity 57

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]



210030 Seq. No. Seq. ID LIB3135-047-Q1-K1-F8 Method BLASTX NCBI GI g3319342 BLAST score 281 4.0e-25 E value 116 Match length 53 % identity (AF077407) similar to mitochondrial carrier proteins (Pfam: NCBI Description mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana] 210031 Seq. No. Seq. ID LIB3135-047-Q1-K1-G1 Method BLASTX NCBI GI g136707 BLAST score 424 9.0e-42 E value 124 Match length 66 % identity CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR NCBI Description (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 280397\_pir\_\_S26199 plastoquinol--plastocyanin reductase (EC 1.10.99.1) iron-sulfur protein precursor - garden pea >gi 20832 emb CAA45151 (X63605) chloroplast Rieske FeS protein [Pisum sativum] 210032 Seq. No. Seq. ID LIB3135-047-Q1-K1-H12 BLASTX Method NCBI GI g3043428 BLAST score 418 3.0e-41E value 100 Match length 81 % identity (AJ005346) 40S ribosomal protein S5 [Cicer arietinum] NCBI Description 210033 Seq. No. Seq. ID LIB3135-047-Q1-K1-H2 BLASTX Method NCBI GI g2827559 BLAST score 270 9.0e-24 E value 127 Match length % identity 42 (AL021635) predicted protein [Arabidopsis thaliana] NCBI Description >gi 3292808 emb CAA19798 (AL031018) putative protein [Arabidopsis thaliana] 210034 Seq. No.

Seq. ID LIB3135-047-Q1-K1-H5

Method BLASTX
NCBI GI g2244847
BLAST score 164
E value 2.0e-11
Match length 115

```
% identity
                  (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
                  210035
Seq. No.
Seq. ID
                  LIB3135-047-Q1-K1-H7
                  BLASTX
Method
NCBI GI
                   g123541
                   206
BLAST score
E value
                   2.0e-16
                   77
Match length
                   49
% identity
                  17.4 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.4)
NCBI Description
                   >gi_81639_pir__JQ0351 heat shock protein 17 - Arabidopsis
                   thaliana >gi_16340_emb_CAA35182_ (X17293) heat shock
                   protein (AA 1 - 156) [Arabidopsis thaliana]
                   210036
Seq. No.
Seq. ID
                   LIB3135-047-Q1-K1-H9
                   BLASTX
Method
NCBI GI
                   g1279654
BLAST score
                   536
                   6.0e-55
E value
                   149
Match length
                   71
% identity
                   (X97351) peroxidase [Populus balsamifera subsp.
NCBI Description
                   trichocarpa]
                   210037
Seq. No.
Seq. ID
                   LIB3135-048-Q1-K1-A10
                   BLASTX
Method
NCBI GI
                   g3868853
BLAST score
                   356
                   8.0e-34
E value
                   98
Match length
                   67
% identity
                  (AB013853) GPI-anchored protein [Vigna radiata]
NCBI Description
                   210038
Seq. No.
                   LIB3135-048-Q1-K1-A11
Seq. ID
Method
                   BLASTX
                   q2160166
NCBI GI
BLAST score
                   381
                   8.0e-37
E value
                   120
Match length
% identity
                   64
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   210039
Seq. No.
Seq. ID
                   LIB3135-048-Q1-K1-A2
                   BLASTX
Method
NCBI GI
                   q2160182
BLAST score
                   199
                   2.0e-15
E value
Match length
                   78
% identity
                   49
                  (AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203
NCBI Description
```





## come from this gene. [Arabidopsis thaliana]

```
210040
Seq. No.
                  LIB3135-048-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g2316016
NCBI GI
                  735
BLAST score
                  3.0e-78
E value
Match length
                  162
                  44
% identity
                  (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
                  210041
Seq. No.
                  LIB3135-048-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  g1524121
NCBI GI
BLAST score
                  154
                  4.0e-10
E value
                  136
Match length
                   40
% identity
                   (X96539) malate dehydrogenase [Mesembryanthemum
NCBI Description
                  crystallinum]
                   210042
Seq. No.
                  LIB3135-048-Q1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1524121
                   689
BLAST score
                   9.0e-73
E value
                   161
Match length
                   79
% identity
                   (X96539) malate dehydrogenase [Mesembryanthemum
NCBI Description
                   crystallinum]
                   210043
Seq. No.
Seq. ID
                   LIB3135-048-Q1-K1-A8
                   BLASTX
Method
                   q722377
NCBI GI
                   427
BLAST score
                   5.0e-42
E value
                   109
Match length
                   69
% identity
                   (U23139) highly similar to beta-ureidopropionase
NCBI Description
                   (SP:BUP_RAT) [Caenorhabditis elegans]
                   210044
Seq. No.
Seq. ID
                   LIB3135-048-Q1-K1-B1
Method
                   BLASTX
                   g3047068
NCBI GI
                   141
BLAST score
                   1.0e-08
E value
                   116
Match length
% identity
                   (AF058825) similar to maize transposon MuDR (GB:M76978)
NCBI Description
```

Seq. No. 210045

[Arabidopsis thaliana]

```
LIB3135-048-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g1709633
NCBI GI
                  236
BLAST score
                  7.0e-20
E value
                  78
Match length
                  60
% identity
                  XAA-PRO DIPEPTIDASE (X-PRO DIPEPTIDASE) (PROLINE
NCBI Description
                  DIPEPTIDASE) (PROLIDASE) (IMIDODIPEPTIDASE) (PEPTIDASE 4)
                  >gi 1236706 (U51014) prolidase [Mus musculus]
                  210046
Seq. No.
                  LIB3135-048-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g1172811
NCBI GI
                   684
BLAST score
                   3.0e-72
E value
                   131
Match length
                   96
% identity
                   60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                   >qi 1076751 pir S49575 ribosomal protein L10.e, cytosolic
                   - rice >gi 575355 emb CAA57339 (X81691) putative tumor
                   suppresser [Oryza sativa]
                   210047
Seq. No.
                   LIB3135-048-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1432058
                   504
BLAST score
                   4.0e-51
E value
                   156
Match length
                   67
% identity
                  (U58540) WRKY2 [Petroselinum crispum]
NCBI Description
                   210048
Seq. No.
Seq. ID
                   LIB3135-048-Q1-K1-B4
                   BLASTX
Method
                   q2244797
NCBI GI
                   276
BLAST score
                   2.0e-24
E value
                   151
Match length
                   40
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   210049
Seq. No.
Seq. ID
                   LIB3135-048-Q1-K1-B8
                   BLASTX
Method
NCBI GI
                   g1362152
BLAST score
                   420
                   3.0e-41
E value
                   111
Match length
                   66
 % identity
                  ribosomal protein S6 kinase homolog (clone Aspk11) - oat
NCBI Description
                   >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal
                   protein S6 kinase [Avena sativa]
                   210050
 Seq. No.
```

29034

an market street



```
LIB3135-048-Q1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g100535
BLAST score
                  289
                  4.0e-26
E value
                  64
Match length
% identity
                  hypothetical protein - swollen duckweed
NCBI Description
                  >gi 1929057 emb_CAA32236_ (X14075) longest ORF (1) [Lemna
                  gibba]
                  210051
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-C11
                  BLASTX
Method
NCBI GI
                  g2464932
                  173
BLAST score
                  2.0e-12
E value
                  123
Match length
                  40
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210052
                  LIB3135-048-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2497752
                  295
BLAST score
                  1.0e-26
E value
                  96
Match length
                  59
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1321911 emb CAA65475 (X96714) lipid transfer protein
                  [Prunus dulcis]
                  210053
Seq. No.
                  LIB3135-048-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                  g2980781
NCBI GI
BLAST score
                  269
                  2.0e-23
E value
                  86
Match length
                  57
% identity
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                  210054
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                  q409574
BLAST score
                   43
                  7.0e-15
E value
                  55
Match length
                  95
% identity
                  Atriplex nummularia glyceraldehyde-3-phosphate
NCBI Description
                  dehydrogenase (GAPDH) mRNA, complete cds.
                  >gi 414606 emb X75597 ANDAP3DH A.nummularia mRNA for
```

Seq. No. 210055

glyceraldehyde-3-phosphate dehydrogenase



```
LIB3135-048-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1321661
                  319
BLAST score
                  1.0e-29
E value
Match length
                  119
% identity
                  52
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
Seq. No.
                  210056
Seq. ID
                  LIB3135-048-Q1-K1-C8
Method
                  BLASTX
                  g2811025
NCBI GI
                  621
BLAST score
                  8.0e-65
E value
                  162
Match length
                  69
% identity
                  ASPARTIC PROTEINASE PRECURSOR >gi 1944181_dbj_BAA19607_
NCBI Description
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                  210057
Seq. ID
                  LIB3135-048-Q1-K1-D1
                  BLASTX
Method
NCBI GI
                  g2983642
                  251
BLAST score
                  2.0e-21
E value
Match length
                  134
                   42
% identity
                  (AE000728) diaminopimelate decarboxylase [Aquifex aeolicus]
NCBI Description
                  210058
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-D10
                  BLASTX
Method
NCBI GI
                  g2702284
BLAST score
                   206
                  7.0e-17
E value
Match length
                   64
                   61
% identity
                   (AC003033) Argonaute (AG01)-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   210059
Seq. No.
                  LIB3135-048-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  q3377797
NCBI GI
BLAST score
                   426
E value
                   4.0e-42
                   95
Match length
% identity
                   86
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
```

A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

210060 Seq. No.

Seq. ID LIB3135-048-Q1-K1-D2



```
BLASTX
Method
                   g1350956
NCBI GI
BLAST score
                   550
                   2.0e-56
E value
                   117
Match length
                   93
% identity
```

40S RIBOSOMAL PROTEIN S20 (S22) NCBI Description

210061 Seq. No.

Seq. ID LIB3135-048-Q1-K1-D3

BLASTX Method NCBI GI q2673868 BLAST score 281 4.0e-25 E value 56 Match length 95 % identity

(Y14856) fimbriata-associated protein [Antirrhinum majus] NCBI Description

210062

Seq. No. Seq. ID LIB3135-048-Q1-K1-D4

Method BLASTX NCBI GI g2129513 BLAST score 280 E value 4.0e-31 Match length 110 % identity 67

peroxidase (EC 1.11.1.7) A3a precursor - Japanese aspen x NCBI Description

large-toothed aspen >gi 1255661 dbj BAA07240 (D38050)

peroidase precursor [Populus kitakamiensis]

210063 Seq. No.

Seq. ID LIB3135-048-Q1-K1-D5

Method BLASTX NCBI GI g3719211 BLAST score 139 1.0e-08 E value 46 Match length 63 % identity

(U97021) UIP2 [Arabidopsis thaliana] NCBI Description

210064 Seq. No.

Seq. ID LIB3135-048-Q1-K1-D7

Method BLASTX g3377797 NCBI GI BLAST score 410 4.0e-40 E value Match length 130 66 % identity

(AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA

H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

210065 Seq. No.

Seq. ID LIB3135-048-Q1-K1-E2

BLASTX Method

NCBI GI

E value

BLAST score

g3043432

210 8.0e-17

```
g2673868
NCBI GI
                  237
BLAST score
                  6.0e-20
E value
                  56
Match length
                  80
% identity
NCBI Description (Y14856) fimbriata-associated protein [Antirrhinum majus]
                  210066
Seq. No.
                  LIB3135-048-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  q2459420
NCBI GI
BLAST score
                  612
                  7.0e-64
E value
Match length
                  120
                  97
% identity
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  210067
                  LIB3135-048-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3785987
BLAST score
                  168
                  1.0e-17 ⊁
E value
Match length
                  120
% identity
                  45
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  210068
                  LIB3135-048-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                  g132944
NCBI GI
BLAST score
                  649
                  4.0e-68
E value
Match length
                  129
                  91
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi 806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
                  210069
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-E9
                  BLASTX
Method
NCBI GI
                  g3046693
BLAST score
                   475
                  7.0e-48
E value
Match length
                  103
                  79
% identity
                  (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  210070
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-F10
                  BLASTX
Method
```

```
Match length
                   100
% identity
                   (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]
NCBI Description
Seq. No.
                   210071
Seq. ID
                   LIB3135-048-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   q1170898
BLAST score
                   364
                   7.0e-35
E value
Match length
                   99
% identity
                   80
                   MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial
- cider tree >gi_473206_emb_CAA55383_ (X78800)
                   mitochondrial malate dehydrogenase [Eucalyptus gunnii]
Seq. No.
                   210072
                   LIB3135-048-Q1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2961300
BLAST score
                   431
E value
                   2.0e-42
Match length
                   139
% identity
                   (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
                   210073
Seq. No.
                   LIB3135-048-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                   g285741
NCBI GI
                   504
BLAST score
E value
                   4.0e-51
                   141
Match length
% identity
                   70
                   (D14550) EDGP precursor [Daucus carota]
NCBI Description
                   210074
Seq. No.
                   LIB3135-048-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g1170898
NCBI GI
BLAST score
                   219
                   5.0e-18
E value
                   74
Match length
                   65
% identity
NCBI Description
                   MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                   >gi 629659 pir S44167 malate dehydrogenase, mitochondrial
                   - cider tree >qi 473206 emb CAA55383 (X78800)
                   mitochondrial malate dehydrogenáse [Eucalyptus gunnii]
                   210075
Seq. No.
Seq. ID
                   LIB3135-048-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g465820
BLAST score
                   462
```

29039

3.0e-46

139

E value Match length



```
% identity
                  HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
NCBI Description
                  >gi 280536_pir__S28301 hypothetical protein C40H1.6 -
                  Caenorhabditis elegans >gi 3874819_emb_CAA79557_ (Z19154)
                  C40H1.6 [Caenorhabditis elegans]
                  210076
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-G3
                  BLASTX
Method
NCBI GI
                  g3021270
BLAST score
                  592
                  2.0e-61
E value
                  162
Match length
% identity
                  69
                   (AL022347) serine/threonine kinase -like protein
NCBI Description
                   [Arabidopsis thaliana]
                  210077
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-G4
Method
                  BLASTX
                  g2465925
NCBI GI
BLAST score
                  193
                  7.0e-15
E value
                  76
Match length
% identity
                  45
                   (AF024649) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                  210078
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-G5
                  BLASTX
Method
NCBI GI
                  g3582340
BLAST score
                  375
                  6.0e-36
E value
                  96
Match length
                  75
% identity
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                  210079
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-G6
                  BLASTX
Method
NCBI GI
                  g4206196
BLAST score
                  474
E value
                  1.0e-47
Match length
                  129
                  72
% identity
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210080
```

LIB3135-048-Q1-K1-G7 Seq. ID

Method BLASTX NCBI GI g82263 BLAST score 355 1.0e-33 E value Match length 99 % identity 73

NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome

NCBI Description





## c1 precursor (clone pC(1)3II) - potato

```
210081
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-G8
                  BLASTX
Method
NCBI GI
                  g465820
BLAST score
                  580
E value
                  5.0e-60
Match length
                  152
                  66
% identity
                  HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
NCBI Description
                  >gi_280536_pir__S28301 hypothetical protein C40H1.6 -
                  Caenorhabditis elegans >gi 3874819 emb CAA79557 (Z19154)
                  C40H1.6 [Caenorhabditis elegans]
Seq. No.
                  210082
Seq. ID
                  LIB3135-048-Q1-K1-H11
Method
                  BLASTX
                  g2673912
NCBI GI
                  432
BLAST score
                  7.0e-43
E value
Match length
                  120
% identity
                  67
                  (AC002561) unknown protein [Arabidopsis thaliana]
NCBI Description
                  210083
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-H7
Method
                  BLASTN
NCBI GI
                  g1204101
BLAST score
                  64
                  2.0e-27
E value
Match length
                  290
% identity
                  83
NCBI Description H.annuus mitochodrial trnW gene
                  210084
Seq. No.
Seq. ID
                  LIB3135-048-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g553111
BLAST score
                  172
                  4.0e-12
E value
Match length
                  128
                  22
% identity
NCBI Description
                  (J03625) hydroproline-rich protein [Glycine max]
                  210085
Seq. No.
                  LIB3135-049-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172571
BLAST score
                  553
                   6.0e-57
E value
Match length
                  122
% identity
```

29041

>gi 1076277 pir S52637 phosphoenolpyruvate carboxykinase

(ATP) (EC 4.1.1.49) - cucumber >gi\_567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus]

PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)



```
210086
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g4138647
BLAST score
                  472
E value
                  2.0e-47
                  117
Match length
% identity
                  74
NCBI Description
                  (AJ011939) peroxidase [Trifolium repens]
                  210087
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1402902
BLAST score
                  123
                  7.0e-14
E value
Match length
                  88
                  46
% identity
                  (X98323) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1419386_emb_CAA67428_ (X98928) peroxidase ATP10a
                   [Arabidopsis thaliana]
                  210088
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  q870726
                  318
BLAST score
                  5.0e-30
E value
                  71
Match length
                  93
% identity
NCBI Description
                  (L38260) biotin carboxylase subunit [Nicotiana tabacum]
                  >gi 1582354 prf 2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                  carboxylase [Nicotiana tabacum]
Seq. No.
                  210089
                  LIB3135-049-Q1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g871468
                  101
BLAST score
E value
                  2.0e-49
                  291
Match length
% identity
                  92
                  H.annuus mitochondrion genes trnH and trnE
NCBI Description
Seq. No.
                  210090
Seq. ID
                  LIB3135-049-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1762945
BLAST score
                  242
                  2.0e-20
E value
Match length
                  79
% identity
                  61
NCBI Description
                   (U66269) ORF; able to induce HR-like lesions [Nicotiana
```

Seq. No. 210091

tabacum]

```
LIB3135-049-Q1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2497752
BLAST score
                  261
                  8.0e-23
E value
                  105
Match length
                  52
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1321911_emb_CAA65475_ (X96714) lipid transfer protein
                  [Prunus dulcis]
                  210092
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-B2
                  BLASTX
Method
                  g1905876
NCBI GI
                  735
BLAST score
                  3.0e-78
E value
                  148
Match length
                  97
% identity
                  (U90879) biotin carboxylase subunit [Arabidopsis thaliana]
NCBI Description
                  >qi 1916300 (U91414) heteromeric acetyl-CoA carboxylase
                  biotin carboxylase subunit [Arabidopsis thaliana]
                  >qi 3047099 (AF058826) Arabidopsis thaliana biotin
                  carboxylase subunit (GB:U90879) [Arabidopsis thaliana]
                  210093
Seq. No.
                  LIB3135-049-Q1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g871468
                  44
BLAST score
                  2.0e-15
E value
Match length
                  130
% identity
                   95
NCBI Description H.annuus mitochondrion genes trnH and trnE
                   210094
Seq. No.
                  LIB3135-049-Q1-K1-B7
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g3776559
BLAST score 295
E value 1.0e-26
Match length 130
% identity 56

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 210095

Seq. ID LIB3135-049-Q1-K1-C10

Method BLASTX
NCBI GI g4138647
BLAST score 456
E value 1.0e-45
Match length 113
% identity 73

NCBI Description (AJ011939) peroxidase [Trifolium repens]

Seq. ID

Method

NCBI GI



```
210096
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-C3
                  BLASTX
Method
                  g3386615
NCBI GI
BLAST score
                  161
                  5.0e-11
E value
Match length
                  40
                  72
% identity
                  (AC004665) putative phosphomannomutase [Arabidopsis
NCBI Description
                  thaliana]
                  210097
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-D4
                  BLASTX
Method
NCBI GI
                  g2245125
BLAST score
                  168
                  8.0e-12
E value
                  47
Match length
                  62
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
                  210098
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-D9
                  BLASTX
Method
                  g4454016
NCBI GI
                  346
BLAST score
                  4.0e-33
E value
                  117
Match length
                   68
% identity
                   (AL035396) UMP/CMP kinase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  210099
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-E11
                  BLASTX
Method
NCBI GI
                  q456568
BLAST score
                   282
                   2.0e-25
E value
Match length
                  86
                   67
% identity
                  (L29077) ubiquitin conjugating enzyme [Pisum sativum]
NCBI Description
                   210100
Seq. No.
                  LIB3135-049-Q1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3043432
                  167
BLAST score
E value
                   6.0e-12
                   38
Match length
% identity
NCBI Description
                  (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]
                   210101
Seq. No.
```

29044

LIB3135-049-Q1-K1-E3

BLASTN

g2264309

BLAST score E value 1.0e-25 189 Match length 83 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MJJ3, complete sequence [Arabidopsis thaliana]

210102 Seq. No.

Seq. ID LIB3135-049-Q1-K1-E4

Method BLASTX g3046693 NCBI GI 571 BLAST score 3.0e-59 E value Match length 110 91 % identity

(AL022140) receptor like protein (fragment) [Arabidopsis NCBI Description

thaliana]

210103 Seq. No.

Seq. ID LIB3135-049-Q1-K1-F1

BLASTX Method NCBI GI g543905 445 BLAST score 3.0e-44E value Match length 113 75 % identity

BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162) NCBI Description

brassinosteroid-regulated protein [Glycine max]

210104 Seq. No.

Seq. ID LIB3135-049-Q1-K1-F10

 ${\tt BLASTX}$ Method g3043432 NCBI GI 179 BLAST score 2.0e-13 E value 38 Match length

84 % identity

NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

210105 Seq. No.

LIB3135-049-Q1-K1-F3 Seq. ID

Method BLASTX NCBI GI g4490705 BLAST score 155 7.0e-11 E value 59 Match length % identity 63

(AL035680) ribosomal protein L14-like protein [Arabidopsis NCBI Description

thaliana]

210106 Seq. No.

Seq. ID LIB3135-049-Q1-K1-F4

BLASTX Method NCBI GI q3894172 BLAST score 457 E value 1.0e-45 Match length 148



% identity 55
NCBI Description (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No. 210107
Seq. ID LIB3135-049-Q1-K1-F6

Method BLASTX
NCBI GI g2981475
BLAST score 334
E value 2.0e-31
Match length 122
% identity 56

NCBI Description (AF053084) putative cinnamyl alcohol dehydrogenase [Malus

domestica]

Seq. No. 210108

Seq. ID LIB3135-049-Q1-K1-F8

Method BLASTX
NCBI GI g2370312
BLAST score 399
E value 7.0e-39
Match length 134
% identity 57

NCBI Description (AJ000995) DnaJ-like protein [Medicago sativa] >gi\_3202020

(AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No. 210109

Seq. ID LIB3135-049-Q1-K1-G3

Method BLASTX
NCBI GI g3327068
BLAST score 162
E value 4.0e-11
Match length 116
% identity 34

NCBI Description (AB014527) KIAA0627 protein [Homo sapiens]

Seq. No. 210110

Seq. ID LIB3135-049-Q1-K1-G7

Method BLASTX
NCBI GI g417073
BLAST score 478
E value 4.0e-48
Match length 121
% identity 79

NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)

>gi\_484529\_pir\_\_JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi\_166412 (L01660) NADH-glutamate

synthase [Medicago sativa]

Seq. No. 210111

Seq. ID LIB3135-049-Q1-K1-H1

Method BLASTX
NCBI GI g4454033
BLAST score 153
E value 1.0e-10
Match length 44
% identity 64

NCBI GI

E value

BLAST score

Match length

q2274998

8.0e-35

361

74

```
(AL035394) putative potassium transport protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  210112
Seq. ID
                  LIB3135-049-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2493144
                  356
BLAST score
                  7.0e-34
E value
                  87
Match length
                  54
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
NCBI Description
                  16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir__S60132
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                  (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana]
                  210113
Seq. No.
Seq. ID
                  LIB3135-049-Q1-K1-H7
                  BLASTX
Method
NCBI GI
                  g4138647
BLAST score
                  445
                  2.0e-44
E value
Match length
                  118
                  69
% identity
                  (AJ011939) peroxidase [Trifolium repens]
NCBI Description
                  210114
Seq. No.
                  LIB3135-050-Q1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3264611
BLAST score
                  396
                  2.0e-38
E value
                  94
Match length
                  79
% identity
NCBI Description (AF061511) seven in absentia homolog [Zea mays]
                  210115
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  g2739279
BLAST score
                  272
E value
                  6.0e-24
Match length
                  114
                  45
% identity
                  (AJ223177) short chain alcohol dehydrogenase [Nicotiana
NCBI Description
                  tabacum] >qi 2791348 emb CAA11154 (AJ223178) short chain
                  alcohol dehydrogenase [Nicotiana tabacum]
                  210116
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-A2
                  BLASTX
Method
```

```
% identity
                  (AJ000233) partial sequence, homology to chromosome
NCBI Description
                  scaffold proteins [Hordeum vulgare]
                  210117
Seq. No.
                  LIB3135-050-Q1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3882081
                  296
BLAST score
                  6.0e-27
E value
                  68
Match length
% identity
                  31
                  (AJ012552) polyubiquitin [Vicia faba]
NCBI Description
                  210118
Seq. No.
                  LIB3135-050-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g4165323
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
                   42
Match length
% identity
                  - 81
NCBI Description (AB022442) p-type H+-ATPase [Vicia faba]
                  210119
Seq. No.
                  LIB3135-050-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1402912
                   410
BLAST score
                   3.0e-40
E value
                   112
Match length
                   73
% identity
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]
                   210120
Seq. No.
Seq. ID
                   LIB3135-050-Q1-K1-B3
                   BLASTX
Method
                   q4538947
NCBI GI
BLAST score
                   163
                   3.0e-11
E value
                   44
Match length
                   64
% identity
                   (AL049483) putative mitochondrial carrier protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   210121
Seq. ID
                   LIB3135-050-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   q1076501
BLAST score
                   315
                   5.0e-29
E value
                   88
Match length
                   67
% identity
                   cell wall protein - alfalfa >gi 3818416 (AF028841)
NCBI Description
                   proline-rich cell wall protein [Medicago sativa]
```

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210122

Seq. No.

```
LIB3135-050-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346172
BLAST score
                  310
                  2.0e-28
E value
Match length
                  64
                  89
% identity
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)
NCBI Description
                  (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)
                  >qi 170384 (L08830) glucose-regulated protein 78
                   [Lycopersicon esculentum]
                  210123
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-C11
                  BLASTX
Method
                  q3759184
NCBI GI
                  165
BLAST score
E value
                  1.0e-16
                  108
Match length
                  46
% identity
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  210124
Seq. No.
                  LIB3135-050-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  q3962377
NCBI GI
                   710
BLAST score
                   3.0e-75
E value
                   149
Match length
                   92
% identity
NCBI Description
                  (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
Seq. No.
                   210125
                   LIB3135-050-Q1-K1-C4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2829205
BLAST score
                   88
                   7.0e-42
E value
Match length
                   314
                   25
% identity
NCBI Description
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
                   precursor (PRP) mRNA, complete cds
Seq. No.
                   210126
Seq. ID
                   LIB3135-050-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   g4432832
```

Method BLASTX
NCBI GI g4432832
BLAST score 228
E value 7.0e-19
Match length 145
% identity 47

NCBI Description (AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No. 210127

Seq. ID LIB3135-050-Q1-K1-D11

Method BLASTX NCBI GI g3107905

```
BLAST score
E value
                  6.0e-15
Match length
                  114
                  41
% identity
                  (D85101) leaf protein [Ipomoea nil]
NCBI Description
                  210128
Seq. No.
                  LIB3135-050-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                  g2160191
NCBI GI
BLAST score
                  173
                  2.0e-12
E value
                  37
Match length
                  84
% identity
                   (AC000132) Identical to A. thaliana AtK-1 (gb_X79279).
NCBI Description
                   [Arabidopsis thaliana]
                   210129
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-D4
                  BLASTN
Method
NCBI GI
                   g1220195
BLAST score
                   156
                   2.0e-82
E value
                   195
Match length
                   95
% identity
                  Gossypium hirsutum alcohol dehydrogenase 2a mRNA, complete
NCBI Description
                   cds
                   210130
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-E1
                   BLASTX
Method
NCBI GI
                   g3236242
BLAST score
                   422
                   2.0e-41
E value
                   96
Match length
                   88
% identity
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
                   210131
Seq. No.
Seq. ID
                   LIB3135-050-Q1-K1-E12
Method
                   BLASTN
NCBI GI
                   g2618602
                   38
BLAST score
                   7.0e-12
E value
Match length
                   66
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
```

Seq. No. 210132

Seq. ID LIB3135-050-Q1-K1-E9

Method BLASTX
NCBI GI g82263
BLAST score 546
E value 4.0e-62
Match length 144

Match length

% identity

73 42

```
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  cl precursor (clone pC(1)3II) - potato
                  210133
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  q1710076
BLAST score
                  273
                  4.0e-24
E value
                  71
Match length
                  75
% identity
                  REHYDRIN HOMOLOG (DORMANCY-ASSOCIATED PROTEIN PBS128)
NCBI Description
                  >gi_82340_pir S22499 hypothetical protein - chess
                  bromegrass (fragment) >gi 17932_emb_CAA44884_ (X63202) ORF
                  [Bromus secalinus]
                  210134
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q129320
BLAST score
                  588
                  5.0e-61
E value
Match length
                  151
                  66
% identity
                  P21 PROTEIN >gi_99943_pir__A33176 P21 protein - soybean
NCBI Description
                  210135
Seq. No.
                  LIB3135-050-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3980393
                  338
BLAST score
                  1.0e-31
E value
Match length
                  110
% identity
                  (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  210136
Seq. ID
                  LIB3135-050-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q4454097
BLAST score
                  164
                  1.0e-11
E value
Match length
                  52
                   67
% identity
                  (X85206) hybrid proline-rich protein [Catharanthus roseus]
NCBI Description
Seq. No.
                  210137
                  LIB3135-050-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2828291
BLAST score
                  147
                  1.0e-09
E value
```

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]



```
210138
Seq. No.
Seq. ID
                  LIB3135-050-Q1-K1-F4
                  BLASTX
Method
                  g4522005
NCBI GI
                  303
BLAST score
                  4.0e-30
E value
                  149 -
Match length
                  48
% identity
                  (AC007069) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  210139
Seq. No.
                  LIB3135-050-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g3201615
NCBI GI
                  180
BLAST score
                  3.0e-13
E value
                  55
Match length
                   67
% identity
                  (AC004669) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210140
                  LIB3135-050-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  q4455364
NCBI GI
                   265
BLAST score
                   4.0e-23
E value
                   104
Match length
                   49
% identity
                   (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                   thaliana]
                   210141
Seq. No.
                   LIB3135-050-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   g3334346
NCBI GI
                   273
BLAST score
                   4.0e-24
E value
                   56
Match length
                   93
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
NCBI Description
                   >gi 2852445_dbj_BAA24697 (AB003378) SUI1 homolog [Salix
                   bakko]
                   210142
Seq. No.
Seq. ID
                   LIB3135-050-Q1-K1-F9
                   BLASTX
Method
NCBI GI
                   g1685003
BLAST score
                   343
                   3.0e-32
E value
                   118
Match length
                   56
% identity
                   (U32643) immediate-early salicylate-induced
NCBI Description
```

Seq. No. 210143

glucosyltransferase [Nicotiana tabacum]

```
LID2125 -050 v01 - W1-
```

Seq. ID LIB3135-050-Q1-K1-G10
Method BLASTN
NCBI GI g2829205
BLAST score 70
E value 5.0e-31

Match length 355 % identity 27

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 210144

Seq. ID LIB3135-050-Q1-K1-G2

Method BLASTX
NCBI GI g1706547
BLAST score 556
E value 3.0e-57
Match length 139
% identity 77

NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM

PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi\_2129912\_pir\_\_S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi\_1184668 (U22147)

beta-1,3-glucanase [Hevea brasiliensis]

Seq. No. 210145

Seq. ID LIB3135-050-Q1-K1-G3

Method BLASTX
NCBI GI g2827139
BLAST score 367
E value 2.0e-35
Match length 87
% identity 79

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi\_4049343\_emb\_CAA22568\_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 210146

Seq. ID LIB3135-050-Q1-K1-G4

Method BLASTN
NCBI GI g3334857
BLAST score 116
E value 5.0e-59
Match length 144
% identity 95

NCBI Description Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2

genes

Seq. No. 210147

Seq. ID LIB3135-050-Q1-K1-H1

Method BLASTX
NCBI GI g2662341
BLAST score 568
E value 8.0e-59
Match length 113
% identity 96



NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 210148

Seq. ID LIB3135-050-Q1-K1-H10

Method BLASTX
NCBI GI g3176708
BLAST score 232
E value 2.0e-19
Match length 80
% identity 56

NCBI Description (AC002392) putative proline-rich protein APG [Arabidopsis

thaliana]

Seq. No. 210149

Seq. ID LIB3135-050-Q1-K1-H11

Method BLASTX
NCBI GI g3334244
BLAST score 250
E value 2.0e-21
Match length 85
% identity 60

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi\_2113825\_emb\_CAA73691\_ (Y13239) Glyoxalase I [Brassica

juncea]

Seq. No. 210150

Seq. ID LIB3135-050-Q1-K1-H6

Method BLASTX
NCBI GI g2213590
BLAST score 137
E value 7.0e-15
Match length 103
% identity 49

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 210151

Seq. ID LIB3135-050-Q1-K1-H9

Method BLASTX
NCBI GI g3132478
BLAST score 320
E value 1.0e-29
Match length 126
% identity 52

NCBI Description (AC003096) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 210152

Seq. ID LIB3135-051-Q1-K1-A4

Method BLASTX
NCBI GI g4006878
BLAST score 250
E value 2.0e-21
Match length 105

```
% identity
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.
                  210153
Seq. ID
                  LIB3135-051-Q1-K1-A5
                  BLASTX
Method
NCBI GI
                  g2292907
BLAST score
                  363
                  1.0e-34
E value
Match length
                  137
% identity
                  30
NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]
                  210154
Seq. No.
                  LIB3135-051-Q1-K1-A8
```

 Seq. ID
 LIB3135-051-Q1-K1-A8

 Method
 BLASTX

 NCBI GI
 g2695711

 BLAST score
 246

 E value
 7.0e-21

E value 7.0
Match length 52
% identity 81

NCBI Description (AJ001370) cytochome b5 [Olea europaea]

Seq. No. 210155

Seq. ID LIB3135-051-Q1-K1-A9

Method BLASTX
NCBI GI g1350680
BLAST score 310
E value 1.0e-28
Match length 90
% identity 68

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 210156

Seq. ID LIB3135-051-Q1-K1-B10

Method BLASTX
NCBI GI g282994
BLAST score 333
E value 1.0e-31
Match length 73
% identity 84

NCBI Description Sip1 protein - barley >gi\_167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 210157

Seq. ID LIB3135-051-Q1-K1-B11

Method BLASTX
NCBI GI g3980391
BLAST score 249
E value 1.0e-21
Match length 85
% identity 60

NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis

thaliana]

Seq. No. 210158

Seq. ID LIB3135-051-Q1-K1-B12

% identity

17

```
BLASTX
Method
                  q464621
NCBI GI
                  376
BLAST score
                  2.0e-36
E value
                  96
Match length
                  75
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                  210159
                  LIB3135-051-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119360
BLAST score
                   486
E value
                  5.0e-49
Match length
                   95
% identity
                   65
                  calmodulin (clone PCM2) - potato (fragment) >gi_687698
NCBI Description
                   (U20291) calmodulin [Solanum tuberosum] >gi 687\overline{7}02 (U20293)
                   calmodulin [Solanum tuberosum]
                   210160
Seq. No.
                   LIB3135-051-Q1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2605932
BLAST score
                   529
                   4.0e-54
E value
                   128
Match length
% identity
                   80
                  (AF029898) aspartate aminotransferase [Lotus corniculatus]
NCBI Description
                   210161
Seq. No.
                   LIB3135-051-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g416650
NCBI GI
                   329
BLAST score
                   1.0e-35
E value
                   142
Match length
                   59
% identity
                   PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
NCBI Description
                   PGNT35/PCNT111) >gi_100304_pir_ S16268 auxin-induced
                   protein (clone pGNT35) - common tobacco
                   >gi 19797 emb CAA39706 (X56265) auxin-induced protein
                   [Nicotiana tabacum] >qi 19801 emb CAA39710 (X56269)
                   auxin-induced protein [Nicotiana Tabacum]
                   210162
Seq. No.
                   LIB3135-051-Q1-K1-C1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2829205
                   123
BLAST score
                   1.0e-62
E value
Match length
                   361
```

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein



## precursor (PRP) mRNA, complete cds

```
210163
Seq. No.
Seq. ID
                  LIB3135-051-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1420887
BLAST score
                  171
                  2.0e-12
E value
Match length
                  80
% identity
                  41
                  (U34334) non-specific lipid transfer-like protein
NCBI Description
                  [Phaseolus vulgaris]
Seq. No.
                  210164
                  LIB3135-051-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168328
BLAST score
                  296
                  4.0e-27
E value
Match length
                  86
% identity
NCBI Description
                  ACTIN-LIKE PROTEIN 3 >gi 629878 pir S48844 actin-like
                  protein - slime mold (Dictyostelium discoideum)
                  >gi 2130164 pir S69002 actin-like protein - slime mold
                   (Dictyostelium discoideum) >gi 563346 emb_CAA86553
                   (Z46418) actin-like protein [Dictyostelium discoideum]
Seq. No.
                  210165
                  LIB3135-051-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                  g2708743
NCBI GI
                  164
BLAST score
E value
                  2.0e-11
                  113
Match length
% identity
                  33
                   (AC003952) putative Tal-1-like reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  210166
Seq. ID
                  LIB3135-051-Q1-K1-C5
                  BLASTX
Method
                  g4115368
NCBI GI
BLAST score
                  363
                  1.0e-34
E value
Match length
                  124
                  56
% identity
NCBI Description (AC005957) hypothetical protein [Arabidopsis thaliana]
                  210167
Seq. No.
Seq. ID
                  LIB3135-051-Q1-K1-C8
                  BLASTX
Method
NCBI GI
                  g3850108
BLAST score
                  367
                  4.0e-35
E value
Match length
                  110
                  62
% identity
NCBI Description (AL033388) putative calcium-transporting atpase
```



## [Schizosaccharomyces pombe]

```
210168
Seq. No.
                   LIB3135-051-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   g4544434
NCBI GI
BLAST score
                   182
                   1.0e-13
E value
                   87
Match length
% identity
                   51
                    (AC006955) putative DNA-directed RNA polymerase II
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    210169
                   LIB3135-051-Q1-K1-D10
Seq. ID
                    BLASTX
Method
                    g464621
NCBI GI
BLAST score
                    213
                    3.0e-17
E value
                    91
Match length
                    53
% identity
                    60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                    ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
                    210170
Seq. No.
                    LIB3135-051-Q1-K1-D12
Seq. ID
Method
                    BLASTX
                    g629483
NCBI GI
                    281
BLAST score
                    4.0e-25
E value
                    113
Match length
% identity
                    51
                    gene 1-Sc3 protein - European white birch
NCBI Description
                    >gi 534898 emb CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                    >qi^{-}158432\overline{2} prf 212237\overline{4}C allergen Bet v 1-Sc3 [Betula
                    pendula]
                    210171
Seq. No.
                    LIB3135-051-Q1-K1-D2
Seq. ID
Method
                    BLASTX
                    g4127781
NCBI GI
BLAST score
                    176
                    9.0e-13
E value
                    38
Match length
% identity
                    23
                    (AJ012588) Notchless protein [Drosophila melanogaster]
NCBI Description
                    210172
Seq. No.
                    LIB3135-051-Q1-K1-D4
Seq. ID
                    BLASTX
Method
                    g122007
NCBI GI
                    227
BLAST score
                    7.0e-19
E value
                    67
Match length
                    67
% identity
```

HISTONE H2A >gi\_100161\_pir\_\_S11498 histone H2A - parsley >gi\_20448\_emb\_CAA37828\_ (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 210173

NCBI Description

Seq. ID LIB3135-051-Q1-K1-D6

Method BLASTX
NCBI GI g82263
BLAST score 365
E value 6.0e-35
Match length 119
% identity 69

NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome

c1 precursor (clone pC(1)3II) - potato

Seq. No. 210174

Seq. ID LIB3135-051-Q1-K1-D7

Method BLASTN
NCBI GI g13193
BLAST score 33
E value 6.0e-09
Match length 33
% identity 100

NCBI Description Mitochondrion Oenothera berteriana gene for ribosomal

protein S14

Seq. No. 210175

Seq. ID LIB3135-051-Q1-K1-E1

Method BLASTX
NCBI GI g2244847
BLAST score 449
E value 1.0e-44
Match length 125
% identity 69

NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

[Arabidopsis thaliana]

Seq. No. 210176

Seq. ID LIB3135-051-Q1-K1-E11

Method BLASTX
NCBI GI g2792185
BLAST score 329
E value 8.0e-31
Match length 108
% identity 12

NCBI Description (AJ002236) Hcr9-9B [Lycopersicon pimpinellifolium]

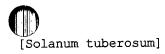
Seq. No. 210177

Seq. ID LIB3135-051-Q1-K1-E3

Method BLASTX
NCBI GI g1076668
BLAST score 674
E value 4.0e-71
Match length 133
% identity 95

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato

>gi 639834 emb CAA58823\_ (X83999) NADH dehydrogenase



```
210178
Seq. No.
                  LIB3135-051-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3608479
BLAST score
                  354
E value
                  1.0e-33
Match length
                  101
                  70
% identity
                  (AF088912) ribosomal protein L15 [Petunia x hybrida]
NCBI Description
                  210179
Seq. No.
                  LIB3135-051-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                   q4455223
NCBI GI
BLAST score
                   407
E value
                   7.0e-40
                   123
Match length
                   25
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   210180
Seq. No.
                   LIB3135-051-Q1-K1-F1
Seq. ID
Method
                   BLASTX
                   q3746069
NCBI GI
BLAST score
                   153
                   5.0e-10
E value
Match length
                   91
                   31
% identity
                   (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   210181
                   LIB3135-051-Q1-K1-F10
Seq. ID
                   BLASTN
Method
                   q2695738
NCBI GI
BLAST score
                   146
                   2.0e-76
E value
                   205
Match length
                   93
% identity
                  Pisum sativum mitochondrial tRNA-Gly gene and flanking
NCBI Description
                   sequences
                   210182
Seq. No.
                   LIB3135-051-Q1-K1-F12
Seq. ID
                   BLASTX
Method
                   g2244831
NCBI GI
BLAST score
                   162
                   4.0e-11
E value
                   49
Match length
                   67
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

210183

LIB3135-051-Q1-K1-F3

Seq. No.

Seq. ID

```
BLASTX
Method
NCBI GI
                  g3522943
BLAST score
                  187
                  4.0e-14
E value
Match length
                  86
% identity
                  49
                  (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
NCBI Description
                  210184
Seq. No.
Seq. ID
                  LIB3135-051-Q1-K1-F5
                  BLASTX
Method
NCBI GI
                  g3184098
BLAST score
                  381
                  1.0e-36
E value
Match length
                  150
                  55
% identity
                  (AL023777) coenzyme a synthetase [Schizosaccharomyces
NCBI Description
                  pombe]
Seq. No.
                  210185
                  LIB3135-051-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  q133867
NCBI GI
                  486
BLAST score
                  4.0e-49
E value
Match length
                  121
                  79
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
                  210186
Seq. No.
                  LIB3135-051-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  q729882
NCBI GI
BLAST score
                   665
                   4.0e-70
E value
                   130
Match length
                   89
% identity
                  CASEIN KINASE II BETA' CHAIN (CK II)
NCBI Description
                   >gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta
                   chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984)
                   casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                   >qi 2245122 emb CAB10544 (Z97343) unnamed protein product
                   [Arabidopsis thaliana]
Seq. No.
                   210187
Seq. ID
                   LIB3135-051-Q1-K1-G3
                   BLASTX
Method
NCBI GI
                   g3522943
BLAST score
                   296
E value
                   9.0e-27
Match length
                   138
```

34 % identity

(AC004411) putative p-glycoprotein [Arabidopsis thaliana] NCBI Description

Seq. No. 210188

```
LIB3135-051-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g2815246
NCBI GI
                  225
BLAST score
                  2.0e-18
E value
                  55
Match length
                  73
% identity
                  (X95709) class I type 2 metallothionein [Cicer arietinum]
NCBI Description
                  210189
Seq. No.
                  LIB3135-051-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g417103
NCBI GI
                  438
BLAST score
                  1.0e-43
E value
                  91
Match length
                  97
% identity
                  HISTONE H3.2, MINOR >gi_282871_pir_ S24346 histone
NCBI Description
                  H3.3-like protein - Arabidopsis thaliana
                  >qi 16324 emb CAA42957 (X60429) histone H3.3 like protein
                   [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                  histone H3.3 like protein [Arabidopsis thaliana] >gi 488563
                   (U09458) histone H3.2 [Medicago sativa] >gi 488567 (\overline{\text{U}}09460)
                  histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
                  H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
                   [Medicago sativa] >gi_488577 (U09465) histone H3.2
                   [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone
                  H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
                  histone H3 variant H3.3 [Lycopersicon esculentum]
                  >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                  >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana
                   tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
                  >gi 4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
                   coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone
                   H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1
                   (AL035708) Histon H3 [Arabidopsis thaliana]
                   210190
Seq. No.
Seq. ID
                   LIB3135-051-Q1-K1-H1
                   BLASTX
Method
                   g1843527
NCBI GI
BLAST score
                   457
                   1.0e-45
E value
Match length
                   119
                   77
% identity
NCBI Description
                  (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   210191
Seq. ID
                   LIB3135-051-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   g1084453
BLAST score
                   401
                   4.0e-39
E value
```

29062

83

% identity 55
NCBI Description calmodulin - rice

Match length % identity

```
210192
Seq. No.
Seq. ID
                  LIB3135-051-Q1-K1-H11:
Method
                  BLASTX
                  g3540219
NCBI GI
BLAST score
                  212
                  3.0e-17
E value
Match length
                  81
                  48
% identity
                  (D87686) KIAA0017 protein [Homo sapiens]
NCBI Description
                  210193
Seq. No.
                  LIB3135-051-Q1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2497543
                  593
BLAST score
                  1.0e-61
E value
                  123
Match length
                   95
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061_pir_ S41379
NCBI Description
                  pyruvate kinase - common tobacco >gi 444023 emb CAA82628
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   210194
Seq. No.
Seq. ID
                  LIB3135-051-Q1-K1-H8
                  BLASTX
Method
                   g1843527
NCBI GI
                   612
BLAST score
                   7.0e-64
E value
                   136
Match length
                   88
% identity
                  (U73747) annexin [Gossypium hirsutum]
NCBI Description
                   210195
Seq. No.
Seq. ID
                   LIB3135-051-Q1-K1-H9
                   BLASTX
Method
NCBI GI
                   q487006
BLAST score
                   469
                   4.0e-47
E value
                   124
Match length
                   79
% identity
                   protoporphyrin IX magnesium chelatase - garden snapdragon
NCBI Description
                   >gi 312129 emb_CAA51664_ (X73144) protoporphyrin IX:Mg
                   Chelatase [Antirrhinum majus]
                   210196
Seq. No.
                   LIB3135-052-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497752
BLAST score
                   230
                   4.0e-19
E value
Match length
                   84
                   55
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
```

[Prunus dulcis]

>gi\_1321911\_emb\_CAA65475 (X96714) lipid transfer protein

```
LIB3135-052-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g1350680
NCBI GI
                  516
BLAST score
                  1.0e-52
E value
Match length
                  117
% identity
                  84
                  60S RIBOSOMAL PROTEIN L1
NCBI Description
Seq. No.
                   210198
                  LIB3135-052-Q1-K1-A6
Seq. ID
Method
                  BLASTX
                   q629483
NCBI GI
                   317
BLAST score
                   3.0e-29
E value
                   120
Match length
% identity
                   53
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi 534898 emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                   >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
Seq. No.
                   210199
                   LIB3135-052-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4469025
BLAST score
                   290
                   4.0e-26
E value
Match length
                   70
                   55
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210200
                   LIB3135-052-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   q4566614
NCBI GI
BLAST score
                   262
                   6.0e-23
E value
                   85
Match length
                   74
% identity
                   (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                   Populus tremula]
                   210201
Seq. No.
                   LIB3135-052-Q1-K1-B10
Seq. ID
                   BLASTN
Method
                   g857394
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
                   86
Match length
                   86
% identity
                  Glycine max mRNA for mitotic cyclin a2-type, complete cds
NCBI Description
```

Seq. ID LIB3135-052-Q1-K1-B5

Method BLASTX NCBI GI g2245132



```
BLAST score
                  2.0e-10
E value
                  44
Match length
                  70
% identity
                  (Z97344) syntaxin [Arabidopsis thaliana]
NCBI Description
                  210203
Seq. No.
                  LIB3135-052-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g2909522
NCBI GI
                  192
BLAST score
                  1.0e-14
E value
                  125
Match length
                   32
% identity
                  (AL021932) ufaAl [Mycobacterium tuberculosis]
NCBI Description
Seq. No.
                   210204
                   LIB3135-052-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   q2052029
NCBI GI
BLAST score
                   515
E value
                   2.0e-52
Match length
                   128
                   73
% identity
                  (Y10820) glutathione transferase [Glycine max]
NCBI Description
                   210205
Seq. No.
                   LIB3135-052-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g1708313
NCBI GI
BLAST score
                   520
                   4.0e-53
E value
Match length
                   109
                   95
% identity
                   HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637
NCBI Description
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                   thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                   thaliana]
                   210206
Seq. No.
Seq. ID
                   LIB3135-052-Q1-K1-C12
                   BLASTX
Method
                   g2351580
NCBI GI
                   159
BLAST score
E value
                   8.0e-11
                   89
Match length
                   39
% identity
                   (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
```

Seq. ID LIB3135-052-Q1-K1-C2

BLASTX Method q1706547 NCBI GI BLAST score 338 1.0e-31 E value 99 Match length

29065

```
% identity
                 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
NCBI Description
                  PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                  ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE)
                  >gi_2129912_pir__S65077 beta-1,3-glucanase class I
                  precursor - Para rubber tree >gi_1184668 (U22147)
                  beta-1,3-glucanase [Hevea brasiliensis]
                  210208
Seq. No.
                  LIB3135-052-Q1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1173187
BLAST score
                  602
                  9.0e-63
E value
Match length
                  118
                  96
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  210209
Seq. No.
Seq. ID
                  LIB3135-052-Q1-K1-C6
Method
                  BLASTX
                  g267070
NCBI GI
                  305
BLAST score
                  4.0e-28
E value
Match length
                  63
                  95
% identity
                  TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin
NCBI Description
                  alpha-6 chain - Arabidopsīs thalīana >gi_166920 (M84699)
                  TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275
                   (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis
                   thaliana]
                  210210
Seq. No.
                  LIB3135-052-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                   g3860315
NCBI GI
                   465
BLAST score
                   1.0e-46
E value
                   103
Match length
                   83
% identity
                  (AJ012684) 40S ribosomal protein S19 [Cicer arietinum]
NCBI Description
                   210211
Seq. No.
                   LIB3135-052-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   g3319882
NCBI GI
BLAST score
                   481
                   9.0e-49
E value
                   96
Match length
                   96
% identity
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
```

```
LIB3135-052-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g2346978
NCBI GI
BLAST score
                  326
                  2.0e-30
E value
                  83
Match length
                  48
% identity
NCBI Description (AB006601) ZPT2-14 [Petunia x hybrida]
                  210213
Seq. No.
                  LIB3135-052-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  g100935
NCBI GI
                  252
BLAST score
                  8.0e-22
E value
                  108
Match length
                  46
% identity
                  vicilin-like storage protein Glb1-S, embryo - maize
NCBI Description
                  >gi_22287_emb_CAA41810_ (X59084) vicilin-like embryo
                  storage protein [Zea mays]
Seq. No.
                  210214
                  LIB3135-052-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  q3885334
NCBI GI
                   471
BLAST score
                   2.0e-47
E value
                   104
Match length
% identity
                   86
                   (ACO05623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   210215
                   LIB3135-052-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   g3183088
NCBI GI
                   206
BLAST score
                   3.0e-16
E value
                   69
Match length
                   58
% identity
                   PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                   cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
```

Seg. No. 210216

Seq. No. 210216 Seq. ID LIB3135-052-Q1-K1-E4

Method BLASTX
NCBI GI g1174867
BLAST score 338
E value 9.0e-32
Match length 72
% identity 88

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING

like protein [Vigna unguiculata]

PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2

KD PROTEIN) >gi\_633687\_emb\_CAA55862\_ (X79275)

29067

ubiquinol--cytochrome c reductase [Solanum tuberosum]

**4** 

```
>qi 1094912 prf 2107179A cytochrome c
oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
210217
LIB3135-052-Q1-K1-E7
BLASTX
g1107526
212
```

% identity (X87931) SIEP1L protein [Beta vulgaris] NCBI Description

210218 Seq. No. LIB3135-052-Q1-K1-E9 Seq. ID BLASTX Method g4185153 NCBI GI

105

69

5.0e-31

171 BLAST score 3.0e-12 E value 50 Match length % identity 66

Seq. No.

Seq. ID

NCBI GI

E value

BLAST score

Match length

Method

(AC005724) hypothetical protein [Arabidopsis thaliana] NCBI Description

210219 Seq. No.

LIB3135-052-Q1-K1-F10 Seq. ID

BLASTX Method g2204224 NCBI GI 214 BLAST score 3.0e-17 E value 82 Match length 50 % identity

(Y13849) alpha-galactosidase [Hordeum vulgare] NCBI Description

210220 Seq. No.

LIB3135-052-Q1-K1-F12 Seq. ID

BLASTX Method q1743354 NCBI GI 578 BLAST score 6.0e-60 E value 133 Match length % identity 82

(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] NCBI Description

210221 Seq. No.

LIB3135-052-Q1-K1-F4 Seq. ID

BLASTX Method q3687251 NCBI GI 391 BLAST score E value 6.0e-38 96 Match length % identity 75

(AC005169) unknown protein [Arabidopsis thaliana] NCBI Description

210222 Seq. No.

LIB3135-052-Q1-K1-F5 Seq. ID

BLASTX Method NCBI GI g629483

29068



```
BLAST score
                  9.0e-32
E value
                  127
Match length
                  54
% identity
                  gene 1-Sc3 protein - European white birch
NCBI Description
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi^-158432^-2 pr^-f 212237^-4C allergen Bet v 1-Sc3 [Betula
                  pendula]
Seq. No.
                  210223
                  LIB3135-052-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629483
                  336
BLAST score
                   2.0e-31
E value
                   127
Match length
% identity
                  gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                   >gi^-158432^-pr^-f 212237^-4C allergen Bet v 1-Sc3 [Betula
                  pendula]
Seq. No.
                   210224
                   LIB3135-052-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   q2981950
NCBI GI
                   198
BLAST score
                   9.0e-16
E value
Match length
                   69
                   54
% identity
NCBI Description Pathogenesis-Related Protein 5d From Nicotiana Tabacum
Seq. No.
                   210225
                   LIB3135-052-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g2369766
NCBI GI
                   202
BLAST score
                   8.0e-16
E value
                   39
Match length
                   95
% identity
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   210226
Seq. No.
Seq. ID
                   LIB3135-052-Q1-K1-G4
                   BLASTX
Method
                   q3043432
NCBI GI
                   318
BLAST score
                   2.0e-29
E value
                   60
Match length
                   100
% identity
                  (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]
```

NCBI Description

210227 Seq. No.

LIB3135-052-Q1-K1-G5 Seq. ID

BLASTX Method NCBI GI q3953471 232 BLAST score



E value 2.0e-19
Match length 68
% identity 66

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 210228

Seq. ID LIB3135-052-Q1-K1-G8

Method BLASTX
NCBI GI g464981
BLAST score 187
E value 2.0e-14
Match length 58
% identity 67

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 210229

Seq. ID LIB3135-052-Q1-K1-H12

Method BLASTX
NCBI GI g2129513
BLAST score 257
E value 2.0e-32
Match length 100
% identity 76

NCBI Description peroxidase (EC 1.11.1.7) A3a precursor - Japanese aspen x

large-toothed aspen >gi\_1255661\_dbj\_BAA07240\_ (D38050)

peroidase precursor [Populus kitakamiensis]

Seq. No. 210230

Seq. ID LIB3135-052-Q1-K1-H2

Method BLASTX
NCBI GI g339878
BLAST score 157
E value 1.0e-10
Match length 78
% identity 41

NCBI Description (M55169) tripeptidyl peptidase II [Homo sapiens]

Seq. No. 210231

Seq. ID LIB3135-052-Q1-K1-H3

Method BLASTX
NCBI GI g3859602
BLAST score 243
E value 1.0e-20
Match length 97
% identity 55

NCBI Description (AF104919) contains similarity to human

DHHC-domain-containing cysteine-rich protein (GB:U90653) and several S. cerevisiae probable membrane proteins (GB:U20865, Z48758, U43491) [Arabidopsis thaliana]

Seq. No. 210232

Seq. ID LIB3135-052-Q1-K1-H4

Method BLASTX NCBI GI g1170507 BLAST score 374



E value 2.0e-36 Match length 76 % identity 97

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)

>gi\_100276\_pir\_\_S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi\_19699\_emb\_CAA43514\_ (X61206)
nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 210233

Seq. ID LIB3135-052-Q1-K1-H5

Method BLASTX
NCBI GI g3878494
BLAST score 224
E value 2.0e-18
Match length 125
% identity 34

NCBI Description (Z79602) predicted using Genefinder; Similarity to Yeast

hypothetical protein YAE2 (SW:YAE2\_YEAST); cDNA EST EMBL:T01631 comes from this gene; cDNA EST EMBL:M88949

comes from this gene [Caenorhabditis elegans]

Seq. No. 210234

Seq. ID LIB3135-053-Q1-K1-A1

Method BLASTX
NCBI GI g2564066
BLAST score 437
E value 2.0e-43
Match length 99
% identity 85

NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Seq. No. 210235

Seq. ID LIB3135-053-Q1-K1-A10

Method BLASTX
NCBI GI g1346735
BLAST score 403
E value 1.0e-53
Match length 146
% identity 76

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi\_1076562\_pir\_\_S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi\_474170\_emb\_CAA49995\_ (X70652)

phosphoglycerate mutase [Ricinus communis]

Seq. No. 210236

Seq. ID LIB3135-053-Q1-K1-A11

Method BLASTX
NCBI GI g1173218
BLAST score 396
E value 1.0e-38
Match length 100
% identity 80

NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi\_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi\_2150130 (AF001412)

cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. ID

Method



```
210237
Seq. No.
                  LIB3135-053-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                  g3204106
NCBI GI
                  401
BLAST score
                  3.0e-39
E value
                  120
Match length
                   65
% identity
                  (AJ006763) putative beta-amilase [Cicer arietinum]
NCBI Description
Seq. No.
                   210238
                  LIB3135-053-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                   q3719211
NCBI GI
                   383
BLAST score
                   3.0e-37
E value
Match length
                   106
% identity
                  (U97021) UIP2 [Arabidopsis thaliana]
NCBI Description
                   210239
Seq. No.
Seq. ID
                   LIB3135-053-Q1-K1-A6
Method
                   BLASTX
                   g2347054
NCBI GI
                   360
BLAST score
                   2.0e-34
E value
                   126
Match length
% identity
                   58
                   (X96791) arginine decarboxylase [Vitis vinifera]
NCBI Description
                   210240
Seq. No.
Seq. ID
                   LIB3135-053-Q1-K1-B1
                   BLASTX
Method
NCBI GI
                   g4467157
                   269
BLAST score
                   1.0e-23
E value
                   134
Match length
% identity
                   46
                   (AL035540) disease resistance response like protein
NCBI Description
                   [Arabidopsis thaliana]
                   210241
Seq. No.
                   LIB3135-053-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g4512661
NCBI GI
                   209
BLAST score
                   6.0e-17
E value
                   55
Match length
                   65
% identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4544468 gb_AAD22375.1 AC006580 7 (AC006580) putative
                   DNA binding protein [Arabidopsis thaliana]
                   210242
Seq. No.
```

29072

LIB3135-053-Q1-K1-B11

BLASTX

```
g567893
NCBI GI
                  186
BLAST score
                  5.0e-14
E value
                  69
Match length
                  59
% identity
                   (L37382) beta-galactosidase-complementation protein
NCBI Description
                   [Cloning vector]
                  210243
Seq. No.
                  LIB3135-053-Q1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1176658
BLAST score
                   161
                   3.0e-11
E value
                   62
Match length
                   48
% identity
                  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                   >gi_726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
                   210244
Seq. No.
                   LIB3135-053-Q1-K1-B5
Seq. ID
Method
                   BLASTX
                   q3047098
NCBI GI
                   240
BLAST score
                   3.0e-20
E value
                   67
Match length
                   66
% identity
                   (AF058826) similar to eukaryotic protein kinase domains
NCBI Description
                   (Pfam: pkinase.hmm, score: 171.43) [Arabidopsis thaliana]
                   210245
Seq. No.
                   LIB3135-053-Q1-K1-B6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4376203
                   188
BLAST score
                   1.0e-17
E value ·
                   104
Match length
 % identity
                   44
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
                   210246
 Seq. No.
                   LIB3135-053-Q1-K1-B7
 Seq. ID
                   BLASTX
 Method
                   g1711572
 NCBI GI
                   514
 BLAST score
                   2.0e-52
 E value
                   119
 Match length
                   82
 % identity
                   SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR
 NCBI Description
                    (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)
                   >gi_1076415_pir__S30579 succinate--CoA ligase (GDP-forming)
                    (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment)
                   >qi 16510 emb CAA48891 (X69138) succinate--CoA ligase
```

29073

(GDP-forming) [Arabidopsis thaliana]

Same of the

```
210247
Seq. No.
                  LIB3135-053-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g2208944
NCBI GI
                  446
BLAST score
                  2.0e-44
E value
                  115
Match length
                  74
% identity
                  (Y11120) nodulin-35 homologue [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   LIB3135-053-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                   q2736147
NCBI GI
BLAST score
                   444
                   4.0e-44
E value
                   119
Match length
% identity
                   (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
NCBI Description
                   thaliana] >gi 3132481 (AC003096) fatty acid hydroxylase,
                   FAH1 [Arabidopsis thaliana]
                   210249
Seq. No.
                   LIB3135-053-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   q2266947
NCBI GI
BLAST score
                   583
                   2.0e-60
E value
                   109
Match length
                   99
% identity
                   (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium
NCBI Description
                   hirsutum]
                   210250
Seq. No.
                   LIB3135-053-Q1-K1-C6
 Seq. ID
 Method
                   BLASTN
                   g2829205
 NCBI GI
                   133
 BLAST score
                   1.0e-68
 E value
                   348
 Match length
                   17
 % identity
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
 NCBI Description
                   precursor (PRP) mRNA, complete cds
 Seq. No.
                   210251
                   LIB3135-053-Q1-K1-C7
 Seq. ID
                   BLASTX
 Method
                   g2244749
 NCBI GI
                   496
 BLAST score
                   3.0e-50
 E value
                   113
 Match length
                   84
 % identity
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
 NCBI Description
                    210252
 Seq. No.
                    LIB3135-053-Q1-K1-D1
 Seq. ID
                    BLASTX
 Method
```

29074

```
g4539302
NCBI GI
BLAST score
                  361
E value
                  1.0e-34
Match length
                  80
% identity
NCBI Description
                  (AL049480) putative protein [Arabidopsis thaliana]
                  210253
Seq. No.
                  LIB3135~053-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                  g3309086
NCBI GI
BLAST score
                  187
E value
                  2.0e-14
Match length
                  49
                  78
% identity
                  (AF076253) calcineurin B-like protein 3 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  210254
Seq. ID
                  LIB3135-053-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                   384
E value
                  4.0e-37
                  119
Match length
% identity
                   65
                  (X87931) SIEP1L protein [Beta vulgaris]
NCBI Description
Seq. No.
                   210255
Seq. ID
                  LIB3135-053-Q1-K1-D8
                  BLASTX
Method
NCBI GI
                  g2661422
BLAST score
                  267
                  2.0e-23
E value
Match length
                   66
% identity
                  82
                   (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
                   [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
```

LIB3135-053-Q1-K1-D9 Seq. ID

Method BLASTX NCBI GI g3309086 BLAST score 269 1.0e-23 E value 140 Match length % identity 52

NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis

thaliana]

210257 Seq. No.

Seq. ID LIB3135-053-Q1-K1-E1

Method BLASTX NCBI GI g123544 BLAST score 516

```
E value
Match length
                  144
% identity
                  69
                  18.5 KD CLASS I HEAT SHOCK PROTEIN (HSP 18.5)
NCBI Description
                  >gi 81788 pir S00646 heat shock protein 18.5-C - soybean
                  >gi 18654 emb CAA30154 (X07160) hsp18.5-C protein (AA 1 -
                  161) [Glycine max]
                  210258
Seq. No.
                  LIB3135-053-Q1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3241939
BLAST score
                  47
E value
                  3.0e-17
Match length
                  147
% identity
                  60
                 Arabidopsis thaliana chromosome II BAC T26J13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  210259
Seq. ID
                  LIB3135-053-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2245125
BLAST score
                  155
                  3.0e-10
E value
                  109
Match length
% identity
                  39
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  210260
Seq. ID
                  LIB3135-053-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q2497543
BLAST score
                  212
                  6.0e-17
E value
Match length
                  104
% identity
                  46
NCBI Description
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir_ S41379
                  pyruvate kinase - common tobacco >qi 444023 emb CAA82628
                  (Z29492) pyruvate kinase [Nicotiana tabacum]
Seq. No.
                  210261
Seq. ID
                  LIB3135-053-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g1706329
BLAST score
                  178
                  4.0e-13
E value
Match length
                  101
% identity
                  45
                  PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
```

NCBI Description

>gi\_2146788\_pir\_\_S65471 pyruvate decarboxylase (EC 4.1.1.1)

(clone PDC2) - Garden pea (fragment)

>gi\_1177605\_emb\_CAA91445\_ (Z66544) pyruvate decarboxylase

[Pisum sativum]

Seq. No. 210262

Seq. ID LIB3135-053-Q1-K1-F1

```
BLASTN
Method
NCBI GI
                  g4455229
BLAST score
                  53
                  5.0e-21
E value
Match length
                  85
                  91
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
                  (ESSAII project)
                  210263
Seq. No.
Seq. ID
                  LIB3135-053-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q2529665
BLAST score
                  665
E value
                  4.0e-70
Match length
                  144
                  90
% identity
NCBI Description
                  (AC002535) putative ribosomal protein L7A [Arabidopsis
                  thaliana]
                  210264
Seq. No.
Seq. ID
                  LIB3135-053-Q1-K1-F3
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  143
E value
                  1.0e-74
                  387
Match length
                  19
% identity
NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
                  precursor (PRP) mRNA, complete cds
Seq. No.
                  210265
                  LIB3135-053-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281115
BLAST score
                  643
                  2.0e-67
E value
Match length
                  150
% identity
                  82
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  210266
Seq. ID
                  LIB3135-053-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1351303
BLAST score
                  379
E value
                  2.0e-36
Match length
                  118
                  69
% identity
                  INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
NCBI Description
                  >gi 619732 (U18770) indole-3-glycerol phosphate synthase
                  [Arabidopsis thaliana]
```

Seq. ID LIB3135-053-Q1-K1-F9

Method BLASTX

```
NCBI GI
                  q2252843
BLAST score
                  169
E value
                  7.0e-12
Match length
                  98
                  45
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210268
                  LIB3135-053-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3757515
BLAST score
                  455
E value
                  2.0e-45
Match length
                  142
% identity
                  64
NCBI Description
                  (AC005167) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  210269
                  LIB3135-053-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g2853081
NCBI GI
BLAST score
                  428
E value
                  3.0e-42
                  115
Match length
% identity
                  69
                  (AL021768) ATP binding protein - like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  210270
Seq. ID
                  LIB3135-053-Q1-K1-G6
Method
                  BLASTX
                  q3986110
NCBI GI
BLAST score
                  271
                  7.0e-24
E value
Match length
                  69
% identity
                  77
NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana]
Seq. No.
                  210271
Seq. ID
                  LIB3135-053-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3913791
BLAST score
                  363
E value
                  1.0e-34
Match length
                  80
                  85
% identity
                  GLUTAMATE--CYSTEINE LIGASE PRECURSOR
NCBI Description
                  (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS)
                  >gi 2407615 (AF017983) gamma-glutamylcysteine synthetase
                  [Lycopersicon esculentum]
Seq. No.
                  210272
```

Seq. ID LIB3135-053-Q1-K1-H1

Method BLASTX NCBI GI g3702326 BLAST score 454 E value 3.0e-48

Seq. ID

210278

LIB3135-053-Q1-K1-H9

```
Match length
% identity
                  72
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  210273
Seq. No.
                  LIB3135-053-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4531444
BLAST score
                  251
E value
                  2.0e-25
Match length
                  101
% identity
                  63
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  210274
Seg. No.
Seq. ID
                  LIB3135-053-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4539545
BLAST score
                  688
                  9.0e-73
E value
Match length
                  143
% identity
                  94
                 (Y16644) PRCI [Nicotiana tabacum]
NCBI Description
                  210275
Seq. No.
                  LIB3135-053-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467129
BLAST score
                  351
E value
                  3.0e-33
Match length
                  121
% identity
                  53
                  (AL035538) calcium-dependent protein kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  210276
                  LIB3135-053-Q1-K1-H6
Seq. ID
Method
                  BLASTX
                  g4531444
NCBI GI
BLAST score
                  534
                  9.0e-55
E value
                  131
Match length
% identity
                  76
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  210277
Seq. ID
                  LIB3135-053-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3935157
BLAST score
                  603
E value
                  9.0e-63
                  144
Match length
% identity
                  81
NCBI Description
                 (AC005106) T25N20.21 [Arabidopsis thaliana]
```

NCBI GI

BLAST score

g81454

213

```
Method
                  BLASTX
NCBI GI
                  q2655098
BLAST score
                  430
                  2.0e-42
E value
Match length
                  144
% identity
                  58
NCBI Description
                  (AF023472) peptide transporter [Hordeum vulgare]
                  210279
Seq. No.
Seq. ID
                  LIB3135-054-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  q871468
BLAST score
                  104
E value
                  3.0e-51
Match length
                  320
% identity
                  88
NCBI Description H.annuus mitochondrion genes trnH and trnE
                  210280
Seq. No.
Seq. ID
                  LIB3135-054-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g124224
BLAST score
                  533
E value
                  1.0e-54
                  107
Match length
                  93
% identity
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi_100345_pir__S21060 translation initiation factor eIF-5A
                  - common tobacco >gi_19887_emb_CAA45105 (X63543)
                  eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.
                  210281
                  LIB3135-054-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455302
BLAST score
                  344
                  2.0e-32
E value
Match length
                  144
% identity
                  42
NCBI Description
                  (AL035528) putative protein [Arabidopsis thaliana]
                  210282
Seq. No.
Seq. ID
                  LIB3135-054-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3901014
BLAST score
                  234
E value
                  2.0e-19
Match length
                  55
% identity
                  76
NCBI Description
                  (AJ130886) metallothionein-like protein class II [Fagus
                  sylvatica]
Seq. No.
                  210283
Seq. ID
                  LIB3135-054-Q1-K1-B10
Method
                  BLASTX
```

29080



```
.0e-17
E value
                  55
Match length
                  80
% identity
                  photosystem II oxygen-evolving complex protein 1 - spinach
NCBI Description
                  >gi 224916 prf 1204192A photosystem II protein 33kD
                  [Spinacia oleracea]
                  210284
Seq. No.
                  LIB3135-054-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                  g2270994
NCBI GI
                  449
BLAST score
                  1.0e-44
E value
                  116
Match length
                  70
% identity
                  (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
                  210285
Seq. No.
                  LIB3135-054-Q1-K1-B3
Seq. ID
Method
                  BLASTX
                  g3885515
NCBI GI
BLAST score
                  228
E value
                  4.0e-36
Match length
                  96
                  83
% identity
                  (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                  sativa]
                   210286
Seq. No.
                  LIB3135-054-Q1-K1-C1
Seq. ID
                  BLASTN
Method
                  g3510339
NCBI GI
BLAST score
                   38
                   6.0e-12
E value
                   157
Match length
                   84
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K3K7, complete sequence [Arabidopsis thaliana]
                   210287
Seq. No.
                   LIB3135-054-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g1161167
NCBI GI
                   314
BLAST score
                   7.0e-29
E value
                   101
Match length
                   53
% identity
NCBI Description (L42466) ethylene-forming enzyme [Picea glauca]
                   210288
Seq. No.
                   LIB3135-054-Q1-K1-C12
Seq. ID
                   BLASTX
Method
```

29081

g2262114

2.0e-14

189

89

45

NCBI GI

E value Match length

BLAST score

% identity

Seq. ID



```
(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                  210289
Seq. No.
Seq. ID
                  LIB3135-054-Q1-K1-C2
                  BLASTX
Method
                  g4006859
NCBI GI
                  263
BLAST score
                  4.0e-23
E value
                  99
Match length
% identity
                  53
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                  210290
Seq. No.
                  LIB3135-054-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g3980415
NCBI GI
BLAST score
                   403
                  2.0e-39
E value
Match length
                  144
                   56
% identity
                   (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                   thaliana]
                   210291
Seq. No.
                  LIB3135-054-Q1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760334
BLAST score
                   407
                   9.0e-40
E value
Match length
                   91
                   78
% identity
                  (AC002130) F1N21.5 [Arabidopsis thaliana]
NCBI Description
                   210292
Seq. No.
                   LIB3135-054-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g2131751
NCBI GI
BLAST score
                   333
                   4.0e-31
E value
                   130
Match length
                   46
% identity
                   hypothetical protein YLR019w - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi 1360322_emb CAA97541 (Z73191) ORF YLR019w
                   [Saccharomyces cerevisiae]
                   210293
Seq. No.
                   LIB3135-054-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   q3063442
NCBI GI
                   185
BLAST score
                   9.0e-14
E value
                   82
Match length
                   51
% identity
NCBI Description (AC003981) F22013.6 [Arabidopsis thaliana]
                   210294
```

29082

LIB3135-054-Q1-K1-D11

Method

NCBI GI

BLASTX

g4467137

```
Method
NCBI GI
                  g2467274
BLAST score
                  324
E value
                  4.0e-30
                  91
Match length
                  69
% identity
NCBI Description (Z99759) rna binding protein [Schizosaccharomyces pombe]
                  210295
Seq. No.
                  LIB3135-054-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915847
BLAST score
                  483
                  5.0e-49
E value
                  97
Match length
                  95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S2 > gi 2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  210296
Seq. ID
                  LIB3135-054-Q1-K1-D4
Method
                  BLASTX
                  g3421109
NCBI GI
                  490
BLAST score
E value
                  2.0e-49
                  103
Match length
% identity
                  91
                 (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                  thaliana)
Seq. No.
                  210297
                  LIB3135-054-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911072
BLAST score
                  297
E value
                  5.0e-27
Match length
                  117
% identity
                  56
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                  210298
                  LIB3135-054-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  g136644
NCBI GI
BLAST score
                  235
E value
                  8.0e-20
Match length
                  54
% identity
                  80
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_100765_pir__A34506
                  23K ubiquitin carrier protein E2 - wheat >gi 170782
                  (M28059) ubiquitin carrier protein [Triticum vulgare]
                  210299
Seg. No.
Seq. ID
                  LIB3135-054-Q1-K1-E1
```

29083



```
BLAST score
                   3.0e-54
E value
                   128
Match length
                   77
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   210300
Seq. No.
                   LIB3135-054-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   q4490738
NCBI GI
BLAST score
                   150
                   7.0e-10
E value
Match length
                   99
                   36
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   210301
Seq. No.
                   LIB3135-054-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                    q1946364
NCBI GI
                    293
BLAST score
                    1.0e-26
E value
                    88
Match length
                    62
% identity
                   (U93215) lipase isolog [Arabidopsis thaliana]
NCBI Description
                    210302
Seq. No.
                    LIB3135-054-Q1-K1-E2
Seq. ID
                    BLASTX
Method
                    g400992
NCBI GI
                    290
BLAST score
                    4.0e-26
E value
Match length
                    60
                    85
% identity
                    50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR (CL28)
NCBI Description
                    >gi_279656_pir__R5NT28 ribosomal protein L28 precursor,
chloroplast - tobacco >gi_20016_emb_CAA48211_ (X68078)
                    ribosomal protein CL28 [Nicotiana tabacum]
                    210303
 Seq. No.
                    LIB3135-054-Q1-K1-E6
 Seq. ID
                    BLASTX
Method
                    g4467137
 NCBI GI
                    370
 BLAST score
                    2.0e-35
 E value
                    139
 Match length
 % identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                    210304
 Seq. No.
                    LIB3135-054-Q1-K1-F1
 Seq. ID
                    BLASTX
 Method
                    g4538929
 NCBI GI
                    246
 BLAST score
```

29084

6.0e-21

63

43

E value

Match length

% identity



NCBI Description (AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No. 210305

Seq. ID LIB3135-054-Q1-K1-F10

Method BLASTX
NCBI GI g4510418
BLAST score 331
E value 5.0e-31

Match length 117 % identity 56

NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No. 210306

Seq. ID LIB3135-054-Q1-K1-F11

Method BLASTX
NCBI GI 94102839
BLAST score 463
E value 2.0e-46
Match length 114
% identity 78

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 210307

Seq. ID LIB3135-054-Q1-K1-F12

Method BLASTX
NCBI GI g131770
BLAST score 344
E value 2.0e-32
Match length 108
% identity 61

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)

(VEGETATIVE SPECIFIC PROTEIN V12) >gi\_70880\_pir\_\_R3D024

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi\_7353\_emb\_CAA29844\_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 210308

Seq. ID LIB3135-054-Q1-K1-F6

Method BLASTN
NCBI GI g2829205
BLAST score 165
E value 9.0e-88
Match length 257
% identity 27

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 210309

Seq. ID LIB3135-054-Q1-K1-H1

Method BLASTX
NCBI GI g167367
BLAST score 483
E value 5.0e-49
Match length 91
% identity 97

NCBI Description (L08199) peroxidase [Gossypium hirsutum]



```
210310
Seq. No.
                  LIB3135-055-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                   g4006890
NCBI GI
BLAST score
                   140
                   4.0e-09
E value
Match length
                   35
                   77
% identity
                   (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   210311
                   LIB3135-055-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2662343
BLAST score
                   696
                   1.0e-73
E value
Match length
                   149
                   91
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
Seq. No.
                   210312
                   LIB3135-055-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131386
BLAST score
                   702
E value
                   2.0e-74
Match length
                   150
% identity
                   91
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN)
Seq. No.
                   210313
                   LIB3135-055-Q1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4559339
BLAST score
                   422
                   1.0e-41
E value
                   86
Match length
                   93
% identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   210314
Seq. No.
                   LIB3135-055-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   g2811025
NCBI GI
BLAST score
                   590
                   3.0e-61
E value
                   145
Match length
                   71
% identity
                  ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607_
```

NCBI Description

(AB002695) aspartic endopeptidase [Cucurbita pepo]

BLAST score

253

```
LIB3135-055-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g4103635
NCBI GI
                  267
BLAST score
                  2.0e-23
E value
                  106
Match length
                  47
% identity
                  (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
                  210316
Seq. No.
                  LIB3135-055-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  q2662343
NCBI GI
                   636
BLAST score
                  1.0e-66
E value
                  135
Match length
% identity
                   88
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   210317
Seq. No.
Seq. ID
                  LIB3135-055-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                   q3122060
                   389
BLAST score
                   6.0e-38
E value
Match length
                   96
                   74
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi 2598657 emb CAA10847 (AJ222579) elongation factor
                   1-alpha (EFI-a) [Vicia faba]
Seq. No.
                   210318
                   LIB3135-055-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g2765837
NCBI GI
                   105
BLAST score
                   8.0e-12
E value
                   87
Match length
                   54
% identity
                  (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210319
Seq. ID
                   LIB3135-055-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   q974782
                   493
BLAST score
                   7.0e-50
E value
                   99
Match length
                   99
% identity
                   (Z49150) cobalamine-independent methionine synthase
NCBI Description
                   [Solenostemon scutellarioides]
                   210320
Seq. No.
                   LIB3135-055-Q1-K1-B9
Seq. ID
                                                        8,1
Method
                   BLASTX
NCBI GI
                   q2829899
```

29087

```
0e-21
E value
                  109
Match length
                   44
% identity
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp AJ001449 2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
                  210321
Seq. No.
                  LIB3135-055-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  g633890
NCBI GI
                  491
BLAST score
                   1.0e-49
E value
                   136
Match length
                  71
% identity
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
                   210322
Seq. No.
                   LIB3135-055-Q1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1709761
BLAST score
                   665
                   5.0e-70
E value
                   147
Match length
                   86
% identity
                   PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX 27 KD SUBUNIT) >gi_1262146_emb_CAA65660_ (X96974)
                   proteasome subunit [Spinacia oleracea]
                   210323
Seq. No.
Seq. ID
                   LIB3135-055-Q1-K1-C12
                   BLASTX
Method
                   g2341028
NCBI GI
                   201
BLAST score
                   7.0e-16
E value
                   39
Match length
                   100
% identity
                   (AC000104) Strong similarity to 60S ribosomal protein L17
NCBI Description
                   (gb_X01694). EST gb_AA042332 comes from this gene.
                   [Arabidopsis thaliana]
                   210324
Seq. No.
Seq. ID
                   LIB3135-055-Q1-K1-C2
                   BLASTX
Method
                   g3757521
NCBI GI
BLAST score
                   602
E value
                   1.0e-62
                   132
Match length
                   81
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
```

Seq. ID LIB3135-055-Q1-K1-C3

Method BLASTX NCBI GI g2407800 BLAST score 437

```
2.0e-43
E value
Match length
                  113
% identity
                  (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                  210326
Seq. No.
                  LIB3135-055-Q1-K1-C4
Seq. ID
                  BLASTX
Method
                  q3924597
NCBI GI
                  202
BLAST score
E value
                  9.0e-16
Match length
                  127
% identity
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                   210327
Seq. No.
                  LIB3135-055-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                   g2274915
NCBI GI
BLAST score
                   412
                   2.0e-40
E value
                   141
Match length
                   60
% identity
                  (AJ000081) beta-1,3-glucanase [Citrus sinensis]
NCBI Description
                   210328
Seq. No.
                   LIB3135-055-Q1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4457221
                   312
BLAST score
                   1.0e-28
E value
                   100
Match length
% identity
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
NCBI Description
                   chinense]
                   210329
Seq. No.
                   LIB3135-055-Q1-K1-D1
Seq. ID
Method
                   BLASTX
                   g4105794
NCBI GI
BLAST score
                   211
                   9.0e-17
E value
Match length
                   115
                   40
 % identity
NCBI Description (AF049928) PGP224 [Petunia x hybrida]
```

Seq. ID LIB3135-055-Q1-K1-D10

Method BLASTX
NCBI GI g3355468
BLAST score 527
E value 8.0e-54
Match length 123
% identity 87

NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis

thaliana]

Seq. ID

Method

NCBI GI



```
210331
Seq. No.
                  LIB3135-055-Q1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2462753
                   650
BLAST score
                   3.0e-68
E value
                  140
Match length
                   81
% identity
                   (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                   210332
Seq. No.
                  LIB3135-055-Q1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2274915
                   438
BLAST score
                   2.0e-43
E value
                   131
Match length
                   67
% identity
                   (AJ000081) beta-1,3-glucanase [Citrus sinensis]
NCBI Description
                   210333
Seq. No.
                   LIB3135-055-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   q508304
NCBI GI
                   236
BLAST score
                   9.0e-20
E value
                   82
Match length
                   56
% identity
                  (L22305) corC [Medicago sativa]
NCBI Description
Seq. No.
                   210334
                   LIB3135-055-Q1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4559358
BLAST score
                   401
                   4.0e-39
E value
                   100
Match length
                   75
% identity
                   (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   210335
Seq. No.
                   LIB3135-055-Q1-K1-D9
Seq. ID
Method
                   BLASTN
                   q2687434
NCBI GI
BLAST score
                   166
                   2.0e-88
E value
                   326
Match length
                   88
% identity
                   Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
Seq. No.
                   210336
```

29090

LIB3135-055-Q1-K1-E1

BLASTX

g629483



```
BLAST score
                  3.0e-14
E value
Match length
                  71
                  56
% identity
                  gene 1-Sc3 protein - European white birch
NCBI Description
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
Seq. No.
                  210337
                  LIB3135-055-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  q430947
NCBI GI
                  336
BLAST score
                  1.0e-31
E value
                  90
Match length
                  78
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  210338
Seq. ID
                  LIB3135-055-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1711355
BLAST score
                  248
                  3.0e-21
E value
Match length
                  83
                  60
% identity
                  SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
NCBI Description
                  >gi_421786_pir__S34678 short-chain alcohol dehydrogenase -
                  Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain
                  alcohol dehydrogenase [Picea abies]
                  210339
Seq. No.
Seq. ID
                  LIB3135-055-Q1-K1-E2
                  BLASTX
Method
NCBI GI
                  q4099914
BLAST score
                   305
                  7.0e-28
E value
Match length
                  109
                   58
% identity
                   (U91857) ethylene-responsive element binding protein
NCBI Description
                  homolog [Stylosanthes hamata]
                   210340
Seq. No.
                  LIB3135-055-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g755150
BLAST score
                   474
                   1.0e-47
E value
```

Match length 130 % identity 78

(U13670) vacuolar H+-ATPase proteolipid (16 kDa) subunit NCBI Description

[Gossypium hirsutum]

Seq. No. 210341

Seq. ID LIB3135-055-Q1-K1-E5

```
BLASTX
Method
                  q3036816
NCBI GI
                   254
BLAST score
                  6.0e-22
E value
Match length
                  113
                   45
% identity
                  (AL022373) myosin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210342
                  LIB3135-055-Q1-K1-E9
Seq. ID
Method
                  BLASTN
                   g1399575
NCBI GI
BLAST score
                   45
                   4.0e-16
E value
                   69
Match length
                   91
% identity
                   Trollius laxus nuclear 26S ribosomal RNA gene, partial
NCBI Description
                   sequence
                   210343
Seq. No.
```

NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

210344 Seq. No. LIB3135-055-Q1-K1-F10 Seq. ID BLASTX Method NCBI GI q2493482 141 BLAST score 1.0e-08 E value Match length 94 38 % identity

NCBI Description GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)

(GLYCEROKINASE) (GK) >gi 1399490 (U49666) glycerol kinase

[Pseudomonas aeruginosa]

Seq. No. 210345

Seq. ID LIB3135-055-Q1-K1-F11

Method BLASTX
NCBI GI g2462762
BLAST score 272
E value 4.0e-24
Match length 67
% identity 78

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 210346

Seq. ID LIB3135-055-Q1-K1-F12

Method BLASTX
NCBI GI g4097579
BLAST score 598



E value 3.0e-62 Match length 133 % identity 83

NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 210347

Seq. ID LIB3135-055-Q1-K1-F5

Method BLASTX
NCBI GI g445613
BLAST score 363
E value 1.0e-34
Match length 141
% identity 49

NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 210348

Seq. ID LIB3135-055-Q1-K1-F6

Method BLASTX
NCBI GI g122770
BLAST score 586
E value 9.0e-61
Match length 137
% identity 84

NCBI Description HEMOGLOBIN II >gi\_99509\_pir\_\_S13378 hemoglobin II - swamp

oak >gi\_18015\_emb\_CAA37898\_ (X53950) hemoglobin [Casuarina

glauca]

Seq. No. 210349

Seq. ID LIB3135-055-Q1-K1-F7

Method BLASTX
NCBI GI g3746059
BLAST score 548
E value 2.0e-56
Match length 139
% identity 68

NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi 4432812 gb\_AAD20662\_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 210350

Seq. ID LIB3135-055-Q1-K1-G4

Method BLASTX
NCBI GI g4539335
BLAST score 357
E value 5.0e-34
Match length 118
% identity 54

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 210351

Seq. ID LIB3135-055-Q1-K1-G9

Method BLASTX
NCBI GI g2662415
BLAST score 175
E value 1.0e-12
Match length 53
% identity 57



```
(U97494) metallothionein-like protein [Prunus armeniaca]
NCBI Description
                  210352
Seq. No.
                  LIB3135-055-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g4240207
NCBI GI
BLAST score
                  186
                  7.0e-14
E value
                  99
Match length
                  36
% identity
                  (AB020666) KIAA0859 protein [Homo sapiens]
NCBI Description
                  210353
Seq. No.
Seq. ID
                  LIB3135-055-Q1-K1-H10
                  BLASTX
Method
                  g4406759
NCBI GI
                  198
BLAST score
                  3.0e-15
E value
                  106
Match length
                  42
% identity
                  (AC006836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210354
                  LIB3135-055-Q1-K1-H3
Seq. ID
                  BLASTX
Method
                  q3377797
NCBI GI
BLAST score
                   423
                  1.0e-41
E value
                  133
Match length
                   68
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                   210355
Seq. No.
                  LIB3135-055-Q1-K1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g421810
                   261
BLAST score
E value
                   6.0e-23
                   51
Match length
                   94
% identity
                   acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor -
NCBI Description
                   cucumber
                   210356
Seq. No.
Seq. ID
                   LIB3135-055-Q1-K1-H5
                   BLASTX
Method
                   g3063698
NCBI GI
BLAST score
                   150
```

1.0e-14 E value Match length 94 51 % identity

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description



```
210357
Seq. No.
                  LIB3135-056-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                   g1514643
NCBI GI
BLAST score
                   362
                   3.0e-35
E value
                  124
Match length
                  38
% identity
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
                  210358
Seq. No.
                  LIB3135-056-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                   q4218951
NCBI GI
                   282
BLAST score
                   3.0e-25
E value
Match length
                   61
% identity
                   89
                   (AF081796) fructose-1,6-bisphosphatase precursor [Brassica
NCBI Description
                   210359
Seq. No.
                   LIB3135-056-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   q2618721
NCBI GI
                   169
BLAST score
                   4.0e-12
E value
Match length
                   59
% identity
                   64
                  (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                   210360
Seq. No.
                   LIB3135-056-Q1-K1-A5
Seq. ID
Method
                   BLASTX
                   g2961300
NCBI GI
                   186
BLAST score
                   6.0e-14
E value
Match length
                   41
                   95
% identity
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
                   210361
Seq. No.
Seq. ID
                   LIB3135-056-Q1-K1-A8
                   BLASTX
Method
                   g3123264
NCBI GI
BLAST score
                   366
                   3.0e-35
E value
Match length
                   83
                   86
% identity
                  60S RIBOSOMAL PROTEIN L27 >qi 2244857 emb CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   210362
Seq. No.
Seq. ID
                   LIB3135-056-Q1-K1-B11
                   BLASTX
Method
NCBI GI
                   g2160158
```

29095

192

BLAST score



E value 4.0e-15 Match length 42 % identity 86

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb EF1G XENLA). ESTs gb\_T20564,gb\_T45940,gb\_T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No. 210363

Seq. ID LIB3135-056-Q1-K1-B5

Method BLASTN
NCBI GI g434344
BLAST score 44
E value 1.0e-15
Match length 64

% identity 92
NCBI Description A.thaliana (Columbia) mRNA for S18 ribosomal protein

(641bp)

Seq. No. 210364

Seq. ID LIB3135-056-Q1-K1-B6

Method BLASTX
NCBI GI g4580523
BLAST score 192
E value 3.0e-16
Match length 120
% identity 42

NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No. 210365

Seq. ID LIB3135-056-Q1-K1-C11

Method BLASTX
NCBI GI g2462753
BLAST score 521
E value 3.0e-53
Match length 125
% identity 74

NCBI Description (AC002292) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 210366

Seq. ID LIB3135-056-Q1-K1-C12

Method BLASTX
NCBI GI g2914701
BLAST score 462
E value 3.0e-46
Match length 105
% identity 84

NCBI Description (AC003974) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No. 210367

Seq. ID LIB3135-056-Q1-K1-C4

Method BLASTX
NCBI GI g2352828
BLAST score 225
E value 1.0e-18
Match length 94
% identity 35



(AF009228) NaCl-inducible Ca2+-binding protein [Arabidopsis NCBI Description thaliana]

210368 Seq. No.

LIB3135-056-Q1-K1-C9 Seq. ID

Method BLASTX g2653446 NCBI GI BLAST score 281 2.0e-25 E value Match length 57

% identity (AB009077) proton pyrophosphatase [Vigna radiata] NCBI Description

210369 Seq. No.

LIB3135-056-Q1-K1-D12 Seq. ID

95

Method BLASTX NCBI GI g399414 378 BLAST score 1.0e-36 E value Match length 84 % identity 90

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_322865\_pir\_\_JC1454 translation elongation factor eEF-1

alpha chain -  $\overline{wh}eat > gi_170776$  (M90077) translation elongation factor 1 alpha-subunit [Triticum aestivum]

>gi 949878 emb CAA90651 (Z50789) elongation factor 1-alpha

[Hordeum vulgare]

210370 Seq. No.

Seq. ID LIB3135-056-Q1-K1-D3

BLASTX Method NCBI GI g3193303 BLAST score 206 2.0e-16 E value Match length 102 40 % identity

(AF069298) similar to several proteins containing a tandem NCBI Description

 $\hbox{\tt repeat region such as Plasmodium falciparum GGM tandem}$ repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

210371 Seq. No.

LIB3135-056-Q1-K1-D4 Seq. ID

BLASTX Method g4539009 NCBI GI 396 BLAST score 9.0e-39 E value 97 Match length 73 % identity

(AL049481) putative protein [Arabidopsis thaliana] NCBI Description

210372 Seq. No.

LIB3135-056-Q1-K1-D7 Seq. ID

Method BLASTX NCBI GI q2688619 BLAST score 176 7.0e-13 E value



Match length 107 % identity 32

NCBI Description (AE001169) conserved hypothetical protein [Borrelia

burgdorferi]

Seq. No.

210373

BLASTX

456

g167381

Seq. ID

LIB3135-056-Q1-K1-D8

Method NCBI GI BLAST score

E value 1.0e-49 Match length 105 % identity 95

NCBI Description (M19387) storage protein [Gossypium hirsutum]

>gi 226555 prf 1601521E Lea D-19 gene [Saguinus oedipus]

Seq. No.

210374

Seq. ID

LIB3135-056-Q1-K1-E3

Method BLASTX
NCBI GI g3759184
BLAST score 370
E value 1.0e-35
Match length 109
% identity 64

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No.

210375

Seq. ID

LIB3135-056-Q1-K1-E5

Method BLASTX
NCBI GI g1706547
BLAST score 508
E value 1.0e-51
Match length 137
% identity 73

NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM

PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi\_2129912\_pir\_\_S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi\_1184668 (U22147)

beta-1,3-qlucanase [Hevea brasiliensis]

Seq. No.

210376

Seq. ID

LIB3135-056-Q1-K1-E6

Method BLASTX
NCBI GI g114093
BLAST score 253
E value 1.0e-21
Match length 57
% identity 84

NCBI Description RAS-RELATED PROTEIN ARA-5 >gi\_217841\_dbj\_BAA00832\_ (D01027)

small GTP-binding protein [Arabidopsis thaliana]

Seq. No.

210377

Seq. ID

LIB3135-056-Q1-K1-E8

Method BLASTX NCBI GI g3033375 BLAST score 245

```
E value
                  124
Match length
% identity
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   210378
Seq. No.
                  LIB3135-056-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3953466
BLAST score
                   441
E value
                   9.0e-59
Match length
                   149
                   72
% identity
NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana]
                   210379
Seq. No.
                   LIB3135-056-Q1-K1-F1
Seq. ID
                   BLASTX
Method
```

 Seq. No.
 210379

 Seq. ID
 LIB3135-056-Q1-K1-F1

 Method
 BLASTX

 NCBI GI
 g1361991

 BLAST score
 361

 E value
 1.0e-34

 Match length
 130

% identity 66
NCBI Description homeotic protein ATK1 - Arabidopsis thaliana

>gi 984046 emb CAA57122 (X81354) ATK1 [Arabidopsis
thaliana] >gi 984048 emb CAA57121 (X81353) ATK1

[Arabidopsis thaliana]

 Seq. No.
 210380

 Seq. ID
 LIB3135-056-Q1-K1-F11

 Method
 BLASTX

 NCBI GI
 g3319774

 BLAST score
 179

NCBI GI g3319774
BLAST score 179
E value 4.0e-13
Match length 39
% identity 87

NCBI Description (Y16228) TOM7 protein [Solanum tuberosum]

Seq. No. 210381

Seq. ID LIB3135-056-Q1-K1-F2

Method BLASTX
NCBI GI g267082
BLAST score 538
E value 2.0e-55
Match length 104
% identity 94

NCBI Description TUBULIN BETA-8 CHAIN >gi\_320189\_pir\_JQ1592 tubulin beta-8

chain - Arabidopsis thalīana >gī\_166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

Seq. No. 210382

Seq. ID LIB3135-056-Q1-K1-F3

Method BLASTX
NCBI GI g529353
BLAST score 244
E value 9.0e-21

```
113
```

Match length 113 % identity 46

NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 210383

Seq. ID LIB3135-056-Q1-K1-F5

Method BLASTX
NCBI GI g2827139
BLAST score 182
E value 3.0e-27
Match length 132
% identity 54

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi\_4049343\_emb\_CAA22568\_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 210384

Seq. ID LIB3135-056-Q1-K1-G3

Method BLASTX
NCBI GI g131772
BLAST score 352
E value 2.0e-33
Match length 87
% identity 84

NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)

>gi\_82723\_pir\_\_A30097 ribosomal protein S14 (clone MCH1) -

maize

Seq. No. 210385

Seq. ID LIB3135-056-Q1-K1-G5

Method BLASTN
NCBI GI g2924257
BLAST score 90
E value 4.0e-43
Match length 249
% identity 91

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 210386

Seq. ID LIB3135-056-Q1-K1-G7

Method BLASTX
NCBI GI g549063
BLAST score 330
E value 5.0e-31
Match length 81
% identity 78

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi 303835 dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 210387

Seq. ID LIB3135-056-Q1-K1-G9

Method BLASTX
NCBI GI g3341490
BLAST score 538



```
E value
                  123
Match length
                  92
% identity
                  (AJ007705) phospoenolpyruvate carboxylase [Triticum
NCBI Description
                  aestivum]
                  210388
Seq. No.
                  LIB3135-056-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                  g3023685
NCBI GI
                  456
BLAST score
                  9.0e-46
E value
                  97
Match length
                  92
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                  >gi 1041245 emb CAA63121 (X92377) enolase [Alnus
                  glutinosa]
                  210389
Seq. No.
Seq. ID
                  LIB3135-056-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g729985
BLAST score
                  201
                  1.0e-15
E value
Match length
                  70
                  57
% identity
                  PROCESSING ALPHA-1,2-MANNOSIDASE (ALPHA-1,2-MANNOSIDASE 1B)
NCBI Description
                  >gi 474278 (U03458) alpha-mannosidase [Mus musculus]
                  >gi 3335696 (AF078095) alpha 1,2-mannosidase IB [Mus
                  musculus]
                  210390
Seq. No.
                  LIB3135-057-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q417148
BLAST score
                   346
E value
                   8.0e-33
                  109
Match length
                   61
% identity
                  PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
NCBI Description
                   (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                   soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.
                   210391
Seq. ID
                  LIB3135-057-Q1-K1-A6
Method
                   BLASTX
```

q4512661 NCBI GI 182 BLAST score 7.0e-14 E value 55 Match length % identity 58

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 4544468 gb AAD22375.1 AC006580 7 (AC006580) putative

DNA binding protein [Arabidopsis thaliana]

Seq. No. 210392

Seq. ID

```
LIB3135-057-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  g3122071
NCBI GI
                  563
BLAST score
                  4.0e-58
E value
Match length
                  111
                  96
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi 2130148 pir S66339 translation elongation factor eEF-1
                  alpha chain - maize >gi 1321656_dbj_BAA08249_ (D45408)
                  alpha subunit of tlanslation elongation factor 1 [Zea mays]
                  210393
Seq. No.
                  LIB3135-057-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                  g3386615
NCBI GI
                  600
BLAST score
                  2.0e-62
E value
                  128
Match length
                  88
% identity
                   (AC004665) putative phosphomannomutase [Arabidopsis
NCBI Description
                  thaliana]
                  210394
Seq. No.
                  LIB3135-057-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  q2244993
NCBI GI
                   252
BLAST score
                  1.0e-21
E value
                   90
Match length
                   52
% identity
                   (Z97341) similarity to AMP-activated protein kinase beta
NCBI Description
                   [Arabidopsis thaliana]
                   210395
Seq. No.
Seq. ID
                   LIB3135-057-Q1-K1-B4
                   BLASTX
Method
                   g2980793
NCBI GI
                   402
BLAST score
                   2.0e-39
E value
Match length
                   94
                   77
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210396
Seq. ID
                   LIB3135-057-Q1-K1-B6
Method
                   BLASTX
                   q2462761
NCBI GI
BLAST score
                   206
                   7.0e-17
E value
                   66
Match length
% identity
                   59
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   210397
```

29102

LIB3135-057-Q1-K1-B7

```
BLASTX
Method
                  q2129742
NCBI GI
BLAST score
                  281
                  5.0e-25
E value
                  77
Match length
% identity
                  66
                  stress-induced protein OZI1 precursor - Arabidopsis
NCBI Description
                  thaliana >qi 790583 (U20347) mRNA corresponding to this
                  gene accumulates in response to ozone stress and pathogen
                   (bacterial) infection; putative pathogenesis-related
                  protein [Arabidopsis thaliana] >gi 2252869 (AF013294) No
                  definition line found [Arabidopsis thaliana]
                  210398
Seq. No.
                  LIB3135-057-Q1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2493738
BLAST score
                  230
                  3.0e-19
E value
Match length
                  102
                   42
% identity
                  ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT
NCBI Description
                   (ENDOPEPTIDASE CLP) >gi 1377852 (U55059) ClpP [Yersinia
                   enterocolitica]
                  210399
Seq. No.
                  LIB3135-057-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                   g2244781
NCBI GI
                   218
BLAST score
                   9.0e-18
E value
                   74
Match length
% identity
                   30
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   210400
Seq. No.
                   LIB3135-057-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   q3980264
NCBI GI
                   525
BLAST score
                   1.0e-53
E value
                   110
Match length
                   89
% identity
                  (AJ011383) 20S proteasome beta subunit [Cicer arietinum]
NCBI Description
                   210401
Seq. No.
                   LIB3135-057-Q1-K1-D1
Seq. ID
```

Method BLASTX
NCBI GI g541816
BLAST score 376
E value 3.0e-36
Match length 85
% identity 76

NCBI Description protein kinase - common ice plant >gi\_457689\_emb\_CAA82990\_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 210402

```
LIB3135-057-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g3851636
NCBI GI
                  269
BLAST score
                  3.0e-24
E value
                  63
Match length
                  79
% identity
                  (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                  210403
Seq. No.
                  LIB3135-057-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  q1350984
NCBI GI
                  138
BLAST score
                  7.0e-09
E value
Match length
                  69
                   42
% identity
                  40S RIBOSOMAL PROTEIN S3A >gi 469248 (L31645) ribosomal
NCBI Description
                  protein S3a [Helianthus annuus]
Seq. No.
                   210404
                  LIB3135-057-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  q417073
NCBI GI
                   404
BLAST score
                   1.0e-39
E value
Match length
                   103
                   72
% identity
                  GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
NCBI Description
                   >gi 484529 pir JQ1977 glutamate synthase (NADH) (EC
                   1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate
                   synthase [Medicago sativa]
                   210405
Seq. No.
                   LIB3135-057-Q1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3603230
                   275
BLAST score
                   2.0e-24
E value
                   129
Match length
                   41
% identity
                   (AF026850) cytochrome oxidase assembly factor [Homo
NCBI Description
                   sapiens]
                   210406
Seq. No.
Seq. ID
                   LIB3135-057-Q1-K1-D9
```

Method BLASTX
NCBI GI g3122326
BLAST score 208
E value 5.0e-17
Match length 59
% identity 66

NCBI Description LEC14B PROTEIN >gi\_1181604\_dbj\_BAA11768\_ (D83074) LEC14B

protein [Lithospermum erythrorhizon]

Seq. No. 210407



LIB3135-057-Q1-K1-E12 Seq. ID BLASTX Method g1076627 NCBI GI 147 BLAST score 7.0e-10 E value 40 Match length % identity inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco NCBI Description >gi 790479 emb\_CAA58701 (X83730) inorganic pyrophosphatase [Nicotiana tabacum] 210408 Seq. No. LIB3135-057-Q1-K1-E5 Seq. ID BLASTX Method g2554835 NCBI GI 398 BLAST score 6.0e-39 E value 108 Match length % identity 72 Chain I, Acetohydroxy Acid Isomeroreductase Complexed With NCBI Description Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi 2554836 pdb\_1YVE\_J Chain J, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi 2554837 pdb 1YVE K Chain K, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi 2554838 pdb 1YVE L Chain L, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) 210409 Seq. No. Seq. ID LIB3135-057-Q1-K1-E8 BLASTXMethod g167367 NCBI GI BLAST score 257 1.0e-22 E value 86 Match length 62 % identity (L08199) peroxidase [Gossypium hirsutum] NCBI Description Seq. No. 210410 Seq. ID LIB3135-057-Q1-K1-E9 BLASTX Method q4544399 NCBI GI BLAST score 521 3.0e-53 E value 138 Match length 71 % identity

(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description

thaliana]

210411 Seq. No.

Seq. ID LIB3135-057-Q1-K1-F11

Method BLASTX NCBI GI g4544436



```
BLAST score
                  1.0e-17
E value
                  132
Match length
                  33
% identity
                  (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,
NCBI Description
                  3' partial [Arabidopsis thaliana]
                  210412
Seq. No.
                  LIB3135-057-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g2062164
NCBI GI
                  282
BLAST score
                  3.0e-25
E value
                  100
Match length
                  19
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  210413
Seq. No.
                  LIB3135-057-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129755
BLAST score
                  384
                  4.0e-37
E value
                  121
Match length
                  70
% identity
                  tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis
NCBI Description
                  thaliana >gi_619753 (U18993) tryptophan synthase alpha
                  chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp
                  synthase:SUBUNIT=alpha [Arabidopsis thaliana]
                  210414
Seq. No.
                  LIB3135-057-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g3785975
NCBI GI
                   233
BLAST score
                  1.0e-19
E value
                   53
Match length
                   89
% identity
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   210415
Seq. No.
                   LIB3135-057-Q1-K1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1143427
BLAST score
                   439
                   1.0e-43
E value
Match length
                   114
```

77 % identity

(X73961) heat shock protein 70 [Cucumis sativus] NCBI Description

Seq. No. 210416

LIB3135-057-Q1-K1-G3 Seq. ID

BLASTX Method NCBI GI g3043415 BLAST score 525 E value 8.0e-54



96

58

hirsutum]

Match length

NCBI Description

% identity

```
Match length
% identity
                  94
                  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
                  210417
Seq. No.
                  LIB3135-057-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  g3023190
NCBI GI
BLAST score
                  502
                  5.0e-51
E value
Match length
                  132
% identity
                  74
                  14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685)
NCBI Description
                  14-3-3 protein [Solanum tuberosum]
                  210418
Seq. No.
                  LIB3135-057-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  q417739
NCBI GI
                  280
BLAST score
                  7.0e-25
E value
                  73
Match length
                  75
% identity
                  MITOCHONDRIAL RIBOSOMAL PROTEIN S19 >gi 319911 pir R3PJ19
NCBI Description
                  ribosomal protein S19 - garden petunia mitochondrion
Seq. No.
                   210419
                   LIB3135-057-Q1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2829205
BLAST score
                   72
E value
                   3.0e-32
Match length
                   273
% identity
                   18
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                   precursor (PRP) mRNA, complete cds
                   210420
Seq. No.
                   LIB3135-057-Q1-K1-H9
Seq. ID
Method
                   BLASTX
                   g1208498
NCBI GI
                   140
BLAST score
                   4.0e-09
E value
Match length
                   54
                   59
% identity
                  (D38126) EREBP-2 [Nicotiana tabacum]
NCBI Description
                   210421
Seq. No.
                   LIB3135-058-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g1469930
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
```

29107

(U48777) fiber-specific acyl carrier protein [Gossypium

% identity

NCBI Description

69



```
210422
Seq. No.
Seq. ID
                  LIB3135-058-Q1-K1-A4
                  BLASTX
Method
NCBI GI
                  g3153902
                  568
BLAST score
                  1.0e-58
E value
                  124
Match length
                  88
% identity
NCBI Description (AF066076) 14-3-3-like protein [Helianthus annuus]
Seq. No.
                  210423
                  LIB3135-058-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  g3135269
NCBI GI
                  245
BLAST score
                  8.0e-21
E value
                  146
Match length
                  44
% identity
                  (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210424
                  LIB3135-058-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  q1172568
NCBI GI
                  235
BLAST score
                  1.0e-19
E value
                  97
Match length
                  51
% identity
                  LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE
NCBI Description
                   (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (PTPASE)
                   (SMALL TYROSINE PHOSPHATASE) >gi 1076916 pir_A55446
                  protein-tyrosine-phosphatase (EC 3.1.3.48), Tow molecular
                  weight - fission yeast (Schizosaccharomyces pombe)
                  >qi 602992 (L33929) low Mr protein tyrosine phosphatase
                   [Schizosaccharomyces pombe]
                  210425
Seq. No.
Seq. ID
                  LIB3135-058-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3953471
                  162
BLAST score
E value
                   4.0e-11
Match length
                   41
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   210426
Seq. No.
                  LIB3135-058-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g416652
BLAST score
                   431
                   1.0e-42
E value
Match length
                   108
```

PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN

PCNT107) >gi 19793 emb\_CAA39707\_ (X56266) auxin-induced



## protein [Nicotiana tabacum]

```
210427
Seq. No.
                  LIB3135-058-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3420982
BLAST score
                  165
E value
                  2.0e-11
Match length
                  94
                  41
% identity
                   (Z97628) Similarity to Brugia peptidylprolyl isomerase
NCBI Description
                   (TR:G984562) [Caenorhabditis elegans]
                  >qi 3876969 emb CAB03088 (Z81080) Similarity to Brugia
                  peptidylprolyl isomerase (TR:G984562) [Caenorhabditis
                  elegans]
                   210428
Seq. No.
                  LIB3135-058-Q1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q585973
BLAST score
                   149
                   2.0e-09
E value
Match length
                   110
% identity
                  FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC
NCBI Description
                   2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823)
                   fructokinase [Solanum tuberosum] >gi 1095321 prf 2108342A
                   fructokinase [Solanum tuberosum]
                   210429
Seq. No.
                   LIB3135-058-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3334146
BLAST score
                   613
                   5.0e-64
E value
Match length
                   130
% identity
                   85
                  ENDOCHITINASE 2 PRECURSOR >gi 1791007 (U78888) class I
NCBI Description
                   endochitinase [Gossypium hirsutum]
                   210430
Seq. No.
                   LIB3135-058-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g4456760
NCBI GI
                   373
BLAST score
                   8.0e-36
E value
Match length
                   80
% identity
                   74
                  (AJ000692) osmotin-like protein [Quercus suber]
NCBI Description
                   210431
Seq. No.
Seq. ID
                   LIB3135-058-Q1-K1-C10
                   BLASTX
Method
                   g2191150
NCBI GI
BLAST score
                   426
```

29109

5.0e-42

100

E value

Match length



% identity (AF007269) similar to mitochondrial carrier family NCBI Description [Arabidopsis thaliana] 210432 Seq. No. LIB3135-058-Q1-K1-C12 Seq. ID Method BLASTX NCBI GI g21839 732 BLAST score E value 7.0e-78 Match length 149 % identity 91 NCBI Description (X57952) phosphoribulokinase [Triticum aestivum] 210433 Seq. No. LIB3135-058-Q1-K1-C2 Seq. ID Method BLASTX NCBI GI g2494076 BLAST score 691 E value 4.0e-73 Match length 138 92 % identity NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE NCBI Description (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi\_1842115 (U87848) non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia] 210434 Seq. No. LIB3135-058-Q1-K1-C3 Seq. ID BLASTX Method NCBI GI g4235093 226 BLAST score 2.0e-18 E value 125 Match length % identity 42 (AF108944) beta-xylosidase [Aspergillus niger] NCBI Description 210435 Seq. No. LIB3135-058-Q1-K1-C4 Seq. ID BLASTX Method NCBI GI g461944 BLAST score 567 2.0e-58 E value Match length 151 74 % identity DNAJ PROTEIN HOMOLOG (DNAJ-1) >gi 18260 emb CAA47925 NCBI Description (X67695) cs DnaJ-1 [Cucumis sativus]

210436 Seq. No.

Seq. ID LIB3135-058-Q1-K1-C6

Method BLASTX NCBI GI g3132696 BLAST score 372 7.0e-36 E value Match length 96



% identity (AF061962) SAR DNA-binding protein-1 [Pisum sativum] NCBI Description 210437 Seq. No. LIB3135-058-Q1-K1-C7 Seq. ID Method BLASTX NCBI GI g3646373 BLAST score 685 2.0e-72 E value Match length 136 % identity (AJ011078) RGP1 protein [Oryza sativa] NCBI Description 210438 Seq. No. LIB3135-058-Q1-K1-D10 Seq. ID Method BLASTN NCBI GI g3869069 BLAST score 33 6.0e-09 E value Match length 190 83 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MEB5, complete sequence [Arabidopsis thaliana] 210439 Seq. No. Seq. ID LIB3135-058-Q1-K1-D12 Method BLASTX NCBI GI q3327204 BLAST score 493 E value 7.0e-50 Match length 145 63 % identity (AB014595) KIAA0695 protein [Homo sapiens] NCBI Description Seq. No. 210440 LIB3135-058-Q1-K1-D3 Seq. ID BLASTX Method q4105683 NCBI GI BLAST score 559 1.0e-57 E value 134 Match length 72 % identity (AF049892) unknown [Oryza sativa] >gi\_4105692 (AF050155) NCBI Description embryo-specific protein [Oryza sativa subsp. indica] 210441 Seq. No. LIB3135-058-Q1-K1-D6 Seq. ID Method BLASTX NCBI GI g3413716 157 BLAST score

2.0e-10 E value Match length 99 12 % identity

(AC004747) unknown protein [Arabidopsis thaliana] NCBI Description

>qi 3643589 (AC005395) unknown protein [Arabidopsis

thaliana]



```
Seq. No.
                  LIB3135-058-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172811
                  731
BLAST score
                  9.0e-78
E value
Match length
                  143
% identity
                  95
                  60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                  >gi 1076751_pir__S49575 ribosomal protein L10.e, cytosolic
                  - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor
                  suppresser [Oryza sativa]
                  210443
Seq. No.
                  LIB3135-058-Q1-K1-E6
Seq. ID
                  BLASTN
Method
                  q1199773
NCBI GI
BLAST score
                  35
                  4.0e-10
E value
Match length
                  55
                  91
% identity
NCBI Description Populus nigra gene for extensin like protein, complete cds
                  210444
Seq. No.
                  LIB3135-058-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                   g2765837
NCBI GI
                   223
BLAST score
                   3.0e-18
E value
                   99
Match length
                   52
% identity
                  (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210445
                   LIB3135-058-Q1-K1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2924784
                   142
BLAST score
                   2.0e-09
E value
Match length
                   70
% identity
                   (AC002334) similar to jasmonate inducible protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   210446
                   LIB3135-058-Q1-K1-F10
Seq. ID
Method
                   BLASTN
                   g2829205
```

NCBI GI BLAST score 110 E value 7.0e-55 Match length 370 % identity 16

Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein NCBI Description

precursor (PRP) mRNA, complete cds

210447 Seq. No.

LIB3135-058-Q1-K1-F2 Seq. ID



```
Method
                  BLASTX
                  g541954
NCBI GI
                  506
BLAST score
E value
                  2.0e-51
Match length
                  136
                  75
% identity
                  ubiquitin extension protein - white lupine
NCBI Description
                  >gi 438111 emb CAA80334 (Z22613) ubiquitin extension
                  protein [Lupinus albus]
Seq. No.
                  210448
Seq. ID
                  LIB3135-058-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2352084
BLAST score
                  159
E value
                  8.0e-11
Match length
                  53
% identity
                   62
                  (U96613) serine/threonine kinase [Arabidopsis thaliana]
NCBI Description
                  210449
Seq. No.
                  LIB3135-058-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q131772
BLAST score
                   502
                   6.0e-51
E value
                   125
Match length
                   83
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                   maize
                   210450
Seq. No.
                   LIB3135-058-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                   g3122914
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
Match length
                   84
% identity
                   50
                   VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
NCBI Description
                   >gi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis
                   thaliana]
                   210451
Seq. No.
                   LIB3135-058-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4263704
                   292
BLAST score
                   3.0e-26
E value
                   118
Match length
                   54
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
```

29113

210452

LIB3135-058-Q1-K1-G2

Seq. No. Seq. ID

BLAST score

648

```
Method
                  q2911054
NCBI GI
BLAST score
                  219
                  9.0e-18
E value
                  128
Match length
                  44
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                  210453
Seq. No.
                  LIB3135-058-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4388717
BLAST score
                   603
E value
                  8.0e-63
Match length
                  133
                  83
% identity
                   (AC006413) putative nuclear phosphoprotein (contains
NCBI Description
                  multiple TPR repeats prosite:QDOC50005) [Arabidopsis
                  thaliana]
Seq. No.
                   210454
Seq. ID
                  LIB3135-058-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1477428
BLAST score
                   689
E value
                   7.0e-73
Match length
                   132
                   97
% identity
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
                   210455
Seq. No.
                   LIB3135-058-Q1-K1-G9
Seq. ID
Method
                   BLASTX
                   g1710590
NCBI GI
BLAST score
                   183
                   2.0e-13
E value
                   92
Match length
                   47
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN P1 (L12) >gi_1209701 (U40147)
NCBI Description
                   ribosomal protein L12 [Zea mays]
                   210456
Seq. No.
                   LIB3135-058-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   g3885517
NCBI GI
                   244
BLAST score
                   1.0e-20
E value
                   71
Match length
                   59
% identity
                   (AF084203) similar to Nicotiana HR lesion-inducing ORF
NCBI Description
                   [Medicago sativa]
                   210457
Seq. No.
                   LIB3135-058-Q1-K1-H10
Seq. ID
                   BLASTX
Method
                   g1169009
NCBI GI
```



E value 4.0e-68
Match length 138
% identity 84

NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi\_542009\_pir\_S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi\_437777\_emb\_CAA52814\_ (X74814) O-Methyltransferase

[Eucalyptus gunnii]

Seq. No. 210458

Seq. ID LIB3135-058-Q1-K1-H2

Method BLASTX
NCBI GI g3123745
BLAST score 306
E value 4.0e-28
Match length 113
% identity 49

NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 210459

Seq. ID LIB3135-058-Q1-K1-H7

Method BLASTX
NCBI GI g3135693
BLAST score 295
E value 1.0e-26
Match length 83
% identity 63

NCBI Description (AF064201) glutathione S-transferase [Gossypium hirsutum]

Seq. No. 210460

Seq. ID LIB3135-059-Q1-K1-A12

Method BLASTX
NCBI GI g4262236
BLAST score 195
E value 8.0e-21
Match length 94
% identity 51

NCBI Description (AC006200) putative ribose 5-phosphate isomerase

[Arabidopsis thaliana]

Seq. No. 210461

Seq. ID LIB3135-059-Q1-K1-B10

Method BLASTX
NCBI GI g4006859
BLAST score 200
E value 2.0e-15
Match length 84
% identity 44

NCBI Description (299707) putative protein [Arabidopsis thaliana]

Seq. No. 210462

Seq. ID LIB3135-059-Q1-K1-B11

Method BLASTX
NCBI GI g3915008
BLAST score 339
E value 5.0e-32



Match length 70 % identity 91

NCBI Description SUPEROXIDE DISMUTASE, CHLOROPLAST [CU-ZN] PRECURSOR >gi 1805502\_dbj\_BAA12745\_ (D85239) superoxide dismutase

precusor [Oryza sativa]

Seq. No. 210463

Seq. ID LIB3135-059-Q1-K1-C12

Method BLASTX
NCBI GI g232278
BLAST score 271
E value 9.0e-33
Match length 127
% identity 59

NCBI Description CHLOROPLAST SMALL HEAT SHOCK PROTEIN PRECURSOR

>gi\_100397\_pir\_\_S16004 heat shock protein 21 - garden

petunia >gi 14158 emb CAA38037 (X54103) heat shock protein

[Petunia x hybrida]

Seq. No. 210464

Seq. ID LIB3135-059-Q1-K1-E10

Method BLASTX
NCBI GI g1076627
BLAST score 677
E value 2.0e-71
Match length 139
% identity 96

NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco

>gi 790479 emb CAA58701 (X83730) inorganic pyrophosphatase

[Nicotiana tabacum]

Seq. No. 210465

Seq. ID LIB3135-059-Q1-K1-E11

Method BLASTX
NCBI GI g1458245
BLAST score 233
E value 2.0e-19
Match length 113
% identity 46

NCBI Description (U64834) coded for by C. elegans cDNA cm17a1; coded for by

C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis

elegans]

Seq. No. 210466

Seq. ID LIB3135-059-Q1-K1-E9

Method BLASTX
NCBI GI g2293566
BLAST score 723
E value 7.0e-77
Match length 140
% identity 99

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 210467

Seq. ID LIB3135-059-Q1-K1-F10

Method BLASTX

```
g4204575
NCBI GI
                  143
BLAST score
                  2.0e-09
E value
                  47
Match length
                  55
% identity
NCBI Description (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
                  210468
Seq. No.
                  LIB3135-059-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  g3123264
NCBI GI
BLAST score
                  421
                  1.0e-41
E value
Match length
                  88
                  89
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi_2244857 emb_CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                  210469
Seq. No.
                  LIB3135-059-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3063396
BLAST score
                   582
E value
                   3.0e-60
Match length
                   128
                   84
% identity
NCBI Description (AB012947) vcCyP [Vicia faba]
                   210470
Seq. No.
                   LIB3135-059-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2262105
BLAST score
                   496
                   1.0e-50
E value
Match length
                   130
                   74
% identity
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                   210471
Seq. No.
Seq. ID
                   LIB3135-059-Q1-K1-H12
                   BLASTX
Method
                   g3759184
NCBI GI
                   339
BLAST score
                   4.0e-32
E value
                   99
Match length
                   64
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                   210472
Seq. No.
Seq. ID
                   LIB3135-059-Q1-K1-H9
                   BLASTX
Method
                   g2462762
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
                   69
Match length
```

29117

NCBI Description (AC002292) Highly similar to auxin-induced protein

74

% identity



(aldo/keto reductase family) [Arabidopsis thaliana] 210473 Seq. No. LIB3135-060-Q1-K1-A10 Seq. ID BLASTX Method NCBI GI g2462929 BLAST score 224 2.0e-18 E value 138 Match length 40 % identity (Y12295) glutathione transferase [Arabidopsis thaliana] NCBI Description 210474 Seq. No. LIB3135-060-Q1-K1-A12 Seq. ID BLASTX Method g3493172 NCBI GI 452 BLAST score 2.0e-45 E value 98 Match length 89 % identity (U89609) fiber annexin [Gossypium hirsutum] NCBI Description 210475 Seq. No. Seq. ID LIB3135-060-Q1-K1-A2 BLASTX Method g2501460 NCBI GI BLAST score 166 2.0e-11 E value Match length 124 36 % identity PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP NCBI Description (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >qi 1545952 emb CAA96580 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens] >gi 4507857 ref NP 003461.1\_pUSP7\_ Herpes virus-associated ubiquitin-specific protease 210476 Seq. No. Seq. ID LIB3135-060-Q1-K1-A5 Method BLASTX

Method BLASTX
NCBI GI g4530595
BLAST score 291
E value 2.0e-26
Match length 105
% identity 55

NCBI Description (AF132477) heme oxygenase 2 [Arabidopsis thaliana]

Seq. No. 210477

Seq. ID LIB3135-060-Q1-K1-A9

Method BLASTX
NCBI GI g72287
BLAST score 386
E value 2.0e-37
Match length 125
% identity 62

```
NCBI Description beta-globulin A precursor (clone 94) - upland cotton
                   (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
                   210478
Seq. No.
Seq. ID
                   LIB3135-060-Q1-K1-B4
                   BLASTX
Method
                   g1174411
NCBI GI
                   297
BLAST score
                   1.0e-27
E value
                   99
Match length
                   67
% identity
                   MICROSOMAL SIGNAL PEPTIDASE 18 KD SUBUNIT (SPC18)
NCBI Description
                   >qi 206978 (L11319) signal peptidase [Rattus norvegicus]
Seq. No.
                   210479
                   LIB3135-060-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g1709493
NCBI GI
                   379
BLAST score
                   1.0e-36
E value
Match length
                   93
% identity
                   70
                   OSMOTIN-LIKE PROTEIN OSML13 PRECURSOR (PA13)
NCBI Description
                   >gi_419783_pir__S30144 osmotin-like protein precursor
(clone pA13) - Commerson's wild potato
                   >qi 21195 emb CAA47601 (X67121) osmotin-like protein
                   [Solanum commersonii] >gi_296772_emb_CAA51432_ (X72928)
                   osmotin-like protein [Solanum commersonii]
                   210480
Seq. No.
Seq. ID
                   LIB3135-060-Q1-K1-B9
                   BLASTN
                   g2829205
                   78
                   9.0e-36
                   254
                   16
% identity
                   Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
```

Method NCBI GI BLAST score E value Match length

precursor (PRP) mRNA, complete cds

Seq. No. 210481

Seq. ID LIB3135-060-Q1-K1-C11

BLASTX Method NCBI GI g3914535 BLAST score 343 2.0e-32 E value Match length 113 57 % identity

60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb CAA11283\_ NCBI Description

(AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No. 210482

Seq. ID LIB3135-060-Q1-K1-C12

BLASTX Method NCBI GI q1762933 BLAST score 219

E value 3.0e-18
Match length 69
% identity 62

NCBI Description (U66263) tumor-related protein [Nicotiana tabacum]

Seq. No.

Seq. ID LIB3135-060-Q1-K1-C5

210483

Method BLASTX
NCBI GI g2739389
BLAST score 295
E value 8.0e-27
Match length 111
% identity 14

NCBI Description (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No. 210484

Seq. ID LIB3135-060-Q1-K1-C6

Method BLASTX
NCBI GI g2586087
BLAST score 130
E value 2.0e-07
Match length 103
% identity 6

NCBI Description (U72724) receptor kinase-like protein [Oryza sativa]

Seq. No. 210485

Seq. ID LIB3135-060-Q1-K1-C7

Method BLASTX
NCBI GI g3834321
BLAST score 174
E value 2.0e-12
Match length 36
% identity 94

NCBI Description (AC005679) Strong similarity to F13P17.9 gi\_3337356

transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb AC004481. [Arabidopsis

thaliana]

Seq. No. 210486

Seq. ID LIB3135-060-Q1-K1-C8

Method BLASTX
NCBI GI g3924597
BLAST score 248
E value 3.0e-21
Match length 106
% identity 49

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 210487

Seq. ID LIB3135-060-Q1-K1-D1

Method BLASTN
NCBI GI g3985957
BLAST score 52
E value 3.0e-20
Match length 92
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:





## MYN8, complete sequence [Arabidopsis thaliana]

```
210488
Seq. No.
                  LIB3135-060-Q1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g434990
BLAST score
                   35
                   3.0e-10
E value
                   52
Match length
                   93
% identity
NCBI Description O.berteriana mitochondrial trnI gene
Seq. No.
                   210489
                   LIB3135-060-Q1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1166450
BLAST score
                   257
                   3.0e-22
E value
                   55
Match length
                   85
% identity
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.
                   210490
                   LIB3135-060-Q1-K1-D8
Seq. ID
                   BLASTN
Method
                   q485861
NCBI GI
BLAST score
                   43
                   6.0e-15
E value
Match length
                   156
                   85
% identity
                   T.aestivum mitochondrial nad7 gene for NADH dehydrogenase
NCBI Description
                   subunit
                   210491
Seq. No.
                   LIB3135-060-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   q2275215
NCBI GI
                   185
BLAST score
                   8.0e-14
E value
                   116
Match length
% identity
                   34
                  (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   210492
Seq. No.
                   LIB3135-060-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g1345787
NCBI GI
BLAST score
                   511
                   2.0e-57
E value
                   135
Match length
                   90
% identity
                   CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)
NCBI Description
                   >gi 567937 dbj BAA05641_ (D26594) chalcone synthase
                   [Camellia sinensis]
```

29121

210493

LIB3135-060-Q1-K1-E3

Seq. No.

Seq. ID

Seq. ID

Method



```
BLASTX
Method
                  g2244754
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
                  111
Match length
                  35
% identity
                  (Z97335) heat shock transcription factor homolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  210494
                  LIB3135-060-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2956717
BLAST score
                  312
                  6.0e-29
E value
                  79
Match length
                  71
% identity
NCBI Description (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
                  210495
Seq. No.
                  LIB3135-060-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2673918
BLAST score
                  210
                  1.0e-16
E value
                  138
Match length
                  39
% identity
NCBI Description (AC002561) unknwon protein [Arabidopsis thaliana]
Seq. No.
                  210496
                  LIB3135-060-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172556
                   346
BLAST score
E value
                   1.0e-32
                   114
Match length
% identity
                   61
                  36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                   (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato
                   >gi 1076681 pir B55364 porin (clone pPOM 36.2) - potato
                   mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin
                   II [Solanum tuberosum]
                   210497
Seq. No.
                   LIB3135-060-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g3643607
NCBI GI
                   366
BLAST score
                   5.0e-35
E value
                   89
Match length
                   76
% identity
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                   210498
Seq. No.
```

29122

LIB3135-060-Q1-K1-F3

BLASTX

```
q3643607
NCBI GI
BLAST score
                  220
                  5.0e-18
E value
                   67
Match length
% identity
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                  210499
Seq. No.
                  LIB3135-060-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2997593
                  255
BLAST score
                   6.0e-22
E value
Match length
                  106
                   47
% identity
                  (AF020816) glucose-6-phosphate/phosphate-translocator
NCBI Description
                  precursor [Solanum tuberosum]
                   210500
Seq. No.
                  LIB3135-060-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g1173256
NCBI GI
                   266
BLAST score
E value
                   2.0e-23
Match length
                   90
                   64
% identity
                   40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   210501
Seq. No.
                   LIB3135-060-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   g3776566
NCBI GI
BLAST score
                   353
E value
                   2.0e-33
                   96
Match length
                   77
% identity
                   (AC005388) Strong similarity to histone H2A gb_AJ006768
NCBI Description
                   from Cicer arietinum. [Arabidopsis thaliana]
                   210502
Seq. No.
Seq. ID
                   LIB3135-060-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g4530585
BLAST score
                   339
                   7.0e-32
E value
Match length
                   85
                   73
% identity
                  (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                   210503
Seq. No.
                   LIB3135-060-Q1-K1-G3
Seq. ID
Method
                   BLASTX
                   g4530585
NCBI GI
                   226
BLAST score
```

NCBI Description

thaliana]



```
0e-19
E value
                  81
Match length
% identity
                  (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                  210504
Seq. No.
                  LIB3135-060-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g2431769
NCBI GI
BLAST score
                  228
                  4.0e-19
E value
Match length
                  56
                  79
% identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
                  210505
Seq. No.
                  LIB3135-060-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g3522938
NCBI GI
BLAST score
                  146
                  2.0e-09
E value
Match length
                  84
% identity
                  39
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
                  210506
Seq. No.
                  LIB3135-060-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467147
BLAST score
                  483
                  9.0e-49
E value
                  133
Match length
% identity
                  71
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  210507
Seq. No.
Seq. ID
                  LIB3135-061-Q1-K1-A1
                  BLASTX
Method
                  g4090884
NCBI GI
                  452
BLAST score
                   4.0e-45
E value
                  116
Match length
% identity
                  76
                  (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                  synaptobrevin 7B [Arabidopsis thaliana]
                  210508
Seq. No.
Seq. ID
                  LIB3135-061-Q1-K1-A11
                  BLASTX
Method
                  g2660670
NCBI GI
BLAST score
                   303
                  1.0e-27
E value
Match length
                  88
% identity
                   68
```

(AC002342) putative Cu2+-transporting ATPase [Arabidopsis

Seq. ID

Method NCBI GI



```
210509
Seq. No.
                  LIB3135-061-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                   g1669655
NCBI GI
                   277
BLAST score
E value
                  1.0e-24
Match length
                  105
% identity
                   55
NCBI Description (X95962) CER3 [Arabidopsis thaliana]
Seq. No.
                   210510
Seq. ID
                  LIB3135-061-Q1-K1-B1
Method
                  BLASTN
NCBI GI
                   q3108273
BLAST score
                   60
E value
                   5.0e-25
Match length
                   115
% identity
                   92
NCBI Description Gossypium barbadense clone pXP095 repetitive DNA sequence
                   210511
Seq. No.
                   LIB3135-061-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                                                                        su<u>t</u>
NCBI GI
                   q218157
BLAST score
                   145
                   3.0e-09
E value
Match length
                   31
                   90
% identity
                  (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
Seq. No.
                   210512
                   LIB3135-061-Q1-K1-B7
Seq. ID
Method
                   BLASTX
                   q602076
NCBI GI
BLAST score
                   657
                   4.0e-69
E value
                   136
Match length
                   23
% identity
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                   210513
Seq. No.
                   LIB3135-061-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g1709767
NCBI GI
                   177
BLAST score
                   7.0e-13
E value
                   39
Match length
                   82
% identity
                   36.4 KD PROLINE-RICH PROTEIN >qi 100249 pir S19129
NCBI Description
                   proline-rich protein TPRP-F1 - tomato
                   >gi 19390 emb CAA43666 (X61395) proline rich protein
                   [Lycopersicon esculentum]
                   210514
Seq. No.
```

29125

LIB3135-061-Q1-K1-B9

BLASTX

g3334259

```
BLAST score 608
E value 2.0e-63
Match length 129
% identity 86
NCBI Description WD-40 REPEAT PROTEIN MSI4 >gi_2599092 (AF028711) WD-40
repeat protein MSI4 [Arabidopsis thaliana]

Seq. No. 210515
Seq. ID LIB3135-061-Q1-K1-C11
```

Method BLASTX
NCBI GI g4522005
BLAST score 173
E value 2.0e-12
Match length 96
% identity 40

NCBI Description (AC007069) putative reverse transcriptase [Arabidopsis

thaliana]

 Seq. No.
 210516

 Seq. ID
 LIB3135-061-Q1-K1-D6

 Method
 BLASTX

 NGDT GT
 T1160403

NCBI GI g1168493 BLAST score 421 E value 1.0e-41 Match length 97 % identity 85

NCBI Description ARGINASE >gi 602422 (U15019) arginase [Arabidopsis

thaliana]  $>g\bar{i}$  4325373 gb AAD17369 (AF128396) Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,

E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No. 210517

Seq. ID LIB3135-061-Q1-K1-E8

Method BLASTX
NCBI GI g3249086
BLAST score 297
E value 3.0e-27
Match length 70
% identity 83

NCBI Description (AC004473) Contains similarity to 21 KD subunit of the

Arp2/3 protein complex (ARC21) gb\_AF006086 from Homo sapiens. EST gb\_Z37222 comes [Arabidopsis thaliana]

Seq. No. 210518

Seq. ID LIB3135-061-Q1-K1-E9

Method BLASTX
NCBI GI 9479713
BLAST score 544
E value 7.0e-56
Match length 128
% identity 81

NCBI Description aspartate carbamoyltransferase - tomato

Seq. No. 210519

Seq. ID LIB3135-061-Q1-K1-F11

Method BLASTN NCBI GI g2687435



```
BLAST score
                  4.0e-36
E value
Match length
                  158
                  87
% identity
                  Hamamelis virginiana large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  210520
                  LIB3135-061-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432866
BLAST score
                  152
                  7.0e-10
E value
                  96
Match length
                  39
% identity
                   (AC006300) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                   210521
Seq. No.
                  LIB3135-061-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  q3913418
NCBI GI
BLAST score
                   160
E value
                   4.0e-11
                  75
Match length
                   47
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1531763 emb CAA69073 (Y07765)
                   S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
Seq. No.
                   210522
Seq. ID
                   LIB3135-061-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3913425
BLAST score
                   365
                   9.0e-40
E value
Match length
                   101
% identity
                   74
                   PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                   HELICASE >gi 2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
Seq. No.
                   210523
Seq. ID
                   LIB3135-061-Q1-K1-F9
Method
                   BLASTN
                   g434989
NCBI GI
BLAST score
                   63
E value
                   7.0e-27
                   107
Match length
% identity
                   90
NCBI Description O.berteriana mitochondrial trnC and trnN genes
```

210524 Seq. No.

LIB3135-061-Q1-K1-G10 Seq. ID

BLASTX Method g1408322 NCBI GI BLAST score 161

```
E value
                  2.0e-11
Match length
                  76
% identity
                  43
                  (D86351) cytochrome P-450 (CYP93A2) [Glycine max]
NCBI Description
                  210525
Seq. No.
Seq. ID
                  LIB3135-061-Q1-K1-G12
Method
                  BLASTX
                  q2695923
NCBI GI
                  394
BLAST score
E value
                  9.0e-39
Match length
                  78
% identity
                  (AJ222775) putative heat shock cognate protein [Hordeum
NCBI Description
                  vulgare]
                  210526
Seq. No.
Seq. ID
                  LIB3135-061-Q1-K1-G7
                  BLASTX
Method
                  q4510428
NCBI GI
                  184
BLAST score
                  4.0e-14
E value
Match length
                  77
% identity
                  45
                  (AC006929) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   210527
Seq. ID
                  LIB3135-061-Q1-K1-G9
                  BLASTX
Method
NCBI GI
                   q2285792
BLAST score
                   374
E value
                   2.0e-39
Match length
                   127
% identity
                   (AB004568) cyanase [Arabidopsis thaliana]
NCBI Description
                   >gi 3287503 dbj BAA31224 (AB015748) cyanase [Arabidopsis
                   thaliana]
                   210528
Seq. No.
                   LIB3135-061-Q1-K1-H1
Seq. ID
Method
                   BLASTX
                   g4376220
NCBI GI
BLAST score
                   263
                   3.0e-23
E value
                   96
Match length
% identity
                   54
                  (AJ001555) pollen allergen, Betv1 [Betula pendula]
NCBI Description
                   210529
Seq. No.
                   LIB3135-061-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   g559684
NCBI GI
BLAST score
                   500
                   6.0e-51
E value
```

29128

105

90

Match length

% identity



```
(L36097) aquaporin [Mesembryanthemum crystallinum]
NCBI Description
                  210530
Seq. No.
                  LIB3135-061-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  q3885884
NCBI GI
BLAST score
                  336
                  2.0e-31
E value
Match length
                  68
                  93
% identity
                  (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                  210531
Seq. No.
                  LIB3135-061-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  g1480347
NCBI GI
BLAST score
                  292
                  9.0e-27
E value
Match length
                  73
                  79
% identity
                  (X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]
NCBI Description
                  210532
Seq. No.
Seq. ID
                  LIB3135-061-Q1-K1-H6
Method
                  BLASTX
                   g2245139
NCBI GI
                   172
BLAST score
                   2.0e-12
E value
Match length
                   62
                   53
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   210533
Seq. No.
                   LIB3135-061-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3023857
BLAST score
                   201
                  4.0e-15
E value
                   50
Match length
% identity
                   84
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN >gi_629591_pir__S48839 guanine nucleotide
                   regulatory protein - rape >gi_563335_emb_CAA83924_
                   quanine nucleotide regulatory protein [Brassica napus]
                   210534
Seq. No.
```

LIB3135-061-Q1-K1-H9 Seq. ID

Method BLASTX NCBI GI q4490292 BLAST score 278 7.0e-25 E value Match length 72 78 % identity

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

210535 Seq. No,

LIB3135-062-Q1-K1-A1 Seq. ID

```
BLASTX
Method
NCBI GI
                  q4388726
                  470
BLAST score
                  3.0e-47
E value
                  127
Match length
                  71
% identity
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  210536
Seq. ID
                  LIB3135-062-Q1-K1-A10
Method
                  BLASTX
                  q3041662
NCBI GI
                  320
BLAST score
                  1.0e-29
E value
                  68
Match length
% identity
                  91
                  14-3-3-LIKE PROTEIN 3 (PBLT3) >gi 1771170 emb CAA65147.1
NCBI Description
                   (X95902) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                  210537
Seq. ID
                  LIB3135-062-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2274915
BLAST score
                   414
E value
                  1.0e-40
Match length
                  130
% identity
                   63
                  (AJ000081) beta-1,3-glucanase [Citrus sinensis]
NCBI Description
                  210538
Seq. No.
Seq. ID
                  LIB3135-062-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g70639
                   668
BLAST score
                  2.0e-72
E value
                  149
Match length
                   26
% identity
                  ubiquitin precursor - Neurospora crassa
NCBI Description
                  >gi 295930 emb CAA31530 (X13140) ubiquitin [Neurospora
                   crassa]
Seq. No.
                   210539
Seq. ID
                  LIB3135-062-Q1-K1-A2
                  BLASTX
Method
                   g1166450
NCBI GI
BLAST score
                   293
                  2.0e-26
E value
                   65
Match length
                  78
% identity
                  (X95262) Tfm5 [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   210540
                  LIB3135-062-Q1-K1-A3
Seq. ID
```

Method BLASTX NCBI GI q710626 BLAST score 284



E value 2.0e-25 Match length 86 % identity 65

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi\_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 210541

Seq. ID LIB3135-062-Q1-K1-A4

Method BLASTX
NCBI GI g4455208
BLAST score 145
E value 3.0e-09
Match length 67
% identity 45

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 210542

Seq. ID LIB3135-062-Q1-K1-A5

Method BLASTX
NCBI GI g3702332
BLAST score 428
E value 2.0e-42
Match length 117
% identity 68

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 210543

Seq. ID LIB3135-062-Q1-K1-A6

Method BLASTX
NCBI GI g2982268
BLAST score 326
E value 2.0e-30
Match length 72
% identity 89

NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea

mariana]

Seq. No. 210544

Seq. ID LIB3135-062-Q1-K1-A7

Method BLASTN
NCBI GI g2829205
BLAST score 133
E value 1.0e-68
Match length 389
% identity 22

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 210545

Seq. ID LIB3135-062-Q1-K1-A9

Method BLASTX
NCBI GI g1256509
BLAST score 621
E value 7.0e-65
Match length 130

```
% identity
                  (X92943) pectate lyase [Musa acuminata]
NCBI Description
                  210546
Seq. No.
                  LIB3135-062-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  q3047318
NCBI GI
BLAST score
                  631
                  4.0e-66
E value
Match length
                  127
% identity
                  22
NCBI Description (AF056625) poly-ubiquitin [Magnaporthe grisea]
```

 Seq. No.
 210547

 Seq. ID
 LIB3135-062-Q1-K1-B11

 Method
 BLASTX

 NCBI GI
 g2281086

 BLAST score
 364

 E value
 8.0e-35

E value 8.00 Match length 128 % identity 55

NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog

[Arabidopsis thaliana]

Seq. No. 210548

Seq. ID LIB3135-062-Q1-K1-B12

Method BLASTX
NCBI GI g2677828
BLAST score 475
E value 9.0e-48
Match length 135
% identity 67

NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 210549

Seq. ID LIB3135-062-Q1-K1-B2

Method BLASTX
NCBI GI 94220535
BLAST score 379
E value 2.0e-36
Match length 78
% identity 94

NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis

thaliana]

Seq. No. 210550

Seq. ID LIB3135-062-Q1-K1-B3

Method BLASTX
NCBI GI g1350956
BLAST score 280
E value 7.0e-25
Match length 117
% identity 79

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 210551

Seq. ID LIB3135-062-Q1-K1-B4



```
Method
                  BLASTX
                  a553107
NCBI GI
BLAST score
                  461
                  4.0e-46
E value
Match length
                  131
                  69
% identity
                  (L04967) triosephosphate isomerase [Oryza sativa]
NCBI Description
Seq. No.
                  210552
Seq. ID
                  LIB3135-062-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q729470
BLAST score
                  604
E value
                  7.0e-63
Match length
                  138
                  84
% identity
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi 542089 pir JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798 emb_CAA79702_
                   (Z21493) mitochondrial formate dehydrogenase precursor
                   [Solanum tuberosum]
Seq. No.
                   210553
                   LIB3135-062-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   q586004
NCBI GI
                   502
BLAST score
E value
                   5.0e-51
Match length
                   104
% identity
                   SUPEROXIDE DISMUTASE [CU-ZN] >gi 421962 pir S34267
NCBI Description
```

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi 542090 pir S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi\_311971\_emb\_CAA51654\_ (X73139)

superoxide dismutase [Ipomoea batatas]

210554 Seq. No.

LIB3135-062-Q1-K1-C4 Seq. ID

BLASTX Method g2829751 NCBI GI 197 BLAST score 4.0e-15 E value Match length 107 39 % identity

MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) NCBI Description

>gi 1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi 2190976 (AF002699) macrophage migration

inhibitory factor [Brugia malayi]

210555 Seq. No.

LIB3135-062-Q1-K1-C5 Seq. ID

BLASTX Method g1296816 NCBI GI 600 BLAST score 1.0e-62 E value 121 Match length

```
% identity
                  (X94995) naringenin-chalcone synthase [Juglans sp.]
NCBI Description
                  210556
Seq. No.
                  LIB3135-062-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                  g2088654
NCBI GI
BLAST score
                  142
                  1.0e-08
E value
Match length
                  75
% identity
                  47
                   (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                   [Arabidopsis thaliana]
                  210557
Seq. No.
Seq. ID
                  LIB3135-062-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3445201
BLAST score
                  227
E value
                  9.0e-19
Match length
                  131
% identity
                  (AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
                  210558
Seq. No.
Seq. ID
                  LIB3135-062-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                   q3925703
BLAST score
                   625
E value
                   2.0e-65
Match length
                  136
% identity
                   89
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                   210559
                  LIB3135-062-Q1-K1-D12
Seq. ID
Method
                   BLASTX
                   q533084
NCBI GI
                   341
BLAST score
                   5.0e-32
E value
                   88
Match length
                   72
% identity
                   (U07597) delta-9 stearoyl-acyl carrier protein desaturase
NCBI Description
                   precursor [Thunbergia alata]
                   210560
Seq. No.
Seq. ID
                   LIB3135-062-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   g576773
                   212
BLAST score
                   4.0e-17
E value
                   92
Match length
                   11
% identity
                  (U16956) polyubiquitin [Filobasidiella neoformans]
NCBI Description
```

29134

210561

LIB3135-062-Q1-K1-D7

Seq. No.

Seq. ID

Match length

97



```
BLASTX
Method
                   q1724100
NCBI GI
                   518
BLAST score
                   7.0e-53
E value
Match length
                  120
% identity
                  82
NCBI Description (U79765) porin [Mesembryanthemum crystallinum]
                   210562
Seq. No.
Seq. ID
                  LIB3135-062-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                   q3901018
BLAST score
                   184
E value
                   4.0e-14
Match length
                   79
                   51
% identity
                   (AJ130889) stress and pathogenesis-related protein [Fagus
NCBI Description
                   sylvatica]
Seq. No.
                   210563
                   LIB3135-062-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3114968
BLAST score
                   461
E value
                   4.0e-46
Match length
                   138
% identity
                   60
NCBI Description
                  (Y14997) prolidase [Suberites domuncula]
                   210564
Seq. No.
                   LIB3135-062-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1542869
                   315
BLAST score
                   5.0e-29
E value
                   126
Match length
% identity
                   51
                  (Z80104) pollen allergen Bet v 1 [Betula pendula]
NCBI Description
                   210565
Seq. No.
Seq. ID
                   LIB3135-062-Q1-K1-E2
                   BLASTX
Method
NCBI GI
                   g2997684
                   149
BLAST score
                   7.0e-10
E value
Match length
                   69
% identity
                   52
                   (AF053302) putative transcriptional co-activator
NCBI Description
                   [Arabidopsis thaliana]
                   210566
Seq. No.
Seq. ID
                   LIB3135-062-Q1-K1-E5
                   BLASTX
Method
NCBI GI
                   g2980770
BLAST score
                   329
                   1.0e-30
E value
```

29135



```
% identity
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  210567
Seq. No.
                  LIB3135-062-Q1-K1-E6
Seq. ID
Method
                  BLASTX
                  g131015
NCBI GI
                  204
BLAST score
                   3.0e-16
E value
Match length
                   37
                   89
% identity
                  PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR
NCBI Description
                   (THAUMATIN-LIKE PROTEIN E22) >gi 100385 pir_JH0230
                   pathogenesis-related protein R precursor - common tobacco
                   >gi 19855_emb_CAA33293_ (X15224) thaumatin-like protein
                   [Nicotiana tabacum] >gi_19980_emb_CAA31235_ (X12739)
                   pathogenesis-related protein \overline{R} (A\overline{A} 1 - 226) [Nicotiana
                   tabacum]
                   210568
Seq. No.
                   LIB3135-062-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982268
BLAST score
                   485
E value
                   5.0e-49
Match length
                   106
                   90
% identity
                   (AF051217) probable 40S ribosomal protein S15 [Picea
NCBI Description
                   mariana]
                   210569
Seq. No.
Seq. ID
                   LIB3135-062-Q1-K1-E8
Method
                   BLASTX
                   q529353
NCBI GI
BLAST score
                   155
                   3.0e-10
E value
                   57
Match length
                   53
% identity
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
                   210570
Seq. No.
Seq. ID
                   LIB3135-062-Q1-K1-F1
                   BLASTX
Method
                   g3236242
NCBI GI
BLAST score
                   425
                   5.0e-42
E value
                   107
Match length
                   80
% identity
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 210571

Seq. ID LIB3135-062-Q1-K1-F10

Method BLASTX
NCBI GI g629597
BLAST score 322
E value 8.0e-30



```
Match length
                   77
% identity
                  proline-rich protein - rape >gi_545029 bbs 142669 (S68113)
NCBI Description
                  proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                   Peptide, 147 aa] [Brassica napus]
                   210572
Seq. No.
                  LIB3135-062-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                   q1173234
NCBI GI
BLAST score
                   324
E value
                   5.0e-30
Match length
                   72
                   88
% identity
                  40S RIBOSOMAL PROTEIN S25 >gi 481909 pir S40089 ribosomal
NCBI Description
                   protein S25 - tomato >gi_4356\overline{7}9_emb_\overline{CAA54132} (X76714)
                   ribosomal protein S25 [Lycopersicon esculentum]
                   >gi 1584836_prf__2123431A ribosomal protein S25
                   [Lycopersicon esculentum]
                   210573
Seq. No.
                   LIB3135-062-Q1-K1-F3
Seq. ID
Method
                   BLASTX
                   g3980254
NCBI GI
BLAST score
                   129
                   1.0e-11
E value
                   71
Match length
                   56
% identity
                   (AJ006053) peroxisomal membrane protein [Arabidopsis
NCBI Description
                   thaliana]
                   210574
Seq. No.
                   LIB3135-062-Q1-K1-F5
Seq. ID
Method
                   BLASTX
                   q548751
NCBI GI
BLAST score
                   220
E value
                   7.0e-18
Match length
                   121
                   40
% identity
                   60S RIBOSOMAL PROTEIN L19 >qi 1079135 pir A61627 ribosomal
NCBI Description
                   protein L19 - fruit fly (Drosophila melanogaster)
                   >gi 400448 emb_CAA52784 (X74776) ribosomal protein L19
                   [Drosophila melanogaster]
Seq. No.
                   210575
                   LIB3135-062-Q1-K1-F6
Seq. ID
Method
                   BLASTX
                   q1710530
NCBI GI
```

BLAST score 235 9.0e-20 E value Match length 61 77 % identity NCBI Description

60S RIBOSOMAL PROTEIN L27A >gi\_2129719 pir \_S71256 ribosomal protein L27a - Arabidopsis thaliana

>gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. ID

Method



```
210576
Seq. No.
                  LIB3135-062-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g119006
NCBI GI
                  393
BLAST score
E value
                  3.0e-38
Match length
                  117
% identity
                   68
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE, BASIC ISOFORM
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi_1197520_emb_CAA37289_ (X53129)
                   1,3,-beta-D-glucanase [Phaseolus vulgaris]
                   210577
Seq. No.
                  LIB3135-062-Q1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1785673
BLAST score
                   55
E value
                   4.0e-22
Match length
                   231
% identity
NCBI Description A.thaliana mitochondrial genome, part A
Seq. No.
                   210578
                  LIB3135-062-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3319882
BLAST score
                   478
E value
                   1.0e-50
                   109
Match length
                   95
% identity
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
Seq. No.
                   210579
Seq. ID
                   LIB3135-062-Q1-K1-G12
Method
                   BLASTN
NCBI GI
                   g18644
BLAST score
                   41
                   1.0e-13
E value
Match length
                   71
                   90
% identity
NCBI Description Soybean mRNA for HMG-1 like protein
                   210580
Seq. No.
Seq. ID
                   LIB3135-062-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g529353
BLAST score
                   304
                   1.0e-27
E value
Match length
                   131
                   47
% identity
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                   210581
Seq. No.
```

29138

LIB3135-062-Q1-K1-G3

BLASTX



```
NCBI GI
                  g2842482
BLAST score
                  373
                  6.0e-36
E value
Match length
                  106
% identity
                  (AL021749) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  210582
Seq. ID
                  LIB3135-062-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2500523
BLAST score
                  267
E value
                  2.0e-23
                  128
Match length
                  47
% identity
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
NCBI Description
                  >gi_2190248_dbj_BAA20371 (D84472) translation initiation
                  factor [Candida albicans]
                  210583
Seq. No.
                  LIB3135-062-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1524176
                  187
BLAST score
                  2.0e-14
E value
                  82
Match length
                  49
% identity
                  (Z71997) DnaJ-like protein [Medicago sativa]
NCBI Description
                  210584
Seq. No.
                  LIB3135-062-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3450889
BLAST score
                  114
E value
                   6.0e-12
Match length
                  74
                   62
% identity
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210585
                  LIB3135-062-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1350736
BLAST score
                   161
                   6.0e-11
E value
Match length
                   34
% identity
                   91
                  60S RIBOSOMAL PROTEIN L37 >gi 629673 pir S44313 ribosomal
NCBI Description
                   protein L37 - tomato >gi_483586_emb CAA55674_ (X79074)
                   ribosomal protein L37 [Lycopersicon esculentum]
                   210586
Seq. No.
Seq. ID
                  LIB3135-062-Q1-K1-H2
                  BLASTX
Method
```

29139

g322551

343

NCBI GI BLAST score



E value 9.0e-33

Match length 73

% identity 88

NCBI Description nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana >gi 16398 emb CAA49173 (X69376) nucleoside

diphosphate kinase [Arabidopsis thaliana]

Seq. No. 210587 Seq. ID LIB3135-062-Q1-K1-H4

Method BLASTX
NCBI GI g1694976
BLAST score 367
E value 4.0e-35
Match length 85
% identity 80

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>gi\_2832361\_emb\_CAA74402\_ (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. 210588

Seq. ID LIB3135-062-Q1-K1-H5

Method BLASTN
NCBI GI g2829205
BLAST score 94
E value 2.0e-45
Match length 296
% identity 17

NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein

precursor (PRP) mRNA, complete cds

Seq. No. 210589

Seq. ID LIB3135-062-Q1-K1-H6

Method BLASTX
NCBI GI g1694976
BLAST score 211
E value 9.0e-17
Match length 82
% identity 52

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>qi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. 210590

Seq. ID LIB3135-062-Q1-K1-H7

Method BLASTX
NCBI GI g3264767
BLAST score 189
E value 3.0e-14
Match length 54
% identity 67

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 210591

Seq. ID LIB3135-062-Q1-K1-H8

Method BLASTX NCBI GI g1710780 BLAST score 373

E value 8.0e-36
Match length 87
% identity 80

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi\_1321917\_emb\_CAA65433\_

(X96613) cytoplasmic ribosomal protein S7 [Podospora

anserina]

Seq. No. 210592

Seq. ID LIB3135-062-Q1-K1-H9

Method BLASTX
NCBI GI g4115563
BLAST score 431
E value 1.0e-42
Match length 141
% identity 61

NCBI Description (AB013598) UDP-glucose:anthocyanin 5-O-glucosyltransferase

[Verbena x hybrida]

Seq. No. 210593

Seq. ID LIB3145-001-P1-K1-B11

Method BLASTX
NCBI GI g2464880
BLAST score 354
E value 1.0e-33
Match length 145
% identity 50

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 210594

Seq. ID LIB3145-001-P1-K1-C8

Method BLASTX
NCBI GI g729882
BLAST score 747
E value 1.0e-79
Match length 150
% identity 87

NCBI Description CASEIN KINASE II BETA' CHAIN (CK II)

>gi\_1076300\_pir\_\_S47968 casein kinase II (EC 2.7.1.-) beta
chain CKB2 - Arabidopsis thaliana >gi\_467975 (U03984)
casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
>gi\_2245122\_emb\_CAB10544\_ (Z97343) unnamed protein product

[Arabidopsis thaliana]

Seq. No. 210595

Seq. ID LIB3145-001-P1-K1-D4

Method BLASTX
NCBI GI g1223926
BLAST score 198
E value 6.0e-16
Match length 64
% identity 58

NCBI Description (U49741) Vigna radiata carboxypeptidase II mRNA, partial

cds [Vigna radiata]

Seq. No. 210596

Seq. ID LIB3145-001-P1-K1-F10

Method BLASTX



```
q4063751
NCBI GI
BLAST score
                  150
                  9.0e-10
E value
                  115
Match length
                  28
% identity
                  (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4510409 gb AAD21495.1 (AC006929) putative white
                  protein [Arabidopsis thaliana]
                  210597
Seq. No.
                  LIB3145-001-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262250
BLAST score
                  690
                  6.0e-73
E value
                  149
Match length
                  89
% identity
                  (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                  210598
Seq. No.
                  LIB3145-001-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2500376
BLAST score
                   361
                   2.0e-34
E value
Match length
                   77
                   88
% identity
                  60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494
NCBI Description
                   (AC005508) 23552 [Arabidopsis thaliana]
                   210599
Seq. No.
                   LIB3145-001-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2500376
BLAST score
                   270
E value
                   1.0e-26
Match length
                   71
                   90
% identity
                   60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494
NCBI Description
                   (AC005508) 23552 [Arabidopsis thaliana]
                   210600
Seq. No.
Seq. ID
                   LIB3145-002-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2827710
BLAST score
                   254
E value
                   7.0e-22
Match length
                   99
% identity
                   54
                   (ALO21684) lysosomal Pro-X carboxypeptidase - like protein
NCBI Description
```

[Arabidopsis thaliana]

Seq. No. 210601

LIB3145-002-P1-K1-A10 Seq. ID

Method BLASTX g2982434 NCBI GI BLAST score 281



```
5.0e-25
E value
Match length
                  119
% identity
                  46
                  (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
                  210602
Seq. No.
                  LIB3145-002-P1-K1-A11
Seq. ID
Method
                  BLASTX
                  g3668086
NCBI GI
                  404
BLAST score
                  2.0e-39
E value
                  131
Match length
% identity
                  62
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  210603
Seq. No.
                  LIB3145-002-P1-K1-A9
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  5.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  210604
Seq. No.
                  LIB3145-002-P1-K1-B11
Seq. ID
                  BLASTX
Method
                  g3093294
NCBI GI
BLAST score
                  157
                   4.0e-11
E value
                   57
Match length
                   56
% identity
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
                   210605
Seq. No.
                   LIB3145-002-P1-K1-C11
Seq. ID
                   BLASTN
Method
                   g2244733
NCBI GI
BLAST score
                   134
E value
                   3.0e-69
                   204
Match length
% identity
NCBI Description Cotton mRNA for actin, clone CF456, partial cds
                   210606
Seq. No.
                   LIB3145-002-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1915960
BLAST score
                   139
                   9.0e-19
E value
```

97 Match length 50 % identity

NCBI Description (Y07636) peptidylprolyl isomerase [Triticum aestivum]

210607 Seq. No.

LIB3145-002-P1-K1-D5 Seq. ID

29143



```
BLASTN
Method
NCBI GI
                  q755147
BLAST score
                  36
                  1.0e-10
E value
                  56
Match length
                  91
% identity
                  Gossypium hirsutum vacuolar H+-ATPase proteolipid (16 kDa)
NCBI Description
                  subunit (cva16-2) mRNA, complete cds
                  210608
Seq. No.
                  LIB3145-002-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3892051
BLAST score
                  472
                  2.0e-47
E value
Match length
                  125
                  76
% identity
                   (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                   [Arabidopsis thaliana]
                  210609
Seq. No.
                  LIB3145-002-P1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g266945
BLAST score
                   637
E value
                   1.0e-66
                   150
Match length
                   83
% identity
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                   >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                   >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                   >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                   [Pisum sativum]
                   210610
Seq. No.
                   LIB3145-002-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3660467
BLAST score
                   352
E value
                   2.0e-33
                   83
Match length
                   83
% identity
                   (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
                   210611
Seq. No.
                   LIB3145-002-P1-K1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3660467
BLAST score
                   349
E value
                   6.0e-33
Match length
                   83
% identity
```

210612 Seq. No.

thaliana]

NCBI Description

(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis



LIB3145-002-P1-K1-F11 Seq. ID Method BLASTX q1170568 NCBI GI 465 BLAST score E value 6.0e-47 91 Match length % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >gi\_2147316\_pir\_\_S60302 D-myo-inositol-3-phosphate synthase (EC 5.5.1.4) - Spirodela polyrrhiza >gi 558648 emb\_CAA77751\_ (Z11693) D-myo-inositol-3-phosphate synthase [Spirodela polyrrhiza] Seq. No. 210613 LIB3145-002-P1-K1-F12 Seq. ID BLASTX Method g1710007 NCBI GI 587 BLAST score 5.0e-61 E value 115 Match length 97 % identity GTP-BINDING NUCLEAR PROTEIN RAN1A >gi 1370203 emb CAA98187 NCBI Description (Z73959) RAN1A [Lotus japonicus] Seq. No. 210614 LIB3145-002-P1-K1-F9 Seq. ID BLASTX Method q1173043 NCBI GI BLAST score 242 2.0e-20 E value 66 Match length 76 % identity 60S RIBOSOMAL PROTEIN L38 >gi\_479441\_pir\_\_S33899 ribosomal NCBI Description protein L38 - tomato (cv. Moneymaker) >gi\_313027\_emb\_CAA49599\_ (X69979) ribosomal protein L38 [Lycopersicon esculentum] 210615 Seq. No. LIB3145-002-P1-K1-G1 Seq. ID Method BLASTX q729010 NCBI GI 373 BLAST score 5.0e-36 E value 84 Match length % identity 47 CALMODULIN >gi\_481907\_pir\_\_S40086 calmodulin - maize NCBI Description >gi\_2119352\_pir\_\_S58924 calmodulin calm1 - maize >gi\_435543\_emb\_CAA52602\_ (X74490) Calmodulin [Zea mays] 210616 Seq. No. LIB3145-002-P1-K1-G10 Seq. ID Method BLASTX

g2146732 NCBI GI 477 BLAST score 4.0e-48 E value

125 Match length 76 % identity



```
FK506-binding protein - Arabidopsis thaliana >gi_1373396
NCBI Description
                  (U57838) rof1 [Arabidopsis thaliana]
                  210617
Seq. No.
                  LIB3145-002-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832664
BLAST score
                  199
                  2.0e-15
E value
                  103
Match length
                  44
% identity
                  (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                  thaliana]
                  210618
Seq. No.
                  LIB3145-002-P1-K1-G12
Seq. ID
                  BLASTX
Method
                  g1815759
NCBI GI
BLAST score
                  156
                  2.0e-10
E value
                  99
Match length
                  36
% identity
NCBI Description (U85499) pollen-specific protein [Phalaris coerulescens]
Seq. No.
                  210619
                  LIB3145-002-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  g115492
NCBI GI
BLAST score
                  253
E value
                  2.0e-22
                  66
Match length
                   44
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                   210620
Seq. ID
                  LIB3145-002-P1-K1-G6
                  BLASTX
Method
                   q1778372
NCBI GI
BLAST score
                   324
                   4.0e-30
E value
                   123
Match length
% identity
NCBI Description
                  (U77679) asparagine synthetase 1 [Glycine max]
                   210621
Seq. No.
Seq. ID
                   LIB3145-002-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g3334323
BLAST score
                   447
                   1.0e-44
```

E value Match length 113 % identity 78

GTP-BINDING PROTEIN SAR1A >gi 1314860 (U56929) Sar1 homolog NCBI Description

[Arabidopsis thaliana] >gi 2104532 gb AAC78700.1

(AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis



## thaliana]

```
210622
Seq. No.
Seq. ID
                   LIB3145-002-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   q3334323
BLAST score
                   390
                   5.0e-38
E value
                   87
Match length
                   85
% identity
                   GTP-BINDING PROTEIN SAR1A >qi 1314860 (U56929) Sar1 homolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_
(AF001308) SAR1/GTP-binding secretory factor [Arabidopsis
                   thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis
                   thaliana]
                   210623
Seq. No.
                   LIB3145-004-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729944
BLAST score
                   231
                   3.0e-19
E value
                   46
Match length
% identity
                   96
                   POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi_478272_pir_
NCBI Description
                   major allergen mI protein - maize >gi_293902 (L14271) Zea
                   mI [Zea mays]
Seq. No.
                   210624
Seq. ID
                   LIB3145-004-P1-K1-A9
                   BLASTX
Method
                   g2244792
NCBI GI
BLAST score
                    488
E value
                    3.0e-49
Match length
                   152
% identity
                   59
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]
Seq. No.
                    210625
                   LIB3145-004-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                    g4176420
BLAST score
                    250
E value
                    2.0e-21
Match length
                    108
                    44
% identity
                   (AB008097) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                    210626
Seq. No.
                    LIB3145-004-P1-K1-C9
Seq. ID
                    BLASTX
Method
                    q548492
NCBI GI
                    840
BLAST score
                    2.0e-90
E value
Match length
                    162
                    97
% identity
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
```



```
(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629853_pir__S30066 polygalacturonase - maize
                  >gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea
                  mays]
                  210627
                  LIB3145-004-P1-K1-D11
                  BLASTX
                  g3386614
                  395
BLAST score
                  3.0e-38
                  115
Match length
                  37
```

% identity (AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description thaliana]

Seq. No. 210628 LIB3145-004-P1-K1-D9 Seq. ID Method BLASTX NCBI GI g1707998

BLAST score 661 2.0e-69 E value 150 Match length 87 % identity

Seq. No. Seq. ID

Method

NCBI GI

E value

SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR NCBI Description

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi\_481944\_pir\_\_S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi\_438247\_emb\_CAA81082\_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

210629 Seq. No.

LIB3145-004-P1-K1-E9 Seq. ID

Method BLASTX q1346109 NCBI GI BLAST score 796 E value 3.0e-85 165 Match length % identity

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE NCBI Description PROTEIN (GPB-LR) (RWD) >gi\_540535\_dbj\_BAA07404 (D38231)

RWD [Oryza sativa]

Seq. No. 210630

LIB3145-004-P1-K1-F11 Seq. ID

Method BLASTX NCBI GI g4510339 BLAST score 361 2.0e-34 E value Match length 119 % identity 57

(AC006921) putative ABC transporter protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 210631

Seq. ID LIB3145-004-P1-K1-F9

BLASTX Method

```
NCBI GI
                  q1531672
BLAST score
                  449
                  1.0e-44
E value
                  89
Match length
                  99
% identity
NCBI Description (U68461) actin [Striga asiatica]
                  210632
Seq. No.
                  LIB3145-005-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1296816
BLAST score
                  405
E value
                  1.0e-39
Match length
                  94
                  83
% identity
                  (X94995) naringenin-chalcone synthase [Juglans sp.]
NCBI Description
Seq. No.
                  210633
                  LIB3145-005-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  q4559381
NCBI GI
                  393
BLAST score
E value
                  3.0e-38
Match length
                  88
                  75
% identity
                  (AC006526) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   210634
Seq. No.
                  LIB3145-005-Q1-K1-A7
Seq. ID
Method
                   BLASTX
                   q4097915
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
Match length
                   116
% identity
                  (U72147) unknown [Anabaena sp. CA]
NCBI Description
                   210635
Seq. No.
Seq. ID
                   LIB3145-005-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g3287826
                   629
BLAST score
                   6.0e-66
E value
Match length
                   125
% identity
                   97
                   (+)-DELTA-CADINENE SYNTHASE ISOZYME C2 (D-CADINENE
NCBI Description
                   SYNTHASE) >qi 2879841 emb CAA76223.1 (Y16432)
                   (+)-delta-cadinene synthase [Gossypium arboreum]
                   210636
Seq. No.
                   LIB3145-005-Q1-K1-B1
Seq. ID
                   BLASTX
Method
                   g3212847
NCBI GI
BLAST score
                   147
                   2.0e-09
E value
                   89
Match length
                   37
% identity
```



NCBI Description (AC004005) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 210637

Seq. ID LIB3145-005-Q1-K1-B10

Method BLASTX
NCBI GI g1928981
BLAST score 515
E value 2.0e-52
Match length 111
% identity 92

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 210638

Seq. ID LIB3145-005-Q1-K1-B11

Method BLASTX
NCBI GI g2827992
BLAST score 196
E value 2.0e-15
Match length 55
% identity 64

NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No. 210639

Seq. ID LIB3145-005-Q1-K1-B2

Method BLASTX
NCBI GI g3608145
BLAST score 177
E value 7.0e-13
Match length 122
% identity 29

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 210640

Seq. ID LIB3145-005-Q1-K1-B9

Method BLASTX
NCBI GI g729974
BLAST score 153
E value 2.0e-10
Match length 96
% identity 45

NCBI Description FLORAL HOMEOTIC PROTEIN PMADS1 (GREEN PETAL HOMEOTIC

PROTEIN) >gi\_322773\_pir\_\_S31693 transcription factor gp - garden petunia >gi\_22665\_emb\_CAA49567\_ (X69946) GP (green

petal) [Petunia x hybrida]

Seq. No. 210641

Seq. ID LIB3145-005-Q1-K1-C1

Method BLASTX
NCBI GI g4006818
BLAST score 293
E value 2.0e-26
Match length 84
% identity 68

NCBI Description (AC005970) putative translation initiation factor eIF-2B,

alpha subunit [Arabidopsis thaliana]



210642

Seq. No.

```
Seq. ID
                  LIB3145-005-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q478809
BLAST score
                  387
E value
                  1.0e-37
Match length
                  96
                  75
% identity
NCBI Description
                  protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449)
                  protein kinase [Glycine max] >gi 444789 prf__1908223A
                  protein kinase [Glycine max]
                  210643
Seq. No.
                  LIB3145-005-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g2244818
NCBI GI
BLAST score
                  349
                  3.0e-33
E value
Match length
                  107
                  64
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210644
                  LIB3145-005-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455207
BLAST score
                  355
                  8.0e-34
E value
Match length
                  73
% identity
                  92
                  (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210645
                  LIB3145-005-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g232202
NCBI GI
BLAST score
                  296
E value
                  4.0e-27
Match length
                  71
                  77
% identity
                  GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI)
NCBI Description
                  >gi_285295_pir__A41789 glutathione transferase (EC
                  2.5.1.18) - common tobacco >gi 218294 dbj BAA01394
                   (D10524) glutathione S-transferase [Nicotiana tabacum]
Seq. No.
                  210646
Seq. ID
                  LIB3145-005-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4406384
BLAST score
                  451
E value
                  6.0e-45
Match length
                  145
% identity
                  64
NCBI Description (AF112303) serine acetyltransferase [Arabidopsis thaliana]
Seq. No.
                  210647
```

29151

```
, ID LIF
```

Seq. ID LIB3145-005-Q1-K1-D9 Method BLASTX

NCBI GI g2921158 BLAST score 504 E value 2.0e-51 Match length 117 % identity 85

NCBI Description (AF022909) ClpC [Arabidopsis thaliana]

Seq. No. 210648

Seq. ID LIB3145-005-Q1-K1-E2

Method BLASTX
NCBI GI g3281868
BLAST score 476
E value 5.0e-48
Match length 122
% identity 79

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 210649

Seq. ID LIB3145-005-Q1-K1-E3

Method BLASTX
NCBI GI g2244806
BLAST score 251
E value 1.0e-21
Match length 106
% identity 49

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 210650

Seq. ID LIB3145-005-Q1-K1-E4

Method BLASTX
NCBI GI g2244806
BLAST score 146
E value 1.0e-09
Match length 55
% identity 49

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 210651

Seq. ID LIB3145-005-Q1-K1-F1

Method BLASTX
NCBI GI g128592
BLAST score 362
E value 1.0e-34
Match length 104
% identity 63

NCBI Description POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR

>gi\_82190\_pir\_\_S22495 pollen-specific protein precursor common tobacco >gi\_19902\_emb\_CAA43454\_ (X61146) pollen

specific protein [Nicotiana tabacum]

Seq. No. 210652

Seq. ID LIB3145-005-Q1-K1-F2

Method BLASTX
NCBI GI g3759184
BLAST score 161

```
E value
                   4.0e-19
Match length
                   84
% identity
                   55
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   210653
Seq. ID
                   LIB3145-005-Q1-K1-G2
Method
                   BLASTX
NCBI GI
                   g2245066
BLAST score
                   227
E value
                   9.0e-19
Match length
                   125
% identity
                   37
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
Seq. No.
                   210654
Seq. ID
                   LIB3145-005-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g4539327
BLAST score
                   188
E value
                   8.0e-17
Match length
                   92
% identity
                   58
                  (AL035679) putative proton pump [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210655
Seq. ID
                   LIB3145-005-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   q2285792
BLAST score
                   147
E value
                   6.0e-10
Match length
                   48
% identity
                   60
NCBI Description
                   (AB004568) cyanase [Arabidopsis thaliana]
                   >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis
                   thaliana]
Seq. No.
                   210656
Seq. ID
                  LIB3145-005-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3860256
BLAST score
                   253
E value
                   9.0e-22
Match length
                  100
% identity
                  55
NCBI Description
                   (AC005824) putative tRNA isopentenylpyrophosphate
                  transferase [Arabidopsis thaliana]
Seq. No.
                  210657
Seq. ID
                  LIB3145-005-Q1-K1-G8
Method
                  BLASTX
```

- - - <del>- -</del>

NCBI GI g2253384 BLAST score 640 E value 4.0e-67 Match length 139 % identity 89

NCBI Description (AF007100) biotin carboxylase precursor [Glycine max]

29153



```
Seq. No.
                  210658
                  LIB3145-005-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1781299
BLAST score
                  163
                  5.0e-16
E value
                  52
Match length
% identity
                  74
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                  tabacum]
                  210659
Seq. No.
Seq. ID
                  LIB3145-005-Q1-K1-H6
Method
                  BLASTX
                  g4176420
NCBI GI
                  250
BLAST score
E value
                   5.0e-22
                  70
Match length
% identity
                   69
                   (AB008097) cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  210660
Seq. No.
                  LIB3145-005-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                   g1079720
NCBI GI
                   501
BLAST score
                   6.0e-51
E value
Match length
                   110
                   87
% identity
                   (U39764) eukaryotic release factor 3 [Ricinus communis]
NCBI Description
                   210661
Seq. No.
                   LIB3145-006-Q1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3618343
BLAST score
                   313
                   8.0e-29
E value
Match length
                   136
                   46
% identity
                   (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]
NCBI Description
                   >qi 4506223 ref NP 002808.1 pPSMD13 proteasome (prosome,
                   macropain) 26S subunit, non-ATPase,
Seq. No.
                   210662
Seq. ID
                   LIB3145-006-Q1-K1-A2
Method
                   BLASTX
                   g4490323
NCBI GI
BLAST score
                   282
                   2.0e-25
E value
Match length
                   88
% identity
                   62
                   (AJ131464) nitrate transporter [Arabidopsis thaliana]
NCBI Description
```

29154

210663

BLASTX

LIB3145-006-Q1-K1-A4

Seq. No.

Seq. ID

Method

BLAST score

361

```
NCBI GI
                    q4104242
BLAST score
                   565
                   2.0e-58
E value
                    123
Match length
% identity
                    (AF034266) palmitoyl-acyl carrier protein thioesterase
NCBI Description
                    [Gossypium hirsutum]
                    210664
Seq. No.
                   LIB3145-006-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                    q4105798
BLAST score
                    506
                    2.0e-51
E value
                    139
Match length
                    53
% identity
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                    210665
Seq. No.
                    LIB3145-006-Q1-K1-A6
Seq. ID
                    BLASTX
Method
NCBI GI
                    q4539315
BLAST score
                    413
                                                                             . (<u>*)</u>
E value
                    1.0e-40
Match length
                    109
                    53
% identity
                    (AL035679) putative zinc finger protein [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    210666
                    LIB3145-006-Q1-K1-B1
Seq. ID
Method
                    BLASTX
                    g549063
NCBI GI
BLAST score
                    317
                    3.0e-29
E value
Match length
                    101
% identity
                    TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                    >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
                    210667
Seq. No.
                    LIB3145-006-Q1-K1-B11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1652942
BLAST score
                    155
E value
                    3.0e-10
Match length
                    135
                    33
% identity
                   (D90909) extragenic suppressor [Synechocystis sp.]
NCBI Description
                    210668
Seq. No.
                    LIB3145-006-Q1-K1-B12
Seq. ID
                    BLASTX
Method
                    g421941
NCBI GI
```

29155

E value 2.0e-34
Match length 74
% identity 95

NCBI Description GTP-binding protein, ras-related - common tobacco

>qi 296878 emb CAA50609\_ (X71609) ras-related GTP-binding

protein [Nicotiana tabacum]

Seq. No. 210669

Seq. ID LIB3145-006-Q1-K1-B2

Method BLASTX
NCBI GI g3402279
BLAST score 574
E value 2.0e-59
Match length 115
% identity 93

NCBI Description (AJ000999) putative beta-subunit of K+ channels [Solanum

tuberosum]

Seq. No. 210670

Seq. ID LIB3145-006-Q1-K1-B8

Method BLASTX
NCBI GI 94455158
BLAST score 215
E value 3.0e-17
Match length 69
% identity 61

NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No. 210671

Seq. ID LIB3145-006-Q1-K1-C10

Method BLASTX
NCBI GI g1946366
BLAST score 150
E value 9.0e-10
Match length 125
% identity 37

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 210672

Seq. ID LIB3145-006-Q1-K1-C4

Method BLASTX
NCBI GI g4104931
BLAST score 147
E value 2.0e-09
Match length 136
% identity 37

NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No. 210673

Seq. ID LIB3145-006-Q1-K1-D1

Method BLASTX
NCBI GI g1052973
BLAST score 160
E value 7.0e-11
Match length 39
% identity 82

NCBI Description (U37838) fructokinase [Beta vulgaris]



```
210674
Seq. No.
                   LIB3145-006-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   q4508083
NCBI GI
                   171
BLAST score
                   4.0e-12
E value
                   67
Match length
% identity
                   (AC005882) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   210675
Seq. No.
                   LIB3145-006-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   g3024385
NCBI GI
                   664
BLAST score
                   6.0e-70
E value
                   141
Match length
                   91
% identity
                   POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi 606652
NCBI Description
                   (U09805) polygalacturonase [Gossypium barbadense]
                   210676
Seq. No.
                   LIB3145-006-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q586004
                   484
BLAST score
                   7.0e-49
E value
                   101
Match length
% identity
                   SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267
NCBI Description
                   superoxide dismutase (EC 1.15.1.\overline{1}) (Cu-\overline{Z}n) \overline{-} sweet potato
                   >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)
                    (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)
                    superoxide dismutase [Ipomoea batatas]
                   210677
Seq. No.
                   LIB3145-006-Q1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                    q3738334
                    175
BLAST score
E value
                    1.0e-12
Match length
                    102
                    48
 % identity
                    (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                    210678
 Seq. No.
Seq. ID
                    LIB3145-006-Q1-K1-D9
 Method
                    BLASTX
                    g400384
 NCBI GI
 BLAST score
                    147
                    2.0e-09
 E value
                    101
Match length
                    32
 % identity
                    NADH-UBIQUINONE OXIDOREDUCTASE B14 SUBUNIT (COMPLEX I-B14)
 NCBI Description
```

(CI-B14) >gi\_346536\_pir\_\_S28245 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B14 - bovine



>gi\_240\_emb\_CAA44896\_ (X63211) NADH dehydrogenase [Bos taurus]

Seq. No. 210679

Seq. ID LIB3145-006-Q1-K1-E10

Method BLASTX
NCBI GI g3201627
BLAST score 484
E value 8.0e-49
Match length 108
% identity 83

NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 210680

Seq. ID LIB3145-006-Q1-K1-E5

Method BLASTX
NCBI GI g3402693
BLAST score 418
E value 4.0e-41
Match length 134
% identity 63

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 210681

Seq. ID LIB3145-006-Q1-K1-E6

Method BLASTX
NCBI GI g3024386
BLAST score 674
E value 4.0e-71
Match length 134
% identity 96

NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)

>gi\_2129500\_pir\_\_S52006 polygalacturonase - upland cotton >gi\_606650 (U09717) polygalacturonase [Gossypium hirsutum]

Seq. No. 210682

Seq. ID LIB3145-006-Q1-K1-F10

Method BLASTX
NCBI GI g4204257
BLAST score 521
E value 3.0e-53
Match length 139
% identity 66

NCBI Description (AC005223) 5493 [Arabidopsis thaliana]

Seq. No. 210683

Seq. ID LIB3145-006-Q1-K1-F3

Method BLASTX
NCBI GI g2398679
BLAST score 708
E value 4.0e-75
Match length 137
% identity 97

NCBI Description (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate

synthase [Morinda citrifolia]

Seq. No. 210684

```
Seq. ID LIB3145-006-Q1-K1-F4 Method BLASTX
```

Method BLASTX

NCBI GI g1168739

BLAST score 461

E value 4.0e-46

Match length 130

% identity 70

NCBI Description CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi\_438449

(L18901) carbonic anhydrase [Arabidopsis thaliana]

 Seq. No.
 210685

 Seq. ID
 LIB3145-006-Q1-K1-F5

 Method
 BLASTX

NCBI GI g1871177 BLAST score 175 E value 1.0e-12 Match length 100 % identity 63

NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 210686

Seq. ID LIB3145-006-Q1-K1-F9

Method BLASTX
NCBI GI g3935170
BLAST score 405
E value 1.0e-39
Match length 112
% identity 62

NCBI Description (AC004557) F17L21.13 [Arabidopsis thaliana]

Seq. No. 210687

Seq. ID LIB3145-006-Q1-K1-G11

Method BLASTX
NCBI GI g1708464
BLAST score 261
E value 1.0e-22
Match length 69
% identity 70

NCBI Description PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD)

(2,3-DIHYDROXY ACID HYDROLYASE) >gi 1213255 emb CAA93689\_

(Z69795) unknown [Schizosaccharomyces pombe]

Seq. No. 210688

Seq. ID LIB3145-006-Q1-K1-G2

Method BLASTX
NCBI GI g100196
BLAST score 266
E value 3.0e-23
Match length 126
% identity 34

NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato

Seq. No. 210689

Seq. ID LIB3145-006-Q1-K1-G3

Method BLASTX NCBI GI g2493144 BLAST score 140



4.0e-09 E value Match length % identity 86 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE NCBI Description 16 KD PROTEOLIPID SUBUNIT) >gi\_2118221\_pir\_\_S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi\_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteol $\overline{ ext{ipid}}$  (Arabidopsis thaliana] 210690 Seq. No. LIB3145-006-Q1-K1-G5 Seq. ID Method BLASTX g4406819 NCBI GI BLAST score 100 5.0e-09 E value 86 Match length 47 % identity (AC006201) unknown protein [Arabidopsis thaliana] NCBI Description 210691 Seq. No. LIB3145-006-Q1-K1-G6 Seq. ID BLASTX Method g2982303 NCBI GI BLAST score 600 2.0e-62 E value 134 Match length 84 % identity (AF051236) hypothetical protein [Picea mariana] NCBI Description 210692 Seq. No. LIB3145-006-Q1-K1-H1 Seq. ID BLASTX Method NCBI GI q2088662 198 BLAST score E value 5.0e-32 Match length 126 61 % identity (AF002109) unknown protein [Arabidopsis thaliana] NCBI Description 210693 Seq. No. LIB3145-006-Q1-K1-H4 Seq. ID Method BLASTX NCBI GI g2191150 BLAST score 346 1.0e-56 E value Match length 135 62 % identity (AF007269) similar to mitochondrial carrier family NCBI Description [Arabidopsis thaliana]

Seq. No. 210694

Seq. ID LIB3145-006-Q1-K1-H5

Method BLASTX
NCBI GI g3746069
BLAST score 141
E value 1.0e-08

E value

Match length

% identity



```
Match length
% identity
                  31
                   (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  210695
Seq. No.
                  LIB3145-007-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  q3980383
NCBI GI
                   358
BLAST score
E value
                   5.0e-34
Match length
                   83
% identity
                   (AC004561) unknown protein [Arabidopsis thaliana]
NCBI Description
                   210696
Seq. No.
                   LIB3145-007-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   g3582436
NCBI GI
                   402
BLAST score
                   3.0e-42
E value
                   129
Match length
                   71
% identity
                   (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
NCBI Description
                   210697
Seq. No.
                   LIB3145-007-Q1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244740
                   407
BLAST score
E value
                   7.0e-40
                   118
Match length
% identity
                   68
                   (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   210698
                   LIB3145-007-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g128592
BLAST score
                   370
E value
                   2.0e-35
                   102
Match length
 % identity
                   POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                   >gi_82190_pir__S22495 pollen-specific protein precursor -
                   common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
                   specific protein [Nicotiana tabacum]
                   210699
 Seq. No.
                   LIB3145-007-Q1-K1-B2
 Seq. ID
                   BLASTX
 Method
                   q3980383
 NCBI GI
 BLAST score
                   369
                   2.0e-35
```

29161

NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]

83

81



```
210700
Seq. No.
                  LIB3145-007-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g2244740
NCBI GI
                  436
BLAST score
                  3.0e-43
E value
                  125
Match length
% identity
                  69
                  (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
NCBI Description
                  210701
Seq. No.
                  LIB3145-007-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  g3738297
NCBI GI
                   365
BLAST score
                   6.0e-35
E value
                   97
Match length
                   22
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   210702
Seq. No.
                   LIB3145-007-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   g4049401
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
                   57
Match length
                   65
% identity
                   (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
NCBI Description
                   thaliana]
                   210703
Seq. No.
                   LIB3145-007-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g4376203
NCBI GI
BLAST score
                   273
                   5.0e-24
E value
                   96
Match length
                   49
% identity
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
                   210704
Seq. No.
                   LIB3145-007-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g1173055
NCBI GI
                   602
BLAST score
E value
                   1.0e-62
                   120
Match length
% identity
                   60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__$42497
NCBI Description
                   ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                   RL5 ribosomal protein - alfalfa >gi_463252_emb CAA55090
                   (X78284) RL5 ribosomal protein [Medicago sativa]
```

Seq. No. 210705



```
LIB3145-007-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  q2052383
NCBI GI
                  177
BLAST score
                  8.0e-13
E value
                  41
Match length
                  76
% identity
                  (U66345) calreticulin [Arabidopsis thaliana]
NCBI Description
                  210706
Seq. No.
                  LIB3145-007-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157928
                  124
BLAST score
                   3.0e-16
E value
Match length
                   57
                   75
% identity
                   (ACO02131) Similar to fumarylacetoacetate hydrolase,
NCBI Description
                   gb L41670 from Emericella nidulans. [Arabidopsis thaliana]
                   210707
Seq. No.
                   LIB3145-007-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g509810
NCBI GI
BLAST score
                   363
                   1.0e-34
E value
                   139
Match length
                   53
% identity
                  (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                   210708
Seq. No.
                   LIB3145-007-Q1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4455313
                   271
BLAST score
E value
                   8.0e-24
Match length
                   103
                   52
% identity
                   (AL035528) fatty acid elongase-like protein (cer2-like)
NCBI Description
                   [Arabidopsis thaliana]
                   210709
Seq. No.
                   LIB3145-007-Q1-K1-C7
Seq. ID
Method
                   BLASTX
                   g4105798
NCBI GI
BLAST score
                   203
E value
                   8.0e-16
Match length
                   72
% identity
                   60
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   210710
Seq. No.
                   LIB3145-007-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g485514
NCBI GI
```

29163

**1**59

1.0e-10

BLAST score

E value



```
Match length
                  97
% identity
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                  >qi 296443 emb CAA49341 (X69640) auxin down regulated
                  [Glycine max]
                  210711
Seq. No.
                  LIB3145-007-Q1-K1-C9
Seq. ID
Method '
                  BLASTX
NCBI GI
                  g2501231
BLAST score
                  408
                  7.0e-40
E value
Match length
                  141
% identity
                  62
                  HYPOTHETICAL 38.1 KD PROTEIN >gi_99505_pir___$24930
NCBI Description
                  hypothetical protein - pink corydalis
                  >gi_18258_emb_CAA45139_ (X63595) protein of unknown
                  function [Corydalis sempervirens] >gi_444333_prf__1906382A
                  pCSC71 protein [Corydalis sempervirens]
Seq. No.
                  210712
                  LIB3145-007-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629561
BLAST score
                  143
E value
                   4.0e-18
                  119
Match length
% identity
                   45
                  SRG1 protein - Arabidopsis thaliana
NCBI Description
                   >qi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                   thaliana]
                   210713
Seq. No.
                   LIB3145-007-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g1076414
NCBI GI
BLAST score
                   534
                   1.0e-54
E value
                   151
Match length
% identity
                   subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
NCBI Description
                   thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)
                   subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                   210714
                   LIB3145-007-Q1-K1-D12
Seq. ID
Method
                   BLASTX
                   g2981463
NCBI GI
```

Method BLASTX
NCBI GI g2981463
BLAST score 316
E value 4.0e-29
Match length 147
% identity 44

NCBI Description (AF052663) gamma-tubulin interacting protein [Xenopus

laevis]

Seq. No. 210715

Seq. ID LIB3145-007-Q1-K1-D2

```
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  734
                  4.0e-78
E value
                  152
Match length
                  96
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  210716
Seq. No.
                  LIB3145-007-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g400976
BLAST score
                  551
E value
                  1.0e-56
                  140
Match length
                  74
% identity
NCBI Description RAS-RELATED PROTEIN RHA1 >gi_478671_pir__S23727 GTP-binding
                  protein RHA1 - Arabidopsis thaliana >gi_16484 emb CAA41863
                  (X59152) RHA1 [Arabidopsis thaliana]
                  >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  210717
Seq. ID
                  LIB3145-007-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  331
                  2.0e-51
E value
                  127
Match length
                  82
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  210718
Seq. No.
Seq. ID
                  LIB3145-007-Q1-K1-D7
Method
                  BLASTX
                  q4262149
NCBI GI
BLAST score
                  164
E value
                  3.0e-11
                  71
Match length
% identity
                  79
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  210719
Seq. ID
                  LIB3145-007-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4558673
BLAST score
                  215
E value
                  3.0e-17
                  105
```

Match length 109 % identity 33

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.

210720

Seq. ID

LIB3145-007-Q1-K1-E1

Method NCBI GI BLASTX g4235430

```
BLAST score
                  6.0e-32
E value
                  77
Match length
% identity
                  83
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
                  210721
Seq. No.
                  LIB3145-007-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g1488043
NCBI GI
                  170
BLAST score
                   4.0e-12
E value
                   47
Match length
                  72
% identity
                  (U63784) PAPS-reductase-like protein [Catharanthus roseus]
NCBI Description
                  210722
Seq. No.
                  LIB3145-007-Q1-K1-E4
Seq. ID
                  BLASTX
Method
                   q4512687
NCBI GI
BLAST score
                   200
                   2.0e-15
E value
                   84
Match length
                   55
% identity
                   (AC006931) floral homeotic protein AGL5 [Arabidopsis
NCBI Description
                   thaliana]
                   210723
Seq. No.
                   LIB3145-007-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   g3935168
NCBI GI
                   350
BLAST score
                   4.0e-33
E value
                   152
Match length
                   53
% identity
                  (AC004557) F17L21.11 [Arabidopsis thaliana]
NCBI Description
                   210724
Seq. No.
                   LIB3145-007-Q1-K1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1296816
                   704
BLAST score
                   1.0e-74
E value
                   147
Match length
                   92
% identity
                  (X94995) naringenin-chalcone synthase [Juglans sp.]
NCBI Description
                   210725
Seq. No.
Seq. ID
                   LIB3145-007-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2827544
                   164
BLAST score
                   3.0e-11
E value
                   84
Match length
                   46
% identity
                   (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
```

thaliana]

Seq. No.

Seq. ID

210731

LIB3145-007-Q1-K1-F9



```
210726
Seq. No.
                  LIB3145-007-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  q167367
NCBI GI
                  579
BLAST score
                  5.0e-60
E value
                  129
Match length
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  210727
Seq. No.
                  LIB3145-007-Q1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244749
BLAST score
                  612
                  8.0e-64
E value
                  127
Match length
                  89
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                  210728
Seq. No.
                  LIB3145-007-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g1617584
NCBI GI
BLAST score
                  345
                  2.0e-32
E value
                  148
Match length
% identity
                  45
NCBI Description (U70675) pectin methylesterase [Lycopersicon esculentum]
                  210729
Seq. No.
                  LIB3145-007-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g231586
NCBI GI
                  362
BLAST score
                  2.0e-34
E value
                  80
Match length
                  91
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain, mitochondrial - Para rubber tree
                   >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
                   210730
Seq. No.
                   LIB3145-007-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1769895
                   477
BLAST score
                   5.0e-48
E value
                   152
Match length
 % identity
                  (X96598) CaLB protein [Arabidopsis thaliana]
NCBI Description
```

```
BLASTX
Method
                   g3132675
NCBI GI
                   541
BLAST score
                   2.0e-62
E value
                   148
Match length
                   80
% identity
                   (AF061740) asparagine synthetase [Elaeagnus umbellata]
NCBI Description
                   210732
Seq. No.
                   LIB3145-007-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   g4455206
NCBI GI
                   268
BLAST score
                   2.0e-23
E value
Match length
                   81
                   56
% identity
                   (AL035440) putative beta-1, 3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   210733
Seq. No.
                   LIB3145-007-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g3914685
NCBI GI
                   307
BLAST score
```

1.0e-36 E value Match length 89 85 % identity

60S RIBOSOMAL PROTEIN L17 >gi\_2668748 (AF034948) ribosomal NCBI Description

protein L17 [Zea mays]

210734 Seq. No. LIB3145-007-Q1-K1-G11 Seq. ID BLASTX Method g115765 NCBI GI BLAST score 626 2.0e-65 E value

136 Match length 53 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR NCBI Description (CAB-7) >gi\_100201\_pir\_\_S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi\_19180\_emb\_CAA32197\_

(X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_226546\_prf\_\_1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

210735 Seq. No.

LIB3145-007-Q1-K1-G12 Seq. ID

Method BLASTX g1864017 NCBI GI 735 BLAST score 3.0e-78 E value 143 Match length 97 % identity

(D63396) elongation factor-1 alpha [Nicotiana tabacum] NCBI Description

NCBI Description



```
210736
Seq. No.
                  LIB3145-007-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g2655008
NCBI GI
                  197
BLAST score
                  4.0e-15
E value
Match length
                  84
% identity
                  42
                  (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  210737
                  LIB3145-007-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1588365
BLAST score
                  174
                  2.0e-12
E value
Match length
                  78
                  41
% identity
NCBI Description signal peptidase:SUBUNIT=12kD [Homo sapiens]
                  210738
Seq. No.
Seq. ID
                  LIB3145-007-Q1-K1-H2
Method
                  BLASTX
                  q3023500
NCBI GI
                  493
BLAST score
                  6.0e-50
E value
                  134
Match length
% identity
                  70
                  ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 2
NCBI Description
                   (ENDOPEPTIDASE CLP 2) >gi_2351823 (U92039) ATP-dependent
                  Clp protease, proteolytic subunit [Synechococcus PCC7942]
                   210739
Seq. No.
Seq. ID
                  LIB3145-007-Q1-K1-H7
Method
                  BLASTX
                   q730290
NCBI GI
                   436
BLAST score
E value
                   6.0e-52
Match length
                   137
% identity
                   65
                   PECTATE LYASE PRECURSOR >gi 322883_pir__S29612 pectate
NCBI Description
                   lyase - trumpet lily >gi_19451_emb_CAA78976_ (Z17328)
                   pectate lyase [Lilium longiflorum] >gi_308902 (L18911)
                   pectate lyase [Lilium longiflorum]
Seq. No.
                   210740
                   LIB3145-007-Q1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3193314
BLAST score
                   316
                   4.0e-29
E value
                   151
Match length
                   47
% identity
                   (AF069299) contains similarity to Arabidopsis scarecrow
```

(GB:U62798) [Arabidopsis thaliana]



```
210741
Seq. No.
                  LIB3145-008-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g4220479
NCBI GI
                  572
BLAST score
                  4.0e-59
E value
                  148
Match length
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  210742
Seq. No.
                  LIB3145-008-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2388586
                   193
BLAST score
                   1.0e-14
E value
                   53
Match length
                   75
% identity
                   (AC000098) Similar to Saccharomyces RAD16 (gb_X78993).
NCBI Description
                   [Arabidopsis thaliana]
                   210743
Seq. No.
                   LIB3145-008-Q1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g730526
BLAST score
                   404
                   2.0e-39
E value
                   102
Match length
                   77
% identity
                   60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
                   >gi 480787_pir__S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >qi 404166 emb CAA53005 (X75162) BBC1 protein
                   [Arabidopsis thaliana]
                   210744
Seq. No.
                   LIB3145-008-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   q3860277
NCBI GI
BLAST score
                   345
                   1.0e-32
E value
Match length
                   83
                   84
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   210745
 Seq. No.
                   LIB3145-008-Q1-K1-A7
 Seq. ID
                   BLASTX
 Method
                   g2702263
 NCBI GI
 BLAST score
                   510
                   6.0e-52
 E value
```

[Arabidopsis thaliana]

125

82

Match length

NCBI Description

% identity

(AC003033) mitochondrial F1-ATPase, gamma subunit



```
210746
Seq. No.
                  LIB3145-008-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g729252
NCBI GI
                  355
BLAST score
                  8.0e-34
E value
                  103
Match length
                  60
% identity
                  CYTOCHROME B5 >gi_167140 (M87514) cytochrome b-5 [Brassica
NCBI Description
                  oleracea] >gi_384338_prf__1905426A cytochrome b5 [Brassica
                  oleracea]
                  210747
Seq. No.
                  LIB3145-008-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g927428
NCBI GI
                   613
BLAST score
                   6.0e-64
E value
Match length
                  145
                   78
% identity
NCBI Description (X86733) fis1 [Linum usitatissimum]
                   210748
Seq. No.
                   LIB3145-008-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g4417268
NCBI GI
                   460
BLAST score
                   5.0e-46
E value
                   117
Match length
                   65
% identity
                   (AC007019) putative cinnamyl-alcohol dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                   210749
Seq. No.
                   LIB3145-008-Q1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2760334
                   415
BLAST score
                   8.0e-41
E value
Match length
                   90
% identity
                   (AC002130) F1N21.5 [Arabidopsis thaliana]
NCBI Description
                   210750
Seq. No.
                   LIB3145-008-Q1-K1-B7
 Seq. ID
                   BLASTX
Method
                   g4567267
NCBI GI
                   471
BLAST score
                   2.0e-47
E value
                   102
Match length
 % identity
                   81
                   (AC006841) putative zinc finger protein [Arabidopsis
 NCBI Description
                   thaliana]
```

210751

BLASTX

LIB3145-008-Q1-K1-B8

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

g2257524

261 9.0e-23



```
q2262172
NCBI GI
BLAST score
                  151
                  7.0e-10
E value
                  95
Match length
                  41
% identity
                  (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                  210752
Seq. No.
                  LIB3145-008-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4105798
BLAST score
                  443
E value
                  5.0e-44
                  117
Match length
                   62
% identity
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
                   210753
Seq. No.
                  LIB3145-008-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g2827139
NCBI GI
                   432
BLAST score
                   1.0e-42
E value
Match length
                   138
                   62
% identity
                  (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_4049343_emb_CAA22568
                                                                     (AL034567)
                   cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                   thalianal
                   210754
Seq. No.
                   LIB3145-008-Q1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1350680
BLAST score
                   532
                   2.0e-54
E value
Match length
                   126
                   78
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                   210755
Seq. No.
                   LIB3145-008-Q1-K1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1685091
                   563
BLAST score
                   4.0e-58
E value
                   139
Match length
 % identity
                  (U45243) diphenol oxidase [Nicotiana tabacum]
NCBI Description
                   210756
 Seq. No.
                   LIB3145-008-Q1-K1-C2
 Seq. ID
Method
                   BLASTX
```



Match length 117 % identity 45

NCBI Description (AB004537) HYPOTHETICAL 47.4KD PROTEIN IN SHP1-SEC17

INTERGENIC REGION [Schizosaccharomyces pombe]

Seq. No. 210757

Seq. ID LIB3145-008-Q1-K1-C3

Method BLASTX
NCBI GI g134944
BLAST score 494
E value 4.0e-50
Match length 120
% identity 75

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi\_100502\_pir\_\_A39173 acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)

precursor - safflower >gi\_167197 (M61109)

stearoyl-acyl-carrier protein desaturase [Carthamus

tinctorius]

Seq. No. 210758

Seq. ID LIB3145-008-Q1-K1-C4

Method BLASTX
NCBI GI g4008159
BLAST score 600
E value 2.0e-62
Match length 123
% identity 89

NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]

Seq. No. 210759

Seq. ID LIB3145-008-Q1-K1-C5

Method BLASTX
NCBI GI g1777312
BLAST score 432
E value 9.0e-43
Match length 118
% identity 66

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 210760

Seq. ID LIB3145-008-Q1-K1-C8

Method BLASTX
NCBI GI g3334261
BLAST score 141
E value 1.0e-08
Match length 48
% identity 56

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi\_1655851 (U61973)

metallothionein-like protein [Malus domestica]

Seq. No. 210761

Seq. ID LIB3145-008-Q1-K1-D10

Method BLASTX
NCBI GI g1685091
BLAST score 123

```
E value
                   60
Match length
                   62
% identity
                  (U45243) diphenol oxidase [Nicotiana tabacum]
NCBI Description
                  210762
Seq. No.
                  LIB3145-008-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                   g3582329
NCBI GI
                  140
BLAST score
                   1.0e-08
E value
                   121
Match length
% identity
                   34
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                   210763
Seq. No.
                   LIB3145-008-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   g4262149
NCBI GI
                   190
BLAST score
                   2.0e-14
E value
                   53
Match length
                   66
% identity
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
                   210764
Seq. No.
                   LIB3145-008-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g3850581
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   69
Match length
                   65
% identity
                   (AC005278) EST gb_N96383 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   210765
Seq. No.
                   LIB3145-008-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g2369766
NCBI GI
                   351
BLAST score
E value
                   3.0e - 33
                   108
Match length
                   63
 % identity
                   (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   210766
 Seq. No.
                   LIB3145-008-Q1-K1-E12
 Seq. ID
Method
                   BLASTX
                   g2695861
 NCBI GI
 BLAST score
                   522
                   3.0e-53
 E value
 Match length
                   124
                   81
 % identity
                   (Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate
 NCBI Description
                   synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273)
```





3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum sativum]

 Seq. No.
 210767

 Seq. ID
 LIB3145-008-Q1-K1-E2

 Method
 BLASTX

 NCBI GI
 g2281334

BLAST score 404
E value 2.0e-39
Match length 126
% identity 59

NCBI Description (U83619) putative pectate lyase [Arabidopsis thaliana]

Seq. No. 210768

Seq. ID LIB3145-008-Q1-K1-E4

Method BLASTX
NCBI GI g2511531
BLAST score 523
E value 2.0e-53
Match length 125
% identity 85

NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]

>gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1

[Eleusine indica]

Seq. No. 210769

Seq. ID LIB3145-008-Q1-K1-E7

Method BLASTX
NCBI GI g1175468
BLAST score 142
E value 9.0e-09
Match length 98
% identity 37

NCBI Description HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I

>gi 2130328 pir S62451 hypothetical protein SPAC22G7.07c -

fission yeast (Schizosaccharomyces pombe)

>gi 1009457 emb CAA91131.1 (Z54328) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 210770

Seq. ID LIB3145-008-Q1-K1-E8

Method BLASTX
NCBI GI g3445212
BLAST score 190
E value 2.0e-14
Match length 52
% identity 69

NCBI Description (AC004786) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No. 210771

Seq. ID LIB3145-008-Q1-K1-F1

Method BLASTX
NCBI GI g2642158
BLAST score 480
E value 2.0e-48
Match length 114

Seq. ID

Method



```
% identity
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  210772
Seq. No.
                  LIB3145-008-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g2384671
NCBI GI
                  538
BLAST score
                  4.0e-55
E value
                  142
Match length
                  73
% identity
                   (AF012657) putative potassium transporter AtKT2p
NCBI Description
                   [Arabidopsis thaliana]
                   210773
Seq. No.
                  LIB3145-008-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g2842490
NCBI GI
                   253
BLAST score
                   8.0e-22
E value
                   67
Match length
                   69
% identity
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   210774
Seq. No.
                   LIB3145-008-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g2369714
NCBI GI
                   154
BLAST score
                   2.0e-10
E value
                   75
Match length
                   49
% identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   210775
Seq. No.
                   LIB3145-008-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   q4126401
NCBI GI
BLAST score
                   406
                   9.0e-40
E value
                   92
Match length
                   85
% identity
                   (AB011795) flavanone 3-hydroxylase [Citrus sinensis]
NCBI Description
                   210776
 Seq. No.
                   LIB3145-008-Q1-K1-F6
 Seq. ID
                   BLASTX
Method
                   g4432834
 NCBI GI
                   203
 BLAST score
                   5.0e-16
 E value
                   79
 Match length
                   57
 % identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   210777
 Seq. No.
```

29176

LIB3145-008-Q1-K1-F7

BLASTX

E value

Match length

```
NCBI GI
                  a2961390
BLAST score
                  495
                  4.0e-50
E value
                  122
Match length
                  66
% identity
                  (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  210778
Seq. No.
                  LIB3145-008-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1871185
BLAST score
                  620
E value
                  1.0e-64
                  135
Match length
                  79
% identity
                  (U90439) seven in absentia isolog [Arabidopsis thaliana]
NCBI Description
                  210779
Seq. No.
                  LIB3145-008-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                   q4455293
NCBI GI
BLAST score
                   376
E value
                   3.0e-36
                   88
Match length
                   90
% identity
                  (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   210780
Seq. No.
                   LIB3145-008-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   q481236
NCBI GI
                   236
BLAST score
E value
                   8.0e-20
                   58
Match length
% identity
                   79
                   hypothetical protein - Madagascar periwinkle
NCBI Description
                   >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
                   [Catharanthus roseus]
                   210781
Seq. No.
                   LIB3145-008-Q1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1666897
BLAST score
                   140
                   1.0e-08
E value
Match length
                   85
% identity
                   33
                  (U75969) CHL1 protein [Homo sapiens]
NCBI Description
                   210782
Seq. No.
                   LIB3145-008-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   g4544460
NCBI GI
                   144
BLAST score
                   5.0e-09
```

NCBI Description

```
% identity
                  (AC006592) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  210783
Seq. No.
                  LIB3145-009-Q1-K1-A10
Seq. ID
                  BLASTX
Method
                  g3080420
NCBI GI
                  359
BLAST score
                  3.0e - 34
E value
                  116
Match length
                   63
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  210784
Seq. No.
                  LIB3145-009-Q1-K1-A6
Seq. ID
                  BLASTN
Method
                  g3108329
NCBI GI
                   180
BLAST score
                   9.0e-97
E value
                   227
Match length
                   95
% identity
NCBI Description Gossypium barbadense clone pXP3-50 repetitive DNA sequence
                   210785
Seq. No.
                   LIB3145-009-Q1-K1-A7
Seq. ID
                   BLASTX
Method
                   q4567229
NCBI GI
                   206
BLAST score
                   3.0e-16
E value
                   89
Match length
                   45
% identity
                   (AC007119) putative pectin methylesterase [Arabidopsis
NCBI Description
                   thaliana]
                   210786
Seq. No.
                   LIB3145-009-Q1-K1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3608479
                   312
BLAST score
E value
                   1.0e-28
                   85
Match length
                   72
% identity
                  (AF088912) ribosomal protein L15 [Petunia x hybrida]
NCBI Description
                   210787
Seq. No.
                   LIB3145-009-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   g729273
NCBI GI
BLAST score
                   701
                   3.0e-74
E value
                   143
Match length
                   90
% identity
```

29178

cardunculus]

CYPRO4 PROTEIN >gi\_322804\_pir\_\_S28592 cypro4 protein -

cardoon >gi\_17959\_emb\_CAA49354\_ (X69672) cypro4 [Cynara



% identity

```
Seq. No.
                  210788
                  LIB3145-009-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2232057
BLAST score
                  157
E value
                  2.0e-10
Match length
                  49
% identity
                  63
NCBI Description
                  (AF000177) CaSm [Homo sapiens]
Seq. No.
                  210789
Seq. ID
                  LIB3145-009-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3212871
BLAST score
                  599
E value
                  3.0e-62
Match length
                  139
                  82
% identity
                   (AC004005) putative translation initiation factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  210790
Seq. ID
                  LIB3145-009-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                   q1170622
BLAST score
                   212
E value
                   6.0e-17
Match length
                   107
                   46
% identity
                  CASEIN KINASE I, DELTA ISOFORM LIKE (CKI-DELTA) >gi_549973
NCBI Description
                   (U12857) casein kinase I-like protein; similar to the rat
                   delta isoform of casein kinase I, Swiss-Prot Accession
                   Number Q06486 [Arabidopsis thaliana]
                   210791
Seq. No.
                   LIB3145-009-Q1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q418854
BLAST score
                   721
                   1.0e-76
E value
                   146
Match length
% identity
                   17
                   ubiquitin precursor - parsley >gi_288112_emb_CAA45621
NCBI Description
                   (X64344) polyubiquitin [Petroselinum crispum]
                   >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
Seq. No.
                   210792
                   LIB3145-009-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g2252866
NCBI GI
BLAST score
                   185
                   9.0e-14
E value
                   54
Match length
```

NCBI Description (AF013294) contains region of similarity to SYT



## [Arabidopsis thaliana]

```
Seq. No.
                  210793
                  LIB3145-009-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g755150
BLAST score
                  401
                  4.0e-39
E value
                  114
Match length
                   51
% identity
                   (U13670) vacuolar H+-ATPase proteolipid (16 kDa) subunit
NCBI Description
                   [Gossypium hirsutum]
                   210794
Seq. No.
                  LIB3145-009-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                   g1706377
NCBI GI
BLAST score
                   558
                   1.0e-60
E value
                   140
Match length
% identity
                   83
                  DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
NCBI Description
                   4-REDUCTASE) >qi 499018 emb CAA53578 (X75964)
                   dihydroflavonol reductase [Vitis vinifera]
                   210795
Seq. No.
                   LIB3145-009-Q1-K1-C8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2656031
BLAST score
                   36
                   1.0e-10
E value
Match length
                   56
                   91
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC20
                   210796
Seq. No.
                   LIB3145-009-Q1-K1-D1
Seq. ID
Method
                   BLASTX
                   g3763916
NCBI GI
                   240
BLAST score
                   3.0e-20
E value
                   140
Match length
% identity
                   41
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4531439 gb AAD22124.1 AC006224_6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
                   210797
Seq. No.
Seq. ID
                   LIB3145-009-Q1-K1-D10
                   BLASTX
Method
                   g114682
NCBI GI
BLAST score
                   304
                   1.0e-27
E value
                   93
Match length
                   67
% identity
NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
```





(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi\_100471\_pir\_\_A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi\_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

NCBI GI g126962
BLAST score 267
E value 1.0e-23
Match length 110
% identity 54

NCBI Description TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7

>gi\_99747\_pir\_\_S13718 probable membrane channel protein Arabidopsis thaliana >gi\_16492\_emb\_CAA38633\_ (X54854)
possible membrane channel protein [Arabidopsis thaliana]

Seq. No. 210799

Seq. ID LIB3145-009-Q1-K1-D8

Method BLASTX
NCBI GI g2136139
BLAST score 321
E value 1.0e-29
Match length 140
% identity 12

NCBI Description sds22 protein homolog - human >gi\_1085028\_emb\_CAA90626\_

(Z50749) yeast sds22 homolog [Homo sapiens]

>gi\_1585165\_prf\_\_2124310A sds22 gene [Homo sapiens]

>gi\_4506013\_ref\_NP\_002703.1\_pPPP1R7\_ protein phosphatase 1,

regulatory subunit

Seq. No. 210800

Seq. ID LIB3145-009-Q1-K1-E1

Method BLASTX
NCBI GI g2500378
BLAST score 256
E value 4.0e-22
Match length 57
% identity 84

NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 210801

Seq. ID LIB3145-009-Q1-K1-E4

Method BLASTN
NCBI GI g642361
BLAST score 40
E value 4.0e-13
Match length 44
% identity 98

NCBI Description T.ranunculoides ITS2 and 28S rRNA gene (partial)

Seq. No. 210802

Seq. ID LIB3145-009-Q1-K1-E7

Method BLASTX NCBI GI g3335367

BLAST score 162 E value 4.0e-11 Match length 54 % identity 46

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.

210803

Seq. ID

LIB3145-009-Q1-K1-F12

Method BLASTX
NCBI GI g135860
BLAST score 513
E value 3.0e-52
Match length 131
% identity 79

NCBI Description

TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi\_99761\_pir\_\_S22202 tonoplast intrinsic

protein gamma - Arabidopsis thaliana

>gi 16312\_emb\_CAA45115\_ (X63552) tonoplast intrinsic

protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi\_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi\_445129\_prf\_\_1908432B tonoplast intrinsic protein gamma

[Arabidopsis thaliana]

Seq. No.

210804

Seq. ID LIB3145-009-Q1-K1-F2

Method BLASTX
NCBI GI g462013
BLAST score 623
E value 4.0e-65
Match length 142
% identity 82

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_542022\_pir\_\_S39558 HSP90 homolog - Madagascar
periwinkle >gi\_348696 (L14594) heat shock protein 90

[Catharanthus roseus]

Seq. No. 210805

Seq. ID LIB3145-009-Q1-K1-F5

Method BLASTX
NCBI GI g1220196
BLAST score 600
E value 2.0e-62
Match length 133
% identity 86

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 210806

Seq. ID LIB3145-009-Q1-K1-F6

Method BLASTX
NCBI GI g399013
BLAST score 549
E value 2.0e-56
Match length 124
% identity 35

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi\_99658\_pir\_\_S21313 ADP,ATP carrier protein - Arabidopsis



thaliana (fragment) >gi\_16175\_emb\_CAA46518\_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi\_445607\_prf\_\_1909354A adenylate translocator [Arabidopsis thaliana]

 Seq. No.
 210807

 Seq. ID
 LIB3145-009-Q1-K1-F7

 Method
 BLASTX

 NCBI GI
 g2339980

 BLAST score
 542

 E value
 1.0e-55

E value 1.06 Match length 141 % identity 74

NCBI Description (Y11337) RGA2 protein [Arabidopsis thaliana]

Seq. No. 210808

Seq. ID LIB3145-009-Q1-K1-F8

Method BLASTX
NCBI GI g2499966
BLAST score 173
E value 2.0e-12
Match length 35
% identity 94

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E

A) >gi\_632722\_bbs\_151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,

141 aa] [Nicotiana sylvestris]

Seq. No. 210809

Seq. ID LIB3145-009-Q1-K1-G1

Method BLASTX
NCBI GI g2213610
BLAST score 211
E value 6.0e-17
Match length 124
% identity 23

NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No. 210810

Seq. ID LIB3145-009-Q1-K1-G12

Method BLASTX
NCBI GI g3885328
BLAST score 239
E value 4.0e-20
Match length 130
% identity 42

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 210811

Seq. ID LIB3145-009-Q1-K1-G3

Method BLASTX
NCBI GI g122085
BLAST score 507
E value 2.0e-51
Match length 120
% identity 85



NCBI Description

HISTONE H3 >gi\_81641\_pir\_ S06250 histone H3 - Arabidopsis thaliana >gi 82482 pir S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi\_168506 (M35388) histone H3 [Zea mays] >gi\_169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi 169659 (M77495) histone H3 [Petroselinum crispum] >gi 387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738 emb\_CAA59111\_ (X84377) histone 3 [Zea mays] >gi  $1\overline{0}40764$  (M35 $\overline{3}87$ ) histone H3 [Arabidopsis thaliana]  $> \overline{g}i$  1314779 (U54827) histone H3 homolog [Brassica napus] >gi 1531754 emb CAA57811 Histone H3 [Asparagus officinalis] >gi\_1667592 (U77296) histone 3 [Oryza sativa] >gi 3249101 ( $\overline{A}$ C003114) Match to histone H3 gene gb\_M17131 and gb\_M35387 from A. thaliana. ESTs gb H76511 gb H76255, gb AA712452, gb N65260 and qb T42306 come from this gene. [Arabidopsis thaliana] >gi 225459 prf 1303352A histone H3 [Helicoverpa zea]
>gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

 Seq. No.
 210812

 Seq. ID
 LIB3145-009-Q1-K1-G8

 Method
 BLASTX

 NCBI GI
 g3901268

 BLAST score
 168

 E value
 9.0e-12

Match length 117 % identity 37

NCBI Description (AF060173) SV2 related protein [Rattus norvegicus]

Seq. No. 210813

Seq. ID LIB3145-009-Q1-K1-G9

Method BLASTX
NCBI GI g1363325
BLAST score 232
E value 3.0e-19
Match length 71
% identity 63

NCBI Description RNA helicase HEL117 - rat >gi\_897915 (U25746) RNA helicase

[Rattus norvegicus]

Seq. No. 210814

Seq. ID LIB3145-009-Q1-K1-H1

Method BLASTX
NCBI GI g2982444
BLAST score 506
E value 2.0e-51
Match length 131
% identity 75

NCBI Description (AL022224) CLV1 receptor kinase like protein [Arabidopsis

thaliana]



```
Seq. No.
                  LIB3145-009-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g3757522
NCBI GI
                  193
BLAST score
E value
                  1.0e-14
Match length
                  60
                  58
% identity
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
                  210816
Seq. No.
                  LIB3145-009-Q1-K1-H3
Seq. ID
Method
                  BLASTX
                   q2655008
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
                   134
Match length
                   49
% identity
                  (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                   esculentum]
                   210817
Seq. No.
                   LIB3145-009-Q1-K1-H6
Seq. ID
Method
                   BLASTX
                   q3402711
NCBI GI
BLAST score
                   307
                   3.0e-28
E value
                   77
Match length
                   33
% identity
                   (ACO04261) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   210818
Seq. No.
                   LIB3145-010-Q1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3413511
BLAST score
                   169
                   5.0e-12
E value
                   86
Match length
% identity
                   58
                   (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
                   oleracea]
                   210819
Seq. No.
                   LIB3145-010-Q1-K1-A10
Seq. ID
Method
                   BLASTX
                   g3386604
NCBI GI
BLAST score
                   144
                   3.0e-09
E value
Match length
                   72
                   39
 % identity
                   (AC004665) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   210820
 Seq. No.
                   LIB3145-010-Q1-K1-A11
 Seq. ID
```

BLASTX

g3738320

Method

NCBI GI

```
BLAST score
                  8.0e-09
E value
                  86
Match length
                  37
% identity
                   (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                   210821
Seq. No.
                  LIB3145-010-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g2961389
NCBI GI
BLAST score
                   480
                   2.0e-48
E value
Match length
                   131
                   64
% identity
                   (AL022141) purple acid phosphatase like protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4006925_emb_CAB16853_ (Z99708)
                   purple acid phosphatase like protein [Arabidopsis thaliana]
                   210822
Seq. No.
                   LIB3145-010-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3367534
BLAST score
                   468
                   4.0e-47
E value
                   111
Match length
                   80
% identity
                   (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                   thaliana]
                   210823
Seq. No.
Seq. ID
                   LIB3145-010-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g3337361
                   499
BLAST score
                   1.0e-50
E value
                   120
Match length
                   73
% identity
                   (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                   210824
Seq. No.
                   LIB3145-010-Q1-K1-B3
Seq. ID
                   BLASTN
Method
                   g18058
NCBI GI
BLAST score
                   36
                   4.0e-11
E value
                   48
Match length
                   94
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
                   210825
Seq. No.
                   LIB3145-010-Q1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244780
BLAST score
                   199
```

1.0e-15

E value



93

Match length

% identity

```
Match length
                  55
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  210826
Seq. No.
                  LIB3145-010-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1814403
BLAST score
                  538
                  3.0e-55
E value
Match length
                  123
% identity
                  83
                  (U84889) methionine synthase [Mesembryanthemum
NCBI Description
                  crystallinum]
                   210827
Seq. No.
Seq. ID
                   LIB3145-010-Q1-K1-C3
Method
                   BLASTX
                   g3334128
NCBI GI
                   199
BLAST score
                   2.0e-15
E value
                   96
Match length
                   52
% identity
                   BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE
NCBI Description
                   PRECURSOR (BCCP) >gi_1066348 (U23155) acetyl-CoA
                   carboxylase biotin-containing subunit [Arabidopsis
                   thaliana]
Seq. No.
                   210828
                   LIB3145-010-Q1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3608479
BLAST score
                   262
                   4.0e-23
E value
                   85
Match length
% identity
                   67
                  (AF088912) ribosomal protein L15 [Petunia x hybrida]
NCBI Description
Seq. No.
                   210829
                   LIB3145-010-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g2244924
NCBI GI
BLAST score
                   391
                   6.0e-38
E value
                   98
Match length
                   71
% identity
                  (Z97339) glutaredoxin [Arabidopsis thaliana]
NCBI Description
                   210830
Seq. No.
                   LIB3145-010-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   q4210948
NCBI GI
                   147
BLAST score
                   1.0e-09
E value
```

29187

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]



```
Seq. No.
                  210831
                  LIB3145-010-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1711507
BLAST score
                  328
E value
                  1.0e-30
Match length
                  75
                  79
% identity
NCBI Description
                  SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19)
                  >qi 624221 (U19030) signal recognition particle 19 kDa
                  protein subunit SRP19 [Oryza sativa]
Seq. No.
                  210832
Seq. ID
                  LIB3145-010-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  157
E value
                  1.0e-10
Match length
                  29
                  100
% identity
NCBI Description
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                  210833
Seq. ID
                  LIB3145-010-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4056468
BLAST score
                  212
                  6.0e-17
E value
Match length
                  108
% identity
                   (AC005990) Contains similarity to gb X66426
NCBI Description
                  polygalacturonase from Persea americana and is a member of
                  the signal peptidase family PF 00461 and polygalacturonase
                  family PF 00295. [Arabidopsis thaliana]
                  210834
Seq. No.
Seq. ID
                  LIB3145-010-Q1-K1-D4
Method
                  BLASTX
                  g2129727
NCBI GI
                  382
BLAST score
                  6.0e-37
E value
Match length
                  87
                  57
% identity
                  RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153
NCBI Description
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  210835
Seq. ID
                  LIB3145-010-Q1-K1-D6
                  BLASTX
Method
NCBI GI
                  g3249098
```

Method BLASTX
NCBI GI g3249098
BLAST score 147
E value 2.0e-09
Match length 82
% identity 43

NCBI Description (AC003114) ESTs gb\_T04610, gb\_N38459, gb\_T45174, gb\_R30481 and gb N64971 come from this gene. [Arabidopsis thaliana]



```
210836
Seq. No.
                  LIB3145-010-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2879811
BLAST score
                  356
                  4.0e-34
E value
Match length
                  70
                                 "My . . .
                  90
% identity
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
Seq. No.
                  210837
                  LIB3145-010-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3869253
                   139
BLAST score
                   3.0e-16
E value
Match length
                   105
% identity
                   50
                   (U39288) ferredoxin-dependent glutamate synthase precursor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   210838
Seq. ID
                   LIB3145-010-Q1-K1-E5
                   BLASTN
Method
                   q18058
NCBI GI
                   237
BLAST score
                   1.0e-131
E value
Match length
                   275
                   97
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
                   210839
Seq. No.
                   LIB3145-010-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729974
BLAST score
                   317
                   2.0e-29
E value
Match length
                   78
% identity
                   76
                   FLORAL HOMEOTIC PROTEIN PMADS1 (GREEN PETAL HOMEOTIC
NCBI Description
                   PROTEIN) >gi_322773_pir__S31693 transcription factor gp -
                   garden petunia >gi_22665_emb_CAA49567_ (X69946) GP (green
                   petal) [Petunia x hybrida]
                   210840
Seq. No.
                   LIB3145-010-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g4406780
NCBI GI
                   566
BLAST score
                   2.0e-58
E value
```

133 Match length 83 % identity

(AC006532) putative multispanning membrane protein NCBI Description

[Arabidopsis thaliana]

210841 Seq. No.

Seq. No. Seq. ID

Method NCBI GI



```
LIB3145-010-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g4006882
NCBI GI
                  196
BLAST score
                  2.0e-16
E value
Match length
                   61
                  75
% identity
                   (Z99707) UDP-glucuronyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   210842
Seq. No.
                  LIB3145-010-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                   q1730109
NCBI GI
                   472
BLAST score
                   1.0e-47
E value
Match length
                   104
                   78
% identity
                   LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                   HYDROXYLASE) >gi_499022_emb_CAA53580 (X75966)
                   leucoanthocyanidin dioxygenase [Vitis vinifera]
Seq. No.
                   210843
                   LIB3145-010-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   q3063453
NCBI GI
                   341
BLAST score
                   4.0e-32
E value
                   136
Match length
                   52
% identity
                  (AC003981) F22013.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210844
                   LIB3145-010-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4432860
NCBI GI
                   276
BLAST score
                   1.0e-24
E value
                   95
Match length
                   29
% identity
                   (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
                   210845
Seq. No.
                   LIB3145-010-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   g1130682
NCBI GI
BLAST score
                   656
                   5.0e-69
E value
                   134
Match length
                   94
 % identity
NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]
                   210846
```

29190

LIB3145-010-Q1-K1-G8

BLASTX

g1209703



```
BLAST score
                  3.0e-29
E value
                   95
Match length
                   61
% identity
                  (U40489) maize gl1 homolog [Arabidopsis thaliana]
NCBI Description
                   210847
Seq. No.
                  LIB3145-010-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                   g3478637
NCBI GI
                   344
BLAST score
                   2.0e-32
E value
                   138
Match length
% identity
                   47
                  (AC005546) R29425_1 [Homo sapiens]
NCBI Description
                   210848
Seq. No.
                   LIB3145-010-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   g462195
NCBI GI
                   367
BLAST score
                   4.0e-35
E value
                   86
Match length
                   84
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
                   210849
Seq. No.
                   LIB3145-010-Q1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q927428
                   473
BLAST score
E value
                   1.0e-47
Match length
                   128
                   80
% identity
                   (X86733) fis1 [Linum usitatissimum]
NCBI Description
                   210850
Seq. No.
                   LIB3145-010-Q1-K1-H6
 Seq. ID
                   BLASTN
Method
                   g4098126
 NCBI GI
 BLAST score
                   62
                   3.0e-26
 E value
                   70
Match length
                   97
 % identity
                   Gossypium hirsutum sucrose synthase mRNA, partial cds
 NCBI Description
 Seq. No.
                    210851
                   LIB3145-010-Q1-K1-H8
 Seq. ID
                   BLASTX
 Method
                    g4204276
 NCBI GI
                    269
 BLAST score
```

1.0e-23

122

E value

Match length



```
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210852
                  LIB3145-011-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  g3738325
NCBI GI
BLAST score
                  197
E value
                  3.0e-15
                  58
Match length
                  67
% identity
                  (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                  thaliana]
                  210853
Seq. No.
                  LIB3145-011-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885340
BLAST score
                  246
                  1.0e-25
E value
                  87
Match length
                  71
% identity
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
Seq. No.
                  210854
Seq. ID
                  LIB3145-011-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4090257
                  286
BLAST score
                  1.0e-25
E value
Match length
                  61
                  89
% identity
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
                  210855
Seq. No.
Seq. ID
                  LIB3145-011-Q1-K1-A6
Method
                  BLASTX
                  q115794
NCBI GI
BLAST score
                  497
                  1.0e-50
E value
Match length
                  99
                  65
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
                   (CAB-13) >gi 72748 pir CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi 19277 emb CAA42818 (X60275) LHCII type III
                   [Lycopersicon esculentum]
Seq. No.
                  210856
                  LIB3145-011-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244956
BLAST score
                  264
E value
                  5.0e-23
Match length
                  98
                   46
% identity
```

NCBI Description (Z97340) strong similarity to pectinesterase [Arabidopsis



## thaliana]

```
Seq. No.
                  210857
                  LIB3145-011-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125887
BLAST score
                  221
E value
                  6.0e-18
                  115
Match length
                  44
% identity
NCBI Description
                 ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                  >gi 82092 pir S04765 LAT52 protein precursor - tomato
                  >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
                  esculentum]
Seq. No.
                  210858
                  LIB3145-011-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g2959324
NCBI GI
BLAST score
                  568
E value
                  9.0e-59
Match length
                  128
% identity
                  34
NCBI Description
                 (Y15224) Importin alpha-like protein [Arabidopsis thaliana]
Seq. No.
                  210859
Seq. ID
                  LIB3145-011-Q1-K1-B2
Method
                  BLASTX
                  g266945
NCBI GI
BLAST score
                  533
E value
                  1.0e-54
Match length
                  124
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                  >gi 100065 pir S19978 ribosomal protein L9 - garden pea
                  >gi 20727 emb CAA46273 (X65155) GA [Pisum sativum]
                  >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
                  210860
Seq. No.
Seq. ID
                  LIB3145-011-01-K1-B7
Method
                  BLASTX
NCBI GI
                  g1731144
BLAST score
                  248
E value
                  4.0e-21
Match length
                  132
% identity
                  40
NCBI Description
                  HYPOTHETICAL 28.6 KD PROTEIN TO7A5.2 IN CHROMOSOME III
                  >qi 3879519 emb CAA88132 (Z48055) similar to the yeast
                  hypothetical protein YK10 (Swiss Prot accession number
```

Seq. No. 210861

Seq. ID LIB3145-011-Q1-K1-B8

Method BLASTX NCBI GI g1742965

[Caenorhabditis elegans]

P36125); cDNA EST EMBL:C11826 comes from this gene

```
BLAST score
E value
                  1.0e-35
                  139
Match length
                  54
% identity
NCBI Description (Y09562) HAPp48,5 protein [Arabidopsis thaliana]
Seq. No.
                  210862
Seq. ID
                  LIB3145-011-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2267567
BLAST score
                  162
E value
                  4.0e-11
Match length
                  62
% identity
                  50
NCBI Description
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
                  x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
Seq. No.
                  210863
                  LIB3145-011-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2290532
BLAST score
                  352
E value
                  2.0e-33
Match length
                  125
% identity
                  60
NCBI Description (U94748) AN11 [Petunia x hybrida]
Seq. No. Seq. ID
                  210864
                  LIB3145-011-Q1-K1-C4
                  BLASTX
Method
NCBI GI
                  g461736
BLAST score
                  310
                  2.0e-28
E value
Match length
                   64
% identity
                  95
NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
                  >gi_478786_pir__$29316 chaperonin 60 - cucurbit
                  >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                   sp.]
Seq. No.
                  210865
                  LIB3145-011-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894612
```

Method BLASTX
NCBI GI g2894612
BLAST score 227
E value 1.0e-18
Match length 57
% identity 74

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 210866

Seq. ID LIB3145-011-Q1-K1-C6

Method BLASTX
NCBI GI g3513744
BLAST score 175
E value 1.0e-12



72 Match length % identity 40

(AF080118) contains similarity to Medicago truncatula MtN3 NCBI Description

(GB:Y08726) [Arabidopsis thaliana]

210867 Seq. No.

Seq. ID LIB3145-011-Q1-K1-D2

Method BLASTX NCBI GI g548774 BLAST score 566 E value 2.0e-58 Match length 128 85 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal

protein L7a - rice >gi 303855 dbj BAA02156 (D12631)

ribosomal protein L7A [Oryza sativa]

Seq. No. 210868

Seq. ID LIB3145-011-Q1-K1-D3

Method BLASTX NCBI GI g4415917 BLAST score 408 E value 6.0e-40 Match length 121 % identity

(AC006282) putative protein containing zinc finger domain NCBI Description

[Arabidopsis thaliana]

Seq. No. 210869

Seq. ID LIB3145-011-Q1-K1-D7

Method BLASTX NCBI GI q3386614 BLAST score 491 E value 1.0e-49 Match length 129

% identity

(AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description

thaliana]

Seq. No. 210870

Seq. ID LIB3145-011-Q1-K1-E12

Method BLASTX NCBI GI g266829 BLAST score 125 E value 2.0e-10 Match length 39 % identity

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1

>gi 81655 pir S20882 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP1) - Arabidopsis thaliana >gi\_16431\_emb\_CAA45611\_ (X64328) protein phosphatase-1 [Arabidopsis thaliana] >gi 166572 (M93408)

phosphoprotein phosphatase 1 [Arabidopsis thaliana] >gi 3980395 (AC004561) phosphoprotein phosphatase-type 1

catalytic subunit [Arabidopsis thaliana]

Seq. No. 210871

```
LIB3145-011-Q1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3643611
                  306
BLAST score
                  5.0e-28
E value
Match length
                  84
% identity
                  68
                  (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
                  210872
Seq. No.
                  LIB3145-011-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3860249
                  403
BLAST score
                  2.0e-39
E value
Match length
                  126
% identity
                  67
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  210873
Seq. ID
                  LIB3145-011-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1142619
BLAST score
                  425
E value
                  6.0e-42
                  141
Match length
                  61
% identity
                  (U18348) phaseolin G-box binding protein PG1 [Phaseolus
NCBI Description
                  vulgaris]
Seq. No.
                  210874
Seq. ID
                  LIB3145-011-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2695711
BLAST score
                  423
E value
                  1.0e-41
Match length
                  124
                  61
% identity
NCBI Description (AJ001370) cytochome b5 [Olea europaea]
                  210875
Seq. No.
Seq. ID
                  LIB3145-011-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2583128
BLAST score
                  227
E value
                  1.0e-18
Match length
                  133
% identity
                   40
NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  210876
Seq. ID
                  LIB3145-011-Q1-K1-E9
                  BLASTX
Method
NCBI GI
                  g4220531
BLAST score
                  192
```

1.0e-14

126

E value Match length

Seq. No.

Seq. ID

210882

LIB3145-011-Q1-K1-F8



```
% identity
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]
                  210877
Seq. No.
Seq. ID
                  LIB3145-011-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  399
E value
                  6.0e-39
Match length
                  103
% identity
                  77
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  210878
Seq. No.
                  LIB3145-011-Q1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334261
BLAST score
                  141
E value
                  1.0e-08
Match length
                  48
                  56
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
NCBI Description
                  metallothionein-like protein [Malus domestica]
Seq. No.
                  210879
Seq. ID
                  LIB3145-011-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q3264611
BLAST score
                  280
                  6.0e-25
E value
Match length
                  60
% identity
                  83
NCBI Description (AF061511) seven in absentia homolog [Zea mays]
Seq. No.
                  210880
                  LIB3145-011-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3337361
BLAST score
                  585
E value
                  1.0e-60
Match length
                  140
                  73
% identity
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  210881
                  LIB3145-011-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185599
BLAST score
                  232
E value
                  3.0e-19
Match length
                  130
                  39
% identity
                  (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana
NCBI Description
                  triflora]
```



```
Method
NCBI GI
                  q3386621
BLAST score
                  424
E value
                  8.0e-42
Match length
                  103
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210883
Seq. ID
                  LIB3145-011-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  q4204295
BLAST score
                  148
E value
                  2.0e-09
                  100
Match length
                  39
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  210884
Seq. ID
                  LIB3145-011-Q1-K1-G4
Method
                  BLASTN
NCBI GI
                  g2829205
BLAST score
                  41
                  6.0e-14
E value
Match length
                  100
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
Seq. No.
                  210885
Seq. ID
                  LIB3145-011-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2827544
BLAST score
                  542
E value
                  1.0e-55
Match length
                  144
% identity
                  73
NCBI Description
                  (AL021635) HSP associated protein like [Arabidopsis
                  thaliana]
                  210886
Seq. No.
Seq. ID
                  LIB3145-011-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2827544
BLAST score
                  513
E value
                  3.0e-52
Match length
                  138
% identity
NCBI Description
                  (AL021635) HSP associated protein like [Arabidopsis
                  thaliana]
Seq. No.
                  210887
```

Seq. ID LIB3145-011-Q1-K1-G8

Method BLASTX NCBI GI g2827544 BLAST score 181

Seq. No.

Seq. ID

Method



```
1.0e-13
E value
                   90
Match length
                   50
% identity
                   (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                   thaliana]
                   210888
Seq. No.
                   LIB3145-011-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g3122638
NCBI GI
                   559
BLAST score
                   9.0e-58
E value
                   118
Match length
                   39
% identity
                   PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1
NCBI Description
                   >gi_1076381_pir__S49820 PRL1 protein - Arabidopsis thaliana
                   >gi_577733 emb CAA58031 (X82824) PRL1 [Arabidopsis
                   thaliana] >gi_577735_emb_CAA58032_ (X82825) PRL1
                    [Arabidopsis \overline{\text{thaliana}}] \overline{\text{gi}}_224494\overline{7} emb_CAB10369.1_ (Z97339)
                   PRL1 protein - Arabidopsis thaliana
Seq. No.
                   210889
                   LIB3145-011-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   q3264769
NCBI GI
                   312
BLAST score
                   4.0e-37
E value
                   100
Match length
                   75
% identity
                    (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                   armeniaca]
Seq. No.
                    210890
                   LIB3145-011-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                    g3763916
NCBI GI
                    227
BLAST score
                    1.0e-18
E value
                    143
Match length
                    39
% identity
                    (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                    >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                    protein [Arabidopsis thaliana]
                    210891
Seq. No.
                    LIB3145-011-Q1-K1-H5
Seq. ID
                    BLASTN
Method
                    q20412
NCBI GI
                    46
BLAST score
                    1.0e-16
E value
                    74
Match length
                    91
 % identity
NCBI Description P.amygdalus mRNA for alpha-tubulin
                    210892
```

29199

LIB3145-011-Q1-K1-H7

BLASTX

```
q2760326
NCBI GI
                   155
BLAST score
                   6.0e-19
E value
                   106
Match length
% identity
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                   210893
Seq. No.
                   LIB3145-011-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   q2702277
NCBI GI
                   178
BLAST score
                   4.0e-13
E value
                   98
Match length
                   44
% identity
                   (AC003033) putative cyclin g-associated kinase [Arabidopsis
NCBI Description
                   thaliana] >gi_2914689 (AC003974) putative cyclin
                   g-associated kinase [Arabidopsis thaliana]
                   210894
Seq. No.
                   LIB3145-012-Q1-K1-A10
Seq. ID
                   BLASTX
Method
                   g3915037
NCBI GI
BLAST score
                   702
                   2.0e-74
E value
                   148
Match length
% identity
                   SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose
                   synthase [Pisum sativum]
                   210895
Seq. No.
                   LIB3145-012-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g2462828
NCBI GI
BLAST score
                   414
                   1.0e-40
E value
                   135
Match length
 % identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   210896
 Seq. No.
                   LIB3145-012-Q1-K1-A5
 Seq. ID
                   BLASTX
 Method
                    g3885334
 NCBI GI
 BLAST score
                    558
 E value
                    1.0e-57
 Match length
                    132
                    77
 % identity
                    (AC005623) putative argonaute protein [Arabidopsis
 NCBI Description
                    thaliana]
                    210897
 Seq. No.
                    LIB3145-012-Q1-K1-A9
 Seq. ID
                    BLASTX
 Method
```

29200

q1184075

292

NCBI GI

BLAST score



E value 3.0e-26 Match lèngth 146 % identity

(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] NCBI Description >qi 1587673 prf 2207203A Cf-2 gene [Lycopersicon

esculentum]

210898 Seq. No.

LIB3145-012-Q1-K1-C10 Seq. ID

Method BLASTX g1345882 NCBI GI BLAST score 344 E value 2.0e-32 Match length 72 % identity 88

NCBI Description CYTOCHROME B5

Seq. No. 210899

LIB3145-012-Q1-K1-C11 Seq. ID

Method BLASTX NCBI GI q3639087 BLAST score 694 E value 2.0e-73 Match length 145 % identity 88

(AF090444) phospholipase D2 [Brassica oleracea] >gi 3924621 NCBI Description

(U85482) phospholipase D [Brassica oleracea var. capitata]

>gi\_4324971\_gb\_AAD17209\_ (AF113919) phospholipase D2 [Brassica oleracea var. capitata]

Seq. No. 210900

Seq. ID LIB3145-012-Q1-K1-C2

Method BLASTX NCBI GI a464986 BLAST score 415 E value 8.0e-41 Match length 80 94 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

> LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi\_4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 210901

Seq. ID LIB3145-012-Q1-K1-C3

Method BLASTX NCBI GI g2827704 BLAST score 424 E value 8.0e-42 Match length 119



```
% identity
NCBI Description
                  (AL021684) LRR-like protein [Arabidopsis thaliana]
Seq. No.
                  210902
                  LIB3145-012-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979558
                  383
BLAST score
E value
                  5.0e-37
Match length
                  124
% identity
                  63
NCBI Description
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  210903
                  LIB3145-012-01-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  317
                  2.0e-29
E value
Match length
                  98
% identity
                  68
NCBI Description (Z81012) unknown [Ricinus communis]
                  210904
Seq. No.
Seq. ID
                  LIB3145-012-Q1-K1-C9
                  BLASTX
Method
NCBI GI
                  g3914685
BLAST score
                  380
E value
                  1.0e-36
Match length
                  79
% identity
                  91
                  60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
NCBI Description
                  protein L17 [Zea mays]
Seq. No.
                  210905
Seq. ID
                  LIB3145-012-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3289993
BLAST score
                  220
                  7.0e-18
E value
                  69
Match length
                  59
% identity
NCBI Description (AC005258) R30783 1 [Homo sapiens]
Seq. No.
                  210906
                  LIB3145-012-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125051
BLAST score
                  521
E value
                  4.0e-53
Match length
                  144
% identity
                  69
NCBI Description
                 ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD)
                  >gi_88038 pir_ A37033 isovaleryl-CoA dehydrogenase (EC
                  1.3.99.10) precursor - human >gi 306897 (M34192)
```

29202

isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]

>gi\_4504799\_ref\_NP\_002216.1\_pIVD\_ isovaleryl Coenzyme A



## dehydrogenase

Seq. No. 210907 Seq. ID LIB3145-012-Q1-K1-D12 Method BLASTX NCBI GI q3212539

BLAST score 310 1.0e-28 E value Match length 111 60 % identity

Chain A, Structure Of Human Isovaleryl-Coa Dehydrogenase At NCBI Description

2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi\_3212540\_pdb\_1IVH\_B Chain B, Structure Of Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi\_3212541\_pdb\_1IVH\_C Chain C, Structure Of Human

Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution:

Structural Basis For Substrate Specificity

>gi\_3212542\_pdb\_1IVH\_D Chain D, Structure Of Human

Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution:

Structural Basis For Substrate Specificity

210908

Seq. No. Seq. ID LIB3145-012-Q1-K1-D2

Method BLASTX NCBI GI q3132478 BLAST score 253 E value 8.0e-22 129 Match length 44 % identity

(AC003096) bZIP-like protein [Arabidopsis thaliana] NCBI Description

210909 Seq. No.

LIB3145-012-Q1-K1-D3 Seq. ID

Method BLASTX g1399267 NCBI GI BLAST score 572 3.0e-59 E value Match length 126 62 % identity

NCBI Description (U31752) calmodulin-domain protein kinase CDPK isoform 4

[Arabidopsis thaliana]

210910 Seq. No.

LIB3145-012-Q1-K1-D4 Seq. ID

Method BLASTX NCBI GI g289920 BLAST score 573 E value 2.0e-59 Match length 110 % identity 98

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

Seq. No. 210911

Seq. ID LIB3145-012-Q1-K1-D5

Method BLASTX

```
q1173256
NCBI GI
                  592
BLAST score
                  1.0e-61
E value
                  117
Match length
                  97
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                  [Gossypium hirsutum]
                  210912
Seq. No.
                  LIB3145-012-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  q1864017
NCBI GI
                   767
BLAST score
                   6.0e-82
E value
                   148
Match length
                   97
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                   210913
Seq. No.
                   LIB3145-012-Q1-K1-E1
Seq. ID
Method
                   BLASTX
                   q1518540
NCBI GI
                   236
BLAST score
                   8.0e-20
E value
                   49
Match length
                   92
% identity
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   210914
Seq. No.
                   LIB3145-012-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g3135311
NCBI GI
                   230
BLAST score
                   3.0e-19
E value
                   90
Match length
                   46
% identity
                   (AF053356) actin like gene [Homo sapiens]
NCBI Description
                   210915
Seq. No.
                   LIB3145-012-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g1743410
NCBI GI
                   654
BLAST score
                   1.0e-68
E value
                   140
Match length
                   82
 % identity
                   (Y09825) amino acid transporter [Solanum tuberosum]
NCBI Description
                   210916
 Seq. No.
                   LIB3145-012-Q1-K1-F1
```

 Seq. ID
 LIB3145-012-Q1 

 Method
 BLASTX

 NCBI GI
 g4056457

BLAST score 341 E value 4.0e-32 Match length 93

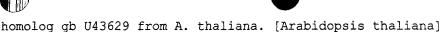
```
% identity
                  (AC005990) ESTs gb_234051 and gb_F13722 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                  210917
Seq. No.
                  LIB3145-012-Q1-K1-F10
Seq. ID
Method
                  BLASTX
                  g3759184
NCBI GI
                  148
BLAST score
                  2.0e-09
E value
                  135
Match length
                  26
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                   210918
Seq. No.
                   LIB3145-012-Q1-K1-F11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3821780
                   36
BLAST score
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   210919
Seq. No.
                   LIB3145-012-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   q3023961
NCBI GI
BLAST score
                   621
E value
                   6.0e-65
                   122
Match length
                   94
% identity
                   HOMEOBOX PROTEIN KNOTTED-1-LIKE >gi_1946222_emb_CAA96512
NCBI Description
                   (Z71980) knotted1-like homeobox protein [Malus domestica]
                   210920
Seq. No.
                   LIB3145-012-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   q82264
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   47
Match length
                   91
 % identity
                   ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
 NCBI Description
                   c1 precursor (clone pC(1)8I) - potato (fragment)
                   >gi_498789_emb_CAA56109_ (X79597) cytochrome c1 [Solanum
                   tuberosum]
                   210921
 Seq. No.
                   LIB3145-012-Q1-K1-F6
 Seq. ID
                   BLASTX
 Method
                   g3776581
 NCBI GI
                   219
 BLAST score
                    4.0e-18
 E value
                   86
 Match length
                    53
 % identity
                   (AC005388) Similar to Beta integral membrane protein
 NCBI Description
```



96

partial sequence

% identity



```
210922
Seq. No.
                  LIB3145-012-Q1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2842700
BLAST score
                  242
E value
                  2.0e-20
                  83
Match length
                  51
% identity
                  HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I
NCBI Description
                  >gi_1644322_emb_CAB03612_ (Z81317) DNA2-NAM7 helicase
                  family protein [Schizosaccharomyces pombe]
Seq. No.
                  210923
                  LIB3145-012-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3643607
BLAST score
                  474
E value
                  1.0e-47
Match length
                  126
                  40
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
                  210924
Seq. No.
Seq. ID
                  LIB3145-012-Q1-K1-G10
Method
                  BLASTX
                  g3033375
NCBI GI
BLAST score
                  541
E value
                  2.0e-55
Match length
                  143
% identity
                  71
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana)
                  210925
Seq. No.
                  LIB3145-012-Q1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4415916
BLAST score
                  449
E value
                  1.0e-44
Match length
                  147
% identity
                  58
NCBI Description
                  (AC006282) putative pectin methylesterase [Arabidopsis
                  thaliana]
                  210926
Seq. No.
Seq. ID
                  LIB3145-012-Q1-K1-G12
Method
                  BLASTN
NCBI GI
                  g2687434
BLAST score
                  308
E value
                  1.0e-173
Match length
                  363
```

NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,



```
210927
Seq. No.
                  LIB3145-012-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g3660471
NCBI GI
BLAST score
                  500
E value
                  7.0e-51
Match length
                  107
                  90
% identity
                  (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
Seq. No.
                  210928
Seq. ID
                  LIB3145-012-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3096949
BLAST score
                   321
E value
                   8.0e-30
Match length
                   108
% identity
                   56
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
                   210929
Seq. No.
Seq. ID
                  LIB3145-012-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                   g4538903
                   393
BLAST score
                   3.0e-38
E value
                   81
Match length
                   89
% identity
NCBI Description
                  (AL049482) putative protein [Arabidopsis thaliana]
                   210930
Seq. No.
Seq. ID
                   LIB3145-012-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g4097547
BLAST score
                   191
                   1.0e-14
E value
Match length
                   55
% identity
                   38
NCBI Description
                  (U64906) ATFP3 [Arabidopsis thaliana]
                   210931
Seq. No.
                  LIB3145-012-Q1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2245115
BLAST score
                   268
                   2.0e-23
E value
Match length
                   124
% identity
                   44
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 210932

Seq. ID LIB3145-012-Q1-K1-H1

Method BLASTX NCBI GI g2689469

```
BLAST score
                  4.0e-58
E value
                  135
Match length
                  80
% identity
                  (U53672) IAA22 [Arabidopsis thaliana]
NCBI Description
                  210933
Seq. No.
                  LIB3145-012-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006894
BLAST score
                  143
E value
                  6.0e-09
Match length
                  84
% identity
                  44
                  (Z99708) homeodomain protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210934
                  LIB3145-012-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432840
BLAST score
                  505
E value
                  2.0e-51
Match length
                  116
% identity
                  81
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  210935
Seq. No.
Seq. ID
                  LIB3145-012-Q1-K1-H5
                  BLASTX
Method
                  g4432840
NCBI GI
BLAST score
                  184
E value
                  1.0e-27
Match length
                  107
% identity
                   62
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   210936
                  LIB3145-012-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006894
BLAST score
                   321
E value
                  1.0e-29
Match length
                  111
                   59
% identity
                  (Z99708) homeodomain protein [Arabidopsis thaliana]
NCBI Description
                  210937
Seq. No.
                  LIB3145-013-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3122703
BLAST score
                   290
                   3.0e-26
E value
Match length
                  81
% identity
                   70
                  60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
NCBI Description
```

protein L23a [Fritillaria agrestís]

```
210938
Seq. No.
Seq. ID
                  LIB3145-013-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2231046
BLAST score
                  227
E value
                  7.0e-19
Match length
                  73
% identity
                  64
NCBI Description (Y12618) PPF-1 protein [Pisum sativum]
Seq. No.
                  210939
                  LIB3145-013-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3004564
BLAST score
                  166
E value
                  1.0e-11
Match length
                  120
                  31
% identity
NCBI Description (AC003673) putative receptor Ser/Thr protein kinase
                  [Arabidopsis thaliana]
                  210940
Seq. No.
Seq. ID
                  LIB3145-013-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q3702121
BLAST score
                  415
                  8.0e-41
E value
Match length
                  124
                  70
% identity
NCBI Description (AJ011681) retinoblastoma-related protein [Chenopodium
                  rubrum]
                  210941
Seq. No.
Seq. ID
                  LIB3145-013-Q1-K1-A6
Method
                  BLASTX
                  g4151319
NCBI GI
BLAST score
                  346
                  1.0e-32
E value
Match length
                  117
% identity
                  58
NCBI Description (AF089084) putative auxin efflux carrier protein; AtPIN1
                  [Arabidopsis thaliana]
                  210942
Seq. No.
Seq. ID
                  LIB3145-013-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q100525
BLAST score
                  671
                  8.0e-71
E value
                  136
Match length
% identity
                  26
NCBI Description ubiquitin precursor UbB2 - common sunflower (fragment)
                  >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein
```

LIB3145-013-Q1-K1-A8

[Helianthus annuus]

210943

Seq. No.

Seq. ID

BLAST score

248



```
Method
NCBI GI
                  q1076264
BLAST score
                  222
E value
                  3.0e-18
Match length
                  67
                  63
% identity
                  carboxyl-terminal processing proteinase D1 precursor -
NCBI Description
                  spinach >gi 2129489 pir S65146 photosystem II D1 protein
                  processing enzyme precursor - spinach
                  >gi_999435_dbj_BAA09134 (D50585) C-terminal protease
                  precursor [Spinacia oleracea]
                  210944
Seq. No.
Seq. ID
                  LIB3145-013-Q1-K1-A9
Method
                  BLASTX
                  g4220527
NCBI GI
BLAST score
                  185
E value
                  9.0e-14
                  54
Match length
% identity
                   67
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210945
Seq. ID
                  LIB3145-013-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3834323
BLAST score
                   193
E value
                   1.0e-14
                  106
Match length
                   42
% identity
NCBI Description (AC005679) F9K20.25 [Arabidopsis thaliana]
                  210946
Seq. No.
                  LIB3145-013-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g2791834
NCBI GI
BLAST score
                   335
                   2.0e-31
E value
Match length
                   103
% identity
                   67
NCBI Description
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  210947
Seq. No.
                  LIB3145-013-Q1-K1-B3
Seq. ID
Method
                  BLASTX
                  g3098571
NCBI GI
BLAST score
                   226
E value
                   1.0e-18
Match length
                  103
% identity
                   43
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]
Seq. No.
                   210948
                   LIB3145-013-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g729092
```



E value 2.0e-21

Match length 91 % identity 52

NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK)

>gi\_477484\_pir\_\_A49082 calcium-dependent protein kinase
isoform AK1 - Arabidopsis thaliana >gi\_304105 (L14771)
calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 210949

Seq. ID LIB3145-013-Q1-K1-C1

Method BLASTX
NCBI GI g1346172
BLAST score 267
E value 2.0e-23
Match length 54
% identity 89

NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)

(IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)

>gi\_170384 (L08830) glucose-regulated protein 78

[Lycopersicon esculentum]

Seq. No. 210950

Seq. ID LIB3145-013-Q1-K1-C2

Method BLASTX
NCBI GI g4510344
BLAST score 225
E value 1.0e-18
Match length 75
% identity 63

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 210951

Seq. ID LIB3145-013-Q1-K1-C4

Method BLASTX
NCBI GI g4191784
BLAST score 358
E value 3.0e-34
Match length 85
% identity 73

NCBI Description (AC005917) putative WD-40 repeat protein [Arabidopsis

thaliana]

Seq. No. 210952

Seq. ID LIB3145-013-Q1-K1-D10

Method BLASTN
NCBI GI g2795836
BLAST score 32
E value 1.0e-08
Match length 60
% identity 88

NCBI Description Allium thunbergii 18S small subunit nuclear ribosomal RNA

gene

Seq. No. 210953

Seq. ID LIB3145-013-Q1-K1-D6

Method BLASTX NCBI GI g3334113

```
BLAST score
E value
                   9.0e-31
Match length
                   89
% identity
                   73
NCBI Description
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                   acyl-CoA-binding protein [Gossypium hirsutum]
                   210954
Seq. No.
                  LIB3145-013-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                   g3201627
NCBI GI
BLAST score
                   240
E value
                   2.0e-20
Match length
                   94
                   47
% identity
                  (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
                   210955
Seq. No.
                   LIB3145-013-Q1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1296816
BLAST score
                   637
E value
                   9.0e-67
Match length
                   132
% identity
                   93
NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]
                   210956
Seq. No.
Seq. ID
                   LIB3145-013-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   q2760322
BLAST score
                   292
                   2.0e-26
E value
Match length
                   102
                   52
% identity
NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]
                   210957
Seq. No.
Seq. ID
                   LIB3145-013-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3024385
BLAST score
                   582
E value
                   3.0e-60
Match length
                   139
% identity
                   73
NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi 606652
                   (U09805) polygalacturonase [Gossypium barbadense]
```

Seq. No. 210958

Seq. ID LIB3145-013-Q1-K1-F1

Method BLASTX
NCBI GI 94467157
BLAST score 163
E value 2.0e-11
Match length 77
% identity 44

NCBI Description (AL035540) disease resistance response like protein



## [Arabidopsis thaliana]

```
210959
Seq. No.
                  LIB3145-013-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543813
BLAST score
                  300
E value
                  3.0e-27
Match length
                  89
% identity
                  73
NCBI Description
                  FLORAL HOMEOTIC PROTEIN APETALA1 (AGL7 PROTEIN)
                  >gi_16162_emb_CAA78909_ (Z16421) AP1 [Arabidopsis thaliana]
                  210960
Seq. No.
                  LIB3145-013-01-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170567
BLAST score
                  209
E value
                  1.0e-16
Match length
                  127
% identity
                  44
NCBI Description
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
                  >gi 1085960 pir S52648 INO1 protein - Citrus paradisi
                  >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                  210961
Seq. ID
                  LIB3145-013-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2104536
BLAST score
                  229
E value
                  6.0e-19
Match length
                  50
% identity
                  78
                  (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  210962
Seq. No.
                  LIB3145-013-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g2388564
NCBI GI
                  152
BLAST score
E value
                  4.0e-10
Match length
                  123
% identity
                  38
NCBI Description
                  (AC000098) ESTs gb_AA042402, gb_ATTS1380 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  210963
Seq. ID
                  LIB3145-013-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4033467
BLAST score
                  436
E value
                  3.0e-43
Match length
                  111
% identity
                  50
NCBI Description
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP31
```

>gi\_1707366\_emb\_CAA67798\_ (X99435) splicing factor



## [Arabidopsis thaliana]

```
210964
Seq. No.
                  LIB3145-013-Q1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2388565
BLAST score
                  290
E value
                  4.0e-26
Match length
                  127
                  45
% identity
                  (ACO00098) Similar to Prunus pectinesterase (gb_X95991).
NCBI Description
                  [Arabidopsis thaliana]
                  210965
Seq. No.
                  LIB3145-013-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220479
BLAST score
                  360
E value
                  3.0e-36
Match length
                  108
% identity
                  73
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
                  210966
Seq. No.
Seq. ID
                  LIB3145-013-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2500579
BLAST score
                  181
                  3.0e-13
E value
                  74
Match length
                  16
% identity
NCBI Description
                  G-RICH SEQUENCE FACTOR-1 (GRSF-1) >gi 517196 (U07231)
                  G-rich sequence factor-1 [Homo sapiens]
                  >gi 4504161 ref NP 002083.1 pGRSF1 G-rich RNA sequence
                  binding factor
                  210967
Seq. No.
                  LIB3145-013-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4388726
BLAST score
                  362
                  7.0e-35
E value
Match length
                  89
                  75
% identity
                  (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
                  210968
Seq. No.
Seq. ID
                  LIB3145-013-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3176668
BLAST score
                  503
E value
                  3.0e-51
Match length
                  111
% identity
                   (AC004393) Similar to ribosomal protein L17 gb_X62724 from
NCBI Description
                  Hordeum vulgare. ESTs gb Z34728, gb_F19974, gb_T75677 and
```

Seq. No.

Seq. ID

Method

210974

BLASTX

LIB3145-013-Q1-K1-H5



gb\_Z33937 come from this gene. [Arabidopsis thaliana]

210969 Seq. No. LIB3145-013-Q1-K1-G5 Seq. ID Method BLASTX g4432834 NCBI GI BLAST score 159 E value 5.0e-11 Match length 72 53 % identity NCBI Description (AC006283) unknown protein [Arabidopsis thaliana] Seq. No. 210970 LIB3145-013-Q1-K1-G7 Seq. ID Method BLASTX NCBI GI q2146731 BLAST score 264 E value 2.0e-23 Match length 89 % identity 25 FK506-binding protein - Arabidopsis thaliana >gi 1354207 NCBI Description (U49453) rof1 [Arabidopsis thaliana] Seq. No. 210971 Seq. ID LIB3145-013-Q1-K1-G9 Method BLASTX NCBI GI g1495366 BLAST score 251 2.0e-21 E value Match length 112 % identity 46 (Z69370) nitrite transporter [Cucumis sativus] NCBI Description Seq. No. 210972 Seq. ID LIB3145-013-Q1-K1-H2 Method BLASTX NCBI GI g3832512 BLAST score 156 E value 5.0e-11 Match length 47 68 % identity (AF097922) granule-bound glycogen (starch) synthase NCBI Description [Astragalus membranaceus] 210973 Seq. No. Seq. ID LIB3145-013-Q1-K1-H4 Method BLASTX NCBI GI g2262105 BLAST score 356 E value 8.0e-34 Match length 101 % identity 60 (AC002343) unknown protein [Arabidopsis thaliana] NCBI Description

```
g3213227
NCBI GI
BLAST score
                  152
                   4.0e-10
E value
                   90
Match length
                   32
% identity
                   (AF035209) putative v-SNARE Vtila [Mus musculus]
NCBI Description
                  >gi 3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
                  210975
Seq. No.
                  LIB3145-013-Q1-K1-H7
Seq. ID
Method
                  BLASTX
```

NCBI GI g2497753
BLAST score 243
E value 9.0e-21
Match length 94
% identity 49

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi 1321915 emb CAA65477 (X96716) lipid transfer protein

[Prunus dulcis]

Seq. No. 210976

Seq. ID LIB3145-013-Q1-K1-H8

Method BLASTX
NCBI GI 93924603
BLAST score 487
E value 2.0e-49
Match length 105
% identity 56

NCBI Description (AF069442) putative WD-repeat protein [Arabidopsis

thaliana]

Seq. No. 210977

Seq. ID LIB3145-013-Q1-K1-H9

Method BLASTN
NCBI GI 94519189
BLAST score 34
E value 2.0e-09
Match length 183
% identity 49

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K5A21, complete sequence

Seq. No. 210978

Seq. ID LIB3145-014-Q1-K1-A10

Method BLASTX
NCBI GI g2760334
BLAST score 411
E value 3.0e-40
Match length 90
% identity 80

NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No. 210979

Seq. ID LIB3145-014-Q1-K1-A11

Method BLASTX NCBI GI g1223926 BLAST score 624

E value 3.0e-65 Match length 150 % identity 75

NCBI Description (U49741) Vigna radiata carboxypeptidase II mRNA, partial

cds [Vigna radiata]

Seq. No. 210980

Seq. ID LIB3145-014-Q1-K1-A2

Method BLASTX
NCBI GI g1895084
BLAST score 687
E value 1.0e-72
Match length 129
% identity 98

NCBI Description (U89897) golqi associated protein se-wap41 [Zea mays]

Seq. No. 210981

Seq. ID LIB3145-014-Q1-K1-A5

Method BLASTX
NCBI GI g729623
BLAST score 399
E value 5.0e-39
Match length 106
% identity 79

NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP

78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 5) (BIP 5) >gi\_100340\_pir\_\_S21880 heat shock protein BiP homolog blp5 - common tobacco >gi\_19813\_emb\_CAA42660\_

(X60058) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No. 210982

Seq. ID LIB3145-014-Q1-K1-A9

Method BLASTX
NCBI GI g1223926
BLAST score 366
E value 2.0e-37
Match length 145
% identity 57

NCBI Description (U49741) Vigna radiata carboxypeptidase II mRNA, partial

cds [Vigna radiata]

Seq. No. 210983

Seq. ID LIB3145-014-Q1-K1-B1

Method BLASTX
NCBI GI g2746826
BLAST score 145
E value 5.0e-09
Match length 91
% identity 34

NCBI Description (AF040646) No definition line found [Caenorhabditis

elegans]

Seq. No. 210984

Seq. ID LIB3145-014-Q1-K1-B10

Method BLASTX NCBI GI g132939 BLAST score 156



E value 6.0e-11 Match length 45 % identity 73 60S RIBOSOMAL PROTEIN L3 >gi\_81657\_pir\_\_JQ0771 ribosomal NCBI Description protein L3 (ARP1) - Arabidopsis thaliana >gi 166858 (M32654) ribosomal protein [Arabidopsis thaliana] 210985 Seq. No. LIB3145-014-Q1-K1-B11 Seq. ID Method BLASTX NCBI GI q1657621 BLAST score 560 E value 1.0e-57 Match length 144 76 % identity (U72505) G6p [Arabidopsis thaliana] >qi 3068711 (AF049236) NCBI Description putative acyl-coA dehydrogenase [Arabidopsis thaliana] 210986 Seq. No. Seq. ID LIB3145-014-Q1-K1-B9 Method BLASTX NCBI GI g3617741 BLAST score 226 E value 3.0e-19 53 Match length 85 % identity (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis NCBI Description thaliana] Seq. No. 210987 LIB3145-014-Q1-K1-C1 Seq. ID Method BLASTX NCBI GI g2245131 BLAST score 252 9.0e-22 E value 76 Match length % identity 68 NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana] 210988 Seq. No. Seq. ID LIB3145-014-Q1-K1-C10 Method BLASTN NCBI GI g296442 BLAST score 33 E value 6.0e-09 Match length 65 % identity 88 NCBI Description G.max ADR11 mRNA Seq. No. 210989 Seq. ID LIB3145-014-Q1-K1-C11 Method BLASTX

Method BLASTX
NCBI GI g3914430
BLAST score 574
E value 2.0e-59
Match length 140
% identity 74



NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON

CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)

>gi\_2285800\_dbj\_BAA21650\_ (D78172) 26S proteasome beta

subunit [Spinacia oleracea]

Seq. No. 210990

Seq. ID LIB3145-014-Q1-K1-C2

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11

Match length 37 % identity 61

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 210991

Seq. ID LIB3145-014-Q1-K1-C4

Method BLASTX
NCBI GI g3327868
BLAST score 154
E value 3.0e-10
Match length 57
% identity 65

NCBI Description (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis

thaliana]

Seq. No. 210992

Seq. ID LIB3145-014-Q1-K1-C7

Method BLASTX
NCBI GI g3169883
BLAST score 339
E value 7.0e-32
Match length 108
% identity 67

NCBI Description (AF033194) dehydroquinate dehydratase/shikimate:NADP

oxidoreductase [Lycopersicon esculentum] >gi\_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP

oxidoreductase [Lycopersicon esculentum]

Seq. No. 210993

Seq. ID LIB3145-014-Q1-K1-D1

Method BLASTX
NCBI GI g4406814
BLAST score 417
E value 4.0e-41
Match length 101
% identity 79

NCBI Description (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis

thaliana]

Seq. No. 210994

Seq. ID LIB3145-014-Q1-K1-D11

Method BLASTX
NCBI GI g2598461
BLAST score 174
E value 2.0e-12

Match length 133

```
% identity
                  (Z98048) HIP (HSC70-INTERACTING PROTEIN (PROGESTERONE
NCBI Description
                  RECEPTOR-ASSOCIATED P48 PROTEIN) [Homo sapiens] >gi 4049268
                  (U17714) putative tumor suppressor ST13 [Homo sapiens]
                  210995
Seq. No.
                  LIB3145-014-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1587206
BLAST score
                  688
E value
                  1.0e-72
Match length
                  146
% identity
                  92
NCBI Description T complex protein [Cucumis sativus]
                  210996
Seq. No.
                  LIB3145-014-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432835
BLAST score
                  247
                  4.0e-21
E value
Match length
                  75
% identity
                  56
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  210997
Seq. No.
                  LIB3145-014-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567250
BLAST score
                  350
E value
                  4.0e-33
Match length
                  111
                  53
% identity
                  (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  210998
                  LIB3145-014-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829870
BLAST score
                  365
                  4.0e-35
E value
Match length
                  110
                  62
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  210999
Seq. No.
Seq. ID
                  LIB3145-014-Q1-K1-D7
Method
                  BLASTX
```

NCBI GI g2342735 BLAST score 191 E value 1.0e-14 Match length 53 74 % identity

(AC002341) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 211000

Seq. ID LIB3145-014-Q1-K1-D9



```
Method
                  BLASTX
NCBI GI
                  q2598461
                   97
BLAST score
                  8.0e-10
E value
Match length
                  104
                  34
% identity
                  (Z98048) HIP (HSC70-INTERACTING PROTEIN (PROGESTERONE
NCBI Description
                  RECEPTOR-ASSOCIATED P48 PROTEIN) [Homo sapiens] >gi 4049268
                   (U17714) putative tumor suppressor ST13 [Homo sapiens]
Seq. No.
                  211001
                  LIB3145-014-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                   417
                   5.0e-41
E value
                  100
Match length
% identity
                   76
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
Seq. No.
                   211002
Seq. ID
                  LIB3145-014-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   g3461821
BLAST score
                   328
                   2.0e-30
E value
Match length
                   91
                   68
% identity
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   211003
Seq. ID
                   LIB3145-014-Q1-K1-E12
Method
                   BLASTX
NCBI GI
                   q124224
BLAST score
                   617
                   2.0e-64
E value
Match length
                   123
                   93
% identity
                   INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_100345_pir__S21060 translation initiation factor eIF-5A
                   - common tobacco >gi_19887_emb_CAA45105_ (X63543)
                   eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.
                   211004
                  LIB3145-014-Q1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3668080
BLAST score
                   424
E value
                   4.0e-42
Match length
                   94
```

% identity 86

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 211005

Seq. ID LIB3145-014-Q1-K1-E4

Method BLASTX

```
g4263714
NCBI GI
BLAST score
                  477
E value
                  3.0e-48
Match length
                  117
% identity
                  78
                  (AC006223) putative integral membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                  211006
Seq. No.
                  LIB3145-014-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097094
BLAST score
                  363
                  9.0e-35
E value
Match length
                  120
% identity
                  61
                  (U45447) vacuolar proton-ATPase subunit D [Oryctolagus
NCBI Description
                  cuniculus]
                  211007
Seq. No.
Seq. ID
                  LIB3145-014-Q1-K1-E9
Method
                  BLASTN
NCBI GI
                  g3449334
BLAST score
                  33
E value
                  6.0e-09
Match length
                  77
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  211008
Seq. ID
                  LIB3145-014-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3281851
BLAST score
                  205
                  2.0e-25
E value
Match length
                  82
                  70
% identity
NCBI Description
                  (AL031004) RNA lariat debranching enzyme - like protein
                   [Arabidopsis thaliana]
                  211009
Seq. No.
Seq. ID
                  LIB3145-014-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3355468
BLAST score
                  522
E value
                  3.0e-53
```

Match length 123 88 % identity

(AC004218) putative ribosomal protein L35 [Arabidopsis NCBI Description

thalianal

Seq. No. 211010

Seq. ID LIB3145-014-Q1-K1-F3

Method BLASTX NCBI GI q2739168 BLAST score 205

```
E value
Match length
                  115
% identity
NCBI Description
                  (AF032386) aldose-1-epimerase-like protein [Nicotiana
                  tabacum]
                  211011
Seq. No.
                  LIB3145-014-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  g4115379
NCBI GI
BLAST score
                  200
                  1.0e-15
E value
Match length
                  61
% identity
                  64
                  (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  211012
                  LIB3145-014-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  g2462756
NCBI GI
BLAST score
                  251
E value
                  2.0e-21
Match length
                  95
% identity
                  73
NCBI Description (AC002292) putative receptor kinase [Arabidopsis thaliana]
Seq. No.
                  211013
Seq. ID
                  LIB3145-014-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2982268
BLAST score
                  624
E value
                  3.0e-65
Match length
                  130
% identity
                  93
NCBI Description
                  (AF051217) probable 40S ribosomal protein S15 [Picea
                  mariana]
Seq. No.
                  211014
Seq. ID
                  LIB3145-014-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g548441
                  775
BLAST score
                  6.0e-83
E value
Match length
                  143
                  99
% identity
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT
NCBI Description
                  >gi_486805_pir__S35502 phosphoprotein phosphatase (EC
                  3.1.3.16) ZA - alfalfa >gi_287811_emb_CAA49849 (X70399)
                  phosphoprotein phosphatase type 2A [Medicago sativa]
```

Seq. No. 211015

Seq. ID LIB3145-014-Q1-K1-G12

Method BLASTX NCBI GI g2392021 BLAST score 426 E value 5.0e-42

V : 1



```
Match length
% identity
                  (D63425) phopholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Spinacia oleracea]
                  211016
Seq. No.
                  LIB3145-014-Q1-K1-G4
Seq. ID
                  BLASTX
Method
                   q4490702
NCBI GI
                   226
BLAST score
                   1.0e-18
E value
                   114
Match length
                   48
% identity
NCBI Description (AL035680) hypothetical protein [Arabidopsis thaliana]
                   211017
Seq. No.
                   LIB3145-014-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   q3355468
NCBI GI
                   305
BLAST score
                   3.0e-28
E value
                   77
Match length
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   211018
 Seq. No.
                   LIB3145-014-Q1-K1-H1
 Seq. ID
                   BLASTX
Method
                   q2583137
NCBI GI
                   161
BLAST score
                   3.0e-11
E value
                   34
Match length
                   79
 % identity
                   (AC002387) similar to symbiosis-related protein, 5' partial
 NCBI Description
                   [Arabidopsis thaliana]
                   211019
 Seq. No.
                   LIB3145-014-Q1-K1-H10
 Seq. ID
 Method
                   BLASTX
                   q2895866
 NCBI GI
                   593
 BLAST score
                   1.0e-61
 E value
                   147
 Match length
 % identity
                    (AF045770) methylmalonate semi-aldehyde dehydrogenase
 NCBI Description
                    [Oryza sativa]
                    211020
 Seq. No.
                   LIB3145-014-Q1-K1-H11
 Seq. ID
                   BLASTX
 Method
                    q1008904
 NCBI GI
                    331
 BLAST score
                    3.0e-57
 E value
 Match length
                    113
                    94
 % identity
 NCBI Description (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
```



```
Seq. No.
                  211021
Seq. ID
                  LIB3145-014-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4263787
BLAST score
                  272
                   6.0e-24
E value
                  78
Match length
% identity
                  77
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211022
Seq. No.
                  LIB3145-014-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500443
BLAST score
                  181
                  2.0e-13
E value
Match length
                  36
                  100
% identity
                  40S RIBOSOMAL PROTEIN S14 >gi 1762931 (U66262) ribosomal
NCBI Description
                  protein S14 [Nicotiana tabacum]
Seq. No.
                   211023
Seq. ID
                  LIB3145-014-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                   g2760326
BLAST score
                   290
E value
                   4.0e-26
Match length
                  112
                   53
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                  211024
Seq. No.
Seq. ID
                  LIB3145-014-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2760326
BLAST score
                   239
                   3.0e-20
E value
Match length
                  97
% identity
                   51
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                   211025
Seq. No.
Seq. ID
                  LIB3145-015-Q1-K1-A10
Method
                  BLASTN
NCBI GI
                  q3386593
BLAST score
                   60
E value
                   5.0e-25
Match length
                  120
                   88
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4I18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No. 211026

Seq. ID LIB3145-015-Q1-K1-A2

Method BLASTX NCBI GI g282946



BLAST score 6.0e-56 E value Match length 124 % identity 78

Ca2+-transporting ATPase (EC 3.6.1.38) - tomato NCBI Description >gi\_423783\_pir\_\_A46284 Ca(2+)-ATPase, LCA1 -

Lycopersicon=tomatoes >gi\_170378 (M96324) Ca2+-ATPase [Lycopersicon esculentum] >gi 4206311 (AF050495) Ca2+ ATP synthase [Lycopersicon esculentum] >gi 4206313 (AF050496)

Ca2+ ATP synthase [Lycopersicon esculentum]

211027 Seq. No.

Seq. ID LIB3145-015-Q1-K1-B1

Method BLASTX q548774 NCBI GI BLAST score 284 2.0e-25 E value Match length 73 75 % identity

60S RIBOSOMAL PROTEIN L7A >gi\_542158\_pir\_\_S38360 ribosomal protein L7a - rice >gi\_303855\_dbj\_BAA02156\_ (D12631) NCBI Description

ribosomal protein L7A [Oryza sativa]

211028 Seq. No.

Seq. ID LIB3145-015-Q1-K1-B10

Method BLASTX NCBI GI q3169178 BLAST score 167 1.0e-11 E value Match length 73 % identity

(AC004401) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 211029

Seq. ID LIB3145-015-Q1-K1-B12

Method BLASTN NCBI GI g2688825 BLAST score 46 E value 1.0e-16 202 Match length 81 % identity

NCBI Description Prunus armeniaca putative NifU protein mRNA, partial cds

Seq. No. 211030

LIB3145-015-Q1-K1-B5 Seq. ID

Method BLASTX NCBI GI g3126969 BLAST score 181 E value 2.0e-13 118 Match length % identity 40

NCBI Description (AF061808) chalcone isomerase [Elaeagnus umbellata]

Seq. No. 211031

Seq. ID LIB3145-015-Q1-K1-B8

Method BLASTX NCBI GI q3647182

Match length

% identity

jakat. \*\*

```
BLAST score
                  1.0e-12
E value
Match length
                  88
% identity
                  45
                  (ALO31178) dJ341E18.2.1 (novel PUTATIVE protein) (isoform
NCBI Description
                  1) [Homo sapiens]
                  211032
Seq. No.
                  LIB3145-015-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1402888
BLAST score
                  145
E value
                  4.0e-09
Match length
                  61
                  44
% identity
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211033
                  LIB3145-015-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2347054
BLAST score
                  486
E value
                  5.0e-49
Match length
                  138
                  72
% identity
                  (X96791) arginine decarboxylase [Vitis vinifera]
NCBI Description
                  211034
Seq. No.
                  LIB3145-015-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g974782
BLAST score
                  684
                  3.0e-72
E value
Match length
                  141
% identity
                  96
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                  [Solenostemon scutellarioides]
Seq. No.
                  211035
                  LIB3145-015-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  640
                  4.0e-67
E value
Match length
                  125
                  56
% identity
NCBI Description
                  CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                  211036
Seq. ID
                  LIB3145-015-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2459417
BLAST score
                  461
E value
                  4.0e-46
```



(AC002332) putative pre-mRNA splicing factor PRP19 NCBI Description [Arabidopsis thaliana]

Seq. No. 211037

LIB3145-015-Q1-K1-D10 Seq. ID

Method BLASTX NCBI GI q3047123 BLAST score 298 E value 5.0e-27 Match length 139 % identity 44

NCBI Description (AF058919) similar to the family of glycosyl hydrolases

[Arabidopsis thaliana]

211038 Seq. No.

Seq. ID LIB3145-015-Q1-K1-D2

Method BLASTX NCBI GI q2924520 BLAST score 680 E value 8.0e-72 Match length 144 % identity 89

NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)

[Arabidopsis thaliana]

Seq. No. 211039

Seq. ID LIB3145-015-Q1-K1-D6

Method BLASTX g2827635 NCBI GI BLAST score 232 E value 3.0e-19 Match length 144 % identity

NCBI Description (AL021636) predicted protein [Arabidopsis thaliana]

Seq. No. 211040

LIB3145-015-Q1-K1-D9 Seq. ID

Method BLASTN NCBI GI g1208681 BLAST score 33 E value 6.0e-09 Match length 65

% identity

NCBI Description Glycine argyrea histone H3 gene, partial cds, clone H3-DARG

211041 Seq. No.

Seq. ID LIB3145-015-Q1-K1-E12

Method BLASTX NCBI GI g543867 BLAST score 520 E value 4.0e-53 Match length 133 % identity 80

ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi\_1076684\_pir\_\_A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi\_303626\_dbj\_BAA03526\_ (D14699) F1-ATPase gammma subunit

```
[Ipomoea batatas]
```

 Seq. No.
 211042

 Seq. ID
 LIB3145-015-Q1-K1-E2

 Method
 BLASTN

 NCBI GI
 g3821780

 BLAST score
 36

 E value
 9.0e-11

 Match length
 36

100

NCBI Description Xenopus laevis cDNA clone 27A6-1

 Seq. No.
 211043

 Seq. ID
 LIB3145-015-Q1-K1-E4

 Method
 BLASTN

 NCBI GI
 g1654303

 BLAST score
 115

 E. value
 7 0e-58

BLAST score 115 E value 7.0e-58 Match length 119 % identity 99

% identity

NCBI Description Gossypium stocksii 5.8S ribosomal RNA gene and internal

34 .

transcribed spacer 1 and

Seq. No. 211044

Seq. ID LIB3145-015-Q1-K1-E6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 211045

Seq. ID LIB3145-015-Q1-K1-E8

Method BLASTX
NCBI GI g3860250
BLAST score 469
E value 5.0e-47
Match length 141
% identity 69

NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 211046

Seq. ID LIB3145-015-Q1-K1-E9

Method BLASTX
NCBI GI g2653738
BLAST score 230
E value 5.0e-19
Match length 124
% identity 38

NCBI Description (AF001688) U4/U6 snRNP 90 kDa protein [Mus musculus]

Seq. No. 211047

Seq. ID LIB3145-015-Q1-K1-F10

Method BLASTX

```
q1771780
NCBI GI
                   307
BLAST score
                   4.0e-28
E value
                   57
Match length
                   96
% identity
                   (Y10024) ubiquitin extension protein [Solanum tuberosum]
NCBI Description
                   211048
Seq. No.
                 _ LIB3145-015-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   q2129495
NCBI GI
BLAST score
                   274
                   3.0e-24
E value
                   54
Match length
                   89
% identity
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                    (U3\overline{0}508) E6 [Gossypium barbadense]
                    211049
Seq. No.
                    LIB3145-015-Q1-K1-F7
Seq. ID
                    BLASTX
Method
NCBI GI
                    q3901014
BLAST score
                    234
                    1.0e-19
E value
Match length
                    55
                    76
% identity
                    (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                    sylvatica]
                    211050
Seq. No.
                    LIB3145-015-Q1-K1-F9
 Seq. ID
Method
                    BLASTX
                    q3175990
 NCBI GI
                    529
 BLAST score
                    4.0e-54
 E value
                    134
 Match length
                    72
 % identity
                    (AJ005836) GDP dissociation inhibitor [Cicer arietinum]
 NCBI Description
                    211051
 Seq. No.
                    LIB3145-015-Q1-K1-G1
 Seq. ID
                    BLASTX
 Method
                    g1174592
 NCBI GI
                    562
 BLAST score
                    5.0e-58
 E value
                    131
 Match length
                    87
 % identity
                    TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
 NCBI Description
                     - garden pea >gi_525332 (\overline{	ext{U}}12589) \overline{	ext{alpha-tubulin}} [Pisum
                    sativum]
                    211052
 Seq. No.
                    LIB3145-015-Q1-K1-G11
 Seq. ID
                    BLASTX
 Method
                     g466160
 NCBI GI
```

29230

373

BLAST score

:--

7.0e-36 E value Match length 84 85 % identity HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III NCBI Description >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis elegans >gi\_289769 (L14429) putative [Caenorhabditis elegans] 211053 Seq. No. LIB3145-015-Q1-K1-G12 Seq. ID Method BLASTN NCBI GI g21308 BLAST score 33 4.0e-09 E value 57 Match length 89 % identity NCBI Description S.oleracea mRNA for a 28kD RNA binding protein, involved in plastid mRNA 3' processing 211054 Seq. No. LIB3145-015-Q1-K1-G2 Seq. ID BLASTX Method q1752734 NCBI GI BLAST score 278 5.0e-25 E value 89 Match length % identity NCBI Description (D78510) beta-glucan-elicitor receptor [Glycine max] 211055 Seq. No. LIB3145-015-Q1-K1-G3 Seq. ID BLASTX Method g3451075 NCBI GI 230 BLAST score 5.0e-19 E value 82 Match length % identity (AL031326) putative protein [Arabidopsis thaliana] NCBI Description 211056 Seq. No. LIB3145-015-Q1-K1-G4 Seq. ID BLASTX Method g4102839 NCBI GI 218 BLAST score 1.0e-17 E value 135 Match length 39 % identity NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

211057 Seq. No.

LIB3145-015-Q1-K1-G6 Seq. ID

BLASTX Method g2346966 NCBI GI 147 BLAST score 2.0e-09 E value 36 Match length 75 % identity

(AB004871) CPC [Arabidopsis thaliana] NCBI Description >gi\_4559383\_gb\_AAD23043.1\_AC006526\_8 (AC006526) putative DNA binding protein CPC [Arabidopsis thaliana] Seq. No. 211058 Seq. ID LIB3145-015-Q1-K1-G9 Method BLASTX NCBI GI q465820 BLAST score 335 E value 2.0e-31 Match length 87 67 % identity HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III NCBI Description >gi\_280536\_pir\_\_S28301 hypothetical protein C40H1.6 -Caenorhabditis elegans >gi 3874819 emb\_CAA79557\_ (Z19154) C40H1.6 [Caenorhabditis elegans] 211059

 Seq. No.
 211059

 Seq. ID
 LIB3145-015-Q1-K1-H1

 Method
 BLASTX

 NCBI GI
 g1220196

 BLAST score
 330

 E value
 7.0e-31

Match length 88 % identity 70

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 211060 Seq. ID LIB3145-015-Q1-K1-H11

Method BLASTX
NCBI GI g3618320
BLAST score 244
E value 7.0e-21
Match length 76
% identity 67

NCBI Description (AB001888) zinc finger protein [Oryza sativa]

Seq. No. 211061

Seq. ID LIB3145-015-Q1-K1-H12

Method BLASTX
NCBI GI g4056420
BLAST score 322
E value 6.0e-30
Match length 96
% identity 66

NCBI Description (AC005322) ESTs gb T144077 and gb T43352 come from this

gene. [Arabidopsis thaliana]

Seq. No. 211062

Seq. ID LIB3145-015-Q1-K1-H2

Method BLASTX
NCBI GI g2117725
BLAST score 552
E value 6.0e-57
Match length 113
% identity 88

NCBI Description 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform



SBE2.2 precursor - Arabidopsis thaliana (fragment) >gi\_726490 (U22428) starch branching enzyme class II [Arabidopsis thaliana]

```
211063
Seq. No.
Seq. ID
                  LIB3145-015-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q3461817
BLAST score
                  333
E value
                  2.0e-31
Match length
                  95
% identity
                   69
                  (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211064
                  LIB3145-015-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244855
BLAST score
                  255
E value
                  2.0e-22
Match length
                  87
% identity
                  61
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   211065
                  LIB3145-015-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g4490330
NCBI GI
BLAST score
                   632
                   3.0e-66
E value
Match length
                  131
% identity
                   95
                  (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   211066
Seq. No.
                  LIB3145-016-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4490332
                   330
BLAST score
                   7.0e-31
E value
                  114
Match length
                   59
% identity
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                   211067
Seq. ID
                   LIB3145-016-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                   g114682
BLAST score
                  184
                   2.0e-13
E value
Match length
                   53
                   70
% identity
```

29233

(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)

>gi\_100471\_pir\_\_A35227 H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, mitochondrial - sweet

NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR



potato >gi\_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No. 211068 Seq. ID LIB3145-016-Q1-K1-A12 Method BLASTX g3874447 NCBI GI BLAST score 185 E value 9.0e-14 115 Match length % identity 36

NCBI Description (Z81039) predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST

yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com

Seq. No. 211069

Seq. ID LIB3145-016-Q1-K1-A2

Method BLASTX
NCBI GI g3201680
BLAST score 190
E value 6.0e-17
Match length 93
% identity 55

NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No. 211070

Seq. ID LIB3145-016-Q1-K1-A3

Method BLASTX
NCBI GI g3819676
BLAST score 485
E value 4.0e-49
Match length 110
% identity 79

NCBI Description (AJ011943) ER auxin binding protein 1 [Lycopersicon

esculentum]

Seq. No. 211071

Seq. ID LIB3145-016-Q1-K1-A7

Method BLASTX
NCBI GI g3395435
BLAST score 306
E value 4.0e-28
Match length 109
% identity 60

NCBI Description (AC004683) myosin heavy chain-like protein [Arabidopsis

thaliana]

Seq. No. 211072

Seq. ID LIB3145-016-Q1-K1-B1

Method BLASTX
NCBI GI g115607
BLAST score 304
E value 9.0e-28
Match length 124
% identity 49

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) (PEPC)

NCBI GI

BLAST score



>gi\_68033\_pir\_QYEC phosphoenolpyruvate carboxylase (EC
4.1.1.31) - Escherichia coli >gi\_4558284\_pdb\_1FIY\_
Three-Dimensional Structure Of Phosphoenolpyruvate
Carboxylase From Escherichia Coli At 2.8 A Resolution.
>gi\_48666\_emb\_CAA29332\_(X05903) PEP carboxylase (AA 1-883)
[Escherichia coli] >gi\_396303 (U00006) phosphoenolpyruvate
carboxylase [Escherichia coli] >gi\_1790393 (AE000469)
phosphoenolpyruvate carboxylase [Escherichia coli]
>gi\_352091\_prf\_1005219A carboxylase,phosphoenolpyruvate
[Escherichia coli]

```
Seq. No.
                   211073
Seq. ID
                  LIB3145-016-01-K1-B5
Method
                  BLASTX
NCBI GI
                   q4008159
BLAST score
                   598
E value
                   4.0e-62
Match length
                   128
% identity
                   88
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
Seq. No.
                   211074
Seq. ID
                  LIB3145-016-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                   g4512707
BLAST score
                   238
                   4.0e-20
E value
Match length
                   55
                   84
% identity
NCBI Description
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   211075
                   LIB3145-016-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g308906
BLAST score
                   241
                   2.0e-20
E value
Match length
                  96
% identity
                   51
NCBI Description (L18909) thioredoxin [Lilium longiflorum]
Seq. No.
                   211076
Seq. ID
                  LIB3145-016-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                   g3885336
BLAST score
                   393
E value
                   4.0e-38
Match length
                   144
% identity
                   51
                  (AC005623) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   211077
Seq. No.
Seq. ID
                   LIB3145-016-Q1-K1-D10
Method
                  BLASTX
```

q3493172

% identity

80

```
E value
Match length
                  129
% identity
                  98
NCBI Description
                  (U89609) fiber annexin [Gossypium hirsutum]
                  211078
Seq. No.
                  LIB3145-016-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  g3252807
NCBI GI'
BLAST score
                  277
E value
                  1.0e-24
Match length
                  120
% identity
                  46
                  (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  211079
Seq. No.
Seq. ID
                  LIB3145-016-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4510363
BLAST score
                  597
                   4.0e-62
E value
Match length
                  125
% identity
                  88
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  211080
Seq. No.
Seq. ID
                  LIB3145-016-Q1-K1-D8
                  BLASTX
Method
NCBI GI
                  q3024386
BLAST score
                  498
                  2.0e-50
E value
Match length
                  104
                   90
% identity
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                  >gi_2129500_pir__S52006 polygalacturonase - upland cotton
                  >gi_606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  211081
                  LIB3145-016-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1706918
BLAST score
                  255
E value
                   6.0e-22
Match length
                  95
% identity
                   48
NCBI Description
                  FLAVONOL SULFOTRANSFERASE-LIKE >gi 498647 (U10277)
                  sulfotransferase-like flavonol [Flaveria bidentis]
Seq. No.
                  211082
Seq. ID
                  LIB3145-016-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1351987
BLAST score
                  491
E value
                  9.0e-50
Match length
                  117
```



```
NCBI Description
                  ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)
                  (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi 507946
                  (L29083) glutamine-dependent asparagine synthetase
                  [Arabidopsis thaliana]
Seq. No.
                  211083
                  LIB3145-016-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3068705
BLAST score
                  258
                  2.0e-22
E value
Match length
                  99
% identity
                  55
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
                  211084
Seq. No.
                  LIB3145-016-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g3789917
NCBI GI
BLAST score
                  144
E value
                  5.0e-09
Match length
                  70
% identity
                  41
                  (AF084928) erythroblast macrophage protein EMP [Homo
NCBI Description
                  sapiens]
                  211085
Seg. No.
Seq. ID
                  LIB3145-016-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2281449
BLAST score
                  199
                  2.0e-15
E value
Match length
                  42
                  93
% identity
NCBI Description
                  (U90214) leucine zipper transcription factor TGA2.1
                  [Nicotiana tabacum]
Seq. No.
                  211086
Seq. ID
                  LIB3145-016-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4204297
BLAST score
                  150
E value
                  1.0e-09
Match length
                  117
% identity
                  42
NCBI Description (AC003027) ADK1 [Arabidopsis thaliana]
Seq. No.
                  211087
                  LIB3145-016-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539315
BLAST score
                  381
E value
```

29237

(AL035679) putative zinc finger protein [Arabidopsis

9.0e-37

thaliana]

92

Match length

% identity NCBI Description

```
211088
Seq. No.
Seq. ID
                  LIB3145-016-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2289008
BLAST score
                  223
                  2.0e-29
E value
                  119
Match length
% identity
                  58
                  (AC002335) putative 3-beta hydroxy-5-ene steriod
NCBI Description
                  dehydrogenase isolog [Arabidopsis thaliana]
                  211089
Seq. No.
                  LIB3145-016-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q285286
BLAST score
                  355
E value
                  8.0e-34
Match length
                  108
                  58
% identity
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
Seq. No.
                  211090
Seq. ID
                  LIB3145-016-Q1-K1-F11
                  BLASTN
Method
                  q3821780
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  211091
Seq. ID
                  LIB3145-016-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                   205
                   3.0e-16
E value
Match length
                   40
                   93-
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
NCBI Description
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                   211092
Seq. No.
Seq. ID
                  LIB3145-016-Q1-K1-F5
```

Method BLASTX NCBI GI g1351222 BLAST score 357 E value 6.0e - 34Match length 70 99 % identity

TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087 NCBI Description

(U31097) transcription factor TFIIB [Glycine max]

211093 Seg. No.

29238

```
LIB3145-016-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  g3236248
NCBI GI
                  306
BLAST score
                  5.0e-28
E value
                  75
Match length
                  81
% identity
NCBI Description
                  (AC004684) unknown protein [Arabidopsis thaliana]
                  211094
Seq. No.
                  LIB3145-016-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4325282
BLAST score
                  177
E value
                  6.0e-17
Match length
                   65
% identity
                  71
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                  >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
Seq. No.
                  211095
                  LIB3145-016-Q1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076498
BLAST score
                  145
E value
                   5.0e-09
Match length
                  72
                   44
% identity
NCBI Description
                  zinc-finger protein (C-terminal) - soybean
                  >gi_558543_emb_CAA85320_ (Z36749) C-terminal zinc-finger
                   [Glycine max]
                   211096
Seq. No.
                  LIB3145-016-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3851636
BLAST score
                   490
E value
                   1.0e-49
Match length
                  111
                   84
% identity
                   (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                   211097
                  LIB3145-016-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2815246
```

Method BLASTX
NCBI GI g2815246
BLAST score 218
E value 9.0e-18
Match length 55
% identity 71

NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No. 211098

Seq. ID LIB3145-016-Q1-K1-G5

Method BLASTX



```
q1351270
NCBI GI
BLAST score
                  251
E value
                  1.0e-21
Match length
                  109
% identity
                  54
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi 478410 pir JQ2255 triose-phosphate isomerase (EC
                  5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                  isomerase [Oryza sativa]
                  211099
Seq. No.
                  LIB3145-016-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g4105190
NCBI GI
BLAST score
                  157
E value
                  1.0e-10
Match length
                  84
% identity
                  42
NCBI Description
                  (AF044127) peroxisomal short-chain alcohol dehydrogenase
                  [Homo sapiens]
Seq. No.
                  211100
Seq. ID
                  LIB3145-016-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g602586
BLAST score
                  232
                  2.0e-19
E value
                  84
Match length
% identity
                  50
                  (X83229) 1-amniocyclopropane-1-carboxylate oxidase
NCBI Description
                  [Nicotiana tabacum]
Seq. No.
                  211101
                  LIB3145-016-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2443880
BLAST score
                  266
E value
                  2.0e-23
Match length
                  68
                  72
% identity
NCBI Description
                  (AC002294) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  211102
Seq. ID
                  LIB3145-016-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g730526
BLAST score
                  187
E value
                  5.0e-14
                  55
Match length
% identity
                  64
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
NCBI Description
```

>gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis

thaliana >gi\_404166\_emb\_CAA53005\_ (X75162) BBC1 protein

[Arabidopsis thaliana]

Seq. No. 211103

LIB3145-016-Q1-K1-H6 Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g2760326
BLAST score
                  335
E value
                  2.0e-31
Match length
                  134
% identity
                  48
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                  211104
Seq. No.
                  LIB3145-016-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3482917
BLAST score
                  501
E value
                  7.0e-51
                  130
Match length
                  75
% identity
                  (AC003970) Similar to Glucose-6-phosphate dehydrogenases,
NCBI Description
                  gi 2276344, gi 2829880, gi 2352919 and others. [Arabidopsis
                  thaliana]
Seq. No.
                  211105
                  LIB3145-016-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482917
BLAST score
                  140
E value
                  1.0e-08
Match length
                  95
% identity
                  41
                   (AC003970) Similar to Glucose-6-phosphate dehydrogenases,
NCBI Description
                  gi_2276344, gi_2829880, gi_2352919 and others. [Arabidopsis
                  thaliana]
Seq. No.
                  211106
Seq. ID
                  LIB3145-017-Q1-K1-A1
                  BLASTX
Method
NCBI GI
                  g950299
BLAST score
                  141
                  3.0e-09
E value
Match length
                  28
% identity
                  89
NCBI Description
                  (L46792) xyloglucan endotransglycosylase precursor
                   [Actinidia deliciosa]
Seq. No.
                  211107
                  LIB3145-017-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642428
BLAST score
                  161
```

E value 2.0e-11 Match length 47 % identity

(AC002391) unknown protein, 3' partial [Arabidopsis NCBI Description

thaliana]

211108 Seq. No.

Seq. ID LIB3145-017-Q1-K1-A11

Method BLASTX



```
q4406775
NCBI GI
BLAST score
                  203
                  6.0e-16
E value
                  98
Match length
% identity
                  42
NCBI Description
                  (AC006836) unknown protein [Arabidopsis thaliana]
                  211109
Seq. No.
Seq. ID
                  LIB3145-017-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3367534
BLAST score
                  558
E value
                  1.0e-57
Match length
                  126
% identity
                  86
                  (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
                  211110
Seq. No.
                  LIB3145-017-Q1-K1-A4
Seq. ID
Metabod
                  BLASTN
NCBI GI
                  g3449329
BLAST score
                  55
E value
                  5.0e-22
Match length
                  270
% identity
                  40
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  211111
Seq. ID
                  LIB3145-017-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3540181
BLAST score
                  248
E value
                  4.0e-21
Match length
                  111
                  47
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211112
                  LIB3145-017-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185511
                  423
BLAST score
E value
                  1.0e-41
Match length
                  114
% identity
                  72
NCBI Description
                  (AF102822) actin depolymerizing factor 4 [Arabidopsis
                  thaliana]
```

Seq. No. 211113

Seq. ID LIB3145-017-Q1-K1-B3

Method BLASTX
NCBI GI g508304
BLAST score 250
E value 2.0e-21

```
Match length
                     52
   % identity
                    (L22305) corC [Medicago sativa]
   NCBI Description
   Seq. No.
                     211114
                     LIB3145-017-Q1-K1-B4
   Seq. ID
   Method
                     BLASTN
NCBI GI
                     q13192
   BLAST score
                     81
                     1.0e-37
  E value
  Match length
                     93
                     97
   % identity
   NCBI Description
                     Oenothera berteriana mitDNA with part of plastid rRNA
                     operon
                     211115
   Seq. No.
                     LIB3145-017-Q1-K1-B8
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g3914303
  BLAST score
                     154
                     4.0e-10
   E value
  Match length
                     98
   % identity
                     36
                     PEROXISOMAL ASSEMBLY PROTEIN PEX3 (PEROXIN-3)
   NCBI Description
                     >gi 3336882 emb CAA04879 (AJ001625) Pex3 protein [Homo
                     sapiens] >gi 4092648 emb CAA10362 (AJ131389) PEX3 protein
                     [Homo sapiens] >gi 4218426 emb CAA08904 (AJ009866) Pex3p
                     [Homo sapiens] >gi 4505727 ref NP 003621.1 pPEX3
                     peroxisomal biogenesis factor
   Seq. No.
                     211116
   Seq. ID
                     LIB3145-017-Q1-K1-C10
   Method
                     BLASTX
                     g2996096
   NCBI GI
   BLAST score
                     617
   E value
                     2.0e-64
   Match length
                     121
   % identity
                     96
   NCBI Description
                     (AF030517) translation elongation factor-1 alpha; EF-1
                     alpha [Oryza sativa]
   Seq. No.
                     211117
   Seq. ID
                     LIB3145-017-Q1-K1-C11
   Method
                     BLASTX
   NCBI GI
                     g3402685
   BLAST score
                     174
                     2.0e-12
   E value
   Match length
                     120
                     37
   % identity
```

Seq. No. 211118

NCBI Description

Seq. ID LIB3145-017-Q1-K1-C4

Method BLASTN
NCBI GI g3249094
BLAST score 37
E value 2.0e-11

(AC004697) unknown protein [Arabidopsis thaliana]



Match length 100 % identity

Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, NCBI Description

complete sequence [Arabidopsis thaliana]

Seq. No. 211119

LIB3145-017-Q1-K1-C6 Seq. ID

BLASTX Method NCBI GI g3024122 BLAST score 587 6.0e-61 E value Match length 134 87 % identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

> ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi\_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

. 4

Seq. No. 211120

Seq. ID LIB3145-017-Q1-K1-C8

Method BLASTX NCBI GI q3540182 BLAST score 335 E value 2.0e-31 Match length 125 % identity 59

(AC004122) Unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 211121

Seq. ID LIB3145-017-Q1-K1-C9

Method BLASTX NCBI GI q3402683 BLAST score 230 E value 4.0e-19 Match length 113 % identity 48

(AC004697) patatin-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 211122

Seq. ID LIB3145-017-Q1-K1-D12

Method BLASTX NCBI GI q122106 404 BLAST score E value 2.0e-39 Match length 82 % identity 98

NCBI Description

HISTONE H4 >gi\_70771\_pir\_\_HSZM4 histone H4 - maize >gi\_81642\_pir\_\_S06904 histone H4 - Arabidopsis thaliana

>gi 2119028 pir S60475 histone H4 - garden pea

>gi 21795 emb CAA24924 (X00043) histone H4 [Triticum aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis thaliana] >gi\_166742 (M17133) histone H4 [Arabidopsis

thaliana] >gi\_168499 (M36659) histone H4 (H4C13) [Zea mays]

>gi 168501 (M13370) histone H4 [Zea mays] >gi 168503 (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone

H4 homolog [Pisum sativum] >qi 1806285 emb CAB01914

(Z79638) histone H4 homologue [Sesbania rostrata]

>gi 3927823 (AC005727) histone H4 [Arabidopsis thaliana]

% identity

NCBI Description

Seq. No.

211123

>gi\_4580385\_gb\_AAD24364.1\_AC007184\_4 (AC007184) histone H4
[Arabidopsis thaliana] >gi\_225838\_prf\_\_1314298A histone H4
[Arabidopsis thaliana]

LIB3145-017-Q1-K1-D4 Seq. ID Method BLASTX g2864608 NCBI GI BLAST score 539 E value 3.0e-55 Match length 139 % identity 71 NCBI Description (AL021811) ferredoxin--NADP+ reductase - like protein [Arabidopsis thaliana] >gi\_4049338\_emb\_CAA22563\_ (AL034567) ferredoxin-NADP+ reductase-like protein [Arabidopsis thalianal Seq. No. 211124 Seq. ID LIB3145-017-Q1-K1-D5 Method BLASTX NCBI GI g3860247 BLAST score 577 1.0e-63 E value 139 Match length 89 % identity NCBI Description (AC005824) unknown protein [Arabidopsis thaliana] Seq. No. 211125 LIB3145-017-Q1-K1-D6 Seq. ID Method BLASTX NCBI GI g1843527 BLAST score 447 2.0e-44E value Match length 116 % identity 78 NCBI Description (U73747) annexin [Gossypium hirsutum] Seq. No. . 211126 Seq. ID LIB3145-017-Q1-K1-D7 Method BLASTX NCBI GI a1708292 BLAST score 281 E value 4.0e-25 Match length 101 % identity 50 HEAT-RESPONSIVE PROTEIN 12 >gi 1255116 (U50631) NCBI Description heat-responsive protein [Mus musculus] Seq. No. 211127 Seq. ID LIB3145-017-Q1-K1-D8 Method BLASTX NCBI GI g2244765 BLAST score 159 E value 1.0e-10 Match length 90

(Z97335) hypothetical protein [Arabidopsis thaliana]



1.2 -Seq. No. 211128 LIB3145-017-Q1-K1-E1 Seq. ID Method BLASTX NCBI GI g4337195 479 BLAST score 3.0e-48E value Match length 138 72 % identity NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana] Seq. No. 211129 Seq. ID LIB3145-017-Q1-K1-E10 Method BLASTX NCBI GI q730558 BLAST score 116 E value 6.0e-12 Match length 63 % identity 65 60S RIBOSOMAL PROTEIN L34 >gi 1076636 pir S48027 ribosomal NCBI Description protein L34 - common tobacco >gi 2129964 pir S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi 436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum] 211130 Seq. No. Seq. ID LIB3145-017-Q1-K1-E12 Method BLASTX NCBI GI q730558 BLAST score 395 E value 2.0e-38 Match length 90 86 % identity 60S RIBOSOMAL PROTEIN L34 >gi 1076636 pir S48027 ribosomal NCBI Description

protein L34 - common tobacco >gi 2129964 pir S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi\_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi 436032 (L27107) 60S ribosomal protein L34

[Nicotiana tabacum]

Seq. No. 211131

Seq. ID LIB3145-017-Q1-K1-E3

Method BLASTX NCBI GI q2760325 BLAST score 446 E value 2.0e-44 Match length 127 69 % identity

(AC002130) F1N21.10 [Arabidopsis thaliana] NCBI Description

Seq. No. 211132

LIB3145-017-Q1-K1-E4 Seq. ID

Method BLASTX NCBI GI g136707 BLAST score 179 E value 4.0e-13

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29246

E value

```
Match length
% identity
                  94
                  CYTOCHROME B6-F COMPLEX IRON-SULFUR SUBUNIT PRECURSOR
NCBI Description
                  (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_280397_pir__S26199
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
                  iron-sulfur protein precursor - garden pea
                  >gi_20832_emb_CAA45151_ (X63605) chloroplast Rieske FeS
                  protein [Pisum sativum]
Seq. No.
                  211133
Seq. ID
                  LIB3145-017-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q1730109
BLAST score
                  307
```

Match length 108 % identity 61 NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN

HYDROXYLASE) >gi\_499022\_emb\_CAA53580\_ (X75966)

leucoanthocyanidin dioxygenase [Vitis vinifera] Seq. No. 211134

Seq. ID LIB3145-017-Q1-K1-E7 Method BLASTX NCBI GI g125887 BLAST score 118 E value 3.0e-12 76 Match length

57

3.0e-28

% identity ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR NCBI Description

> >gi 82092 pir S04765 LAT52 protein precursor - tomato >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 211135

Seq. ID LIB3145-017-Q1-K1-E8

Method BLASTX NCBI GI q266579 BLAST score 159 E value 8.0e-11 78 Match length 45 % identity

METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 169713 (L02306) NCBI Description

metallothionein [Ricinus communis]

Seq. No. 211136

Seq. ID LIB3145-017-Q1-K1-F1

Method BLASTX NCBI GI q2661840 BLAST score 410 E value 3.0e-40 Match length 125 % identity 58

(Y15430) adenosine kinase [Physcomitrella patens] NCBI Description

Seq. No. 211137

Seq. ID LIB3145-017-Q1-K1-F12

Match length

129

```
BLASTX
Method
NCBI GI
                  g1843527
BLAST score
                  438
                  2.0e-43
E value
Match length
                  104
                  51
% identity
                 (U73747) annexin [Gossypium hirsutum]
NCBI Description
                  211138
Seq. No.
                  LIB3145-017-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2661840
BLAST score
                  234
                  1.0e-19
E value
Match length
                  90
                  44
% identity
NCBI Description
                 (Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.
                  211139
                  LIB3145-017-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g349379
BLAST score
                  159
                  9.0e-11
E value
                  93
Match length
                  55
% identity
                 (L22847) HAHB-1 [Helianthus annuus]
NCBI Description
                  211140
Seq. No.
Seq. ID
                  LIB3145-017-Q1-K1-F4
Method
                  BLASTN
                  g407800
NCBI GI
BLAST score
                  63
E value
                  7.0e-27
Match length
                  79
                  95
% identity
                  G.hirsutum mRNA for ribosomal protein 41, large subunit
NCBI Description
                   (RL41)
Seq. No.
                  211141
                  LIB3145-017-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703375
BLAST score
                  337
E value
                  4.0e-38
Match length
                  89
% identity
NCBI Description
                  ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
                  211142
Seq. No.
Seq. ID
                  LIB3145-017-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g464734
BLAST score
                  622
E value
                  4.0e-65
```



```
% identity
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                  HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379
                  adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle
                  >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine
                  hydrolase [Catharanthus roseus]
Seq. No.
                  211143
                  LIB3145-017-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2459421
BLAST score
                  368
E value
                  2.0e-35
Match length
                  99
                  67
% identity
                  (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  211144
Seq. ID
                  LIB3145-017-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g1174621
BLAST score
                  373
E value
                  7.0e-36
Match length
                  127
                  54
% identity
                  T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                  (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing
                  cytosolic chaperonin (CCT) theta chain - mouse
                  >gi 695625 emb CAA85521 (Z37164) CCTtheta, theta subunit
                  of the chaperonin containing TCP-1 (CCT) [Mus musculus]
Seq. No.
                  211145
                  LIB3145-017-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1565225
BLAST score
                  159
E value
                  2.0e-17
Match length
                  108
% identity
                  36
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                  211146
Seq. ID
                  LIB3145-018-Q1-K1-A12
Method
                  BLASTN
NCBI GI
                  g18058
BLAST score
                  189
E value
                  1.0e-102
                  293
Match length
                  91
% identity
NCBI Description Citrus limon cistron for 26S ribosomal RNA
```

Seq. No. 211147

Seq. ID LIB3145-018-Q1-K1-A2

Method BLASTX NCBI GI g951427 BLAST score 475

29249



E value 8.0e-48
Match length 124
% identity 71

NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus

communis]

Seq. No. 211148

Seq. ID LIB3145-018-Q1-K1-A4

Method BLASTX
NCBI GI g1709970
BLAST score 444
E value 4.0e-44
Match length 121
% identity 74

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 211149

Seq. ID LIB3145-018-Q1-K1-A7

Method BLASTX
NCBI GI g3850111
BLAST score 239
E value 3.0e-20
Match length 84
% identity 49

NCBI Description (AL033388) hypothetical integral membrane protein, putative

involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No. 211150

Seq. ID LIB3145-018-Q1-K1-A8

Method BLASTX
NCBI GI g3482979
BLAST score 142
E value 1.0e-08
Match length 121
% identity 34

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

>gi\_4567258\_gb\_AAD23672.1\_AC007070\_21 (AC007070)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 211151

Seq. ID LIB3145-018-Q1-K1-B1

Method BLASTX
NCBI GI g3850111
BLAST score 260
E value 1.0e-22
Match length 86
% identity 51

NCBI Description (AL033388) hypothetical integral membrane protein, putative

involvement in lipid metabolism [Schizosaccharomyces pombe]

Seq. No. 211152

Seq. ID LIB3145-018-Q1-K1-B10

Method BLASTX
NCBI GI g1174621
BLAST score 345
E value 1.0e-32
Match length 135



% identity T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) NCBI Description (CCT-THETA) >gi\_1083259 pir\_\_JC4073 TCP-1 containing cytosolic chaperonin ( $\overline{\text{CCT}}$ )  $\overline{\text{th}}$ eta chain - mouse >gi\_695625\_emb\_CAA85521\_ (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus] Seq. No. 211153 LIB3145-018-Q1-K1-B3 Seq. ID Method BLASTX g1354510 NCBI GI 553 BLAST score 6.0e-57 E value 138 Match length 74 % identity (U55205) HAL2-like protein [Arabidopsis thaliana] NCBI Description 211154 Seq. No. LIB3145-018-Q1-K1-B4 Seq. ID BLASTX Method g4204288 NCBI GI BLAST score 389 E value 1.0e-37 144 Match length 53 % identity (AC003027) lcl\_prt\_seq No definition line found NCBI Description [Arabidopsis thaliana] 211155 Seq. No. LIB3145-018-Q1-K1-B5 Seq. ID BLASTX Method g3850111 NCBI GI BLAST score 149 1.0e-09 E value 89 Match length 37 % identity (AL033388) hypothetical integral membrane protein, putative NCBI Description involvement in lipid metabolism [Schizosaccharomyces pombe] 211156 Seq. No. LIB3145-018-Q1-K1-B8 Seq. ID BLASTX Method g1351408 NCBI GI BLAST score 527 7.0e-54E value 124 Match length 79 % identity

VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) NCBI Description

>gi\_1076563\_pir\_\_S51117 cystein proteinase - sweet orange >gi\_633185\_emb\_CAA87720\_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi\_1588548\_prf\_\_2208463A

vascular processing protease [Citrus sinensis]

211157 Seq. No.

Seq. ID LIB3145-018-Q1-K1-B9

BLASTX Method q1946359 NCBI GI



```
BLAST score
                  2.0e-24
E value
                  92
Match length
                  58
% identity
                  (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211158
Seq. No.
                  LIB3145-018-Q1-K1-C10
Seq. ID
                  BLASTN
Method
                   g12292
NCBI GI
                   275
BLAST score
                   1.0e-153
E value
                   382
Match length
                   93
% identity
                   Spinach chloroplast DNA homologous to ARS and ARC elements
NCBI Description
                   upstream of rDNA operon
                   211159
Seq. No.
                   LIB3145-018-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g4510363
NCBI GI
BLAST score
                   538
                   3.0e-55
E value
                   106
Match length
                   90
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   211160
Seq. No.
                   LIB3145-018-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g1694976
NCBI GI
BLAST score
                   383
                   4.0e-37
E value
                   106
Match length
                   68
% identity
                   (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   211161
 Seq. No.
                   LIB3145-018-Q1-K1-D1
 Seq. ID
                   BLASTX
Method
                   q3292832
NCBI GI
 BLAST score
                   247
                   5.0e-21
 E value
                   94
 Match length
                   63
 % identity
                   (AL031018) putative protein [Arabidopsis thaliana]
 NCBI Description
```

Seq. No. 211162

Seq. ID LIB3145-018-Q1-K1-D2

Method BLASTX
NCBI GI g2317908
BLAST score 624
E value 3.0e-65
Match length 145

NCBI Description

```
% identity
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]
                  211163
Seq. No.
                  LIB3145-018-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3075398
NCBI GI
                  155
BLAST score
                  3.0e-10
E value
Match length
                  66
% identity
                  45
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
                  211164
Seq. No.
                  LIB3145-018-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g1843527
NCBI GI
                   457
BLAST score
                   1.0e-45
E value
                   119
Match length
                   77
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
                   211165
Seq. No.
                   LIB3145-018-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g2244956
NCBI GI
                   327
BLAST score
                   2.0e-30
E value
                   122
Match length
                   50
% identity
                   (Z97340) strong similarity to pectinesterase [Arabidopsis
NCBI Description
                   thaliana]
                   211166
Seq. No.
                   LIB3145-018-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   q123620
NCBI GI
                   567
BLAST score
                   1.0e-58
E value
                   138
Match length
                   82
 % identity
                   HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950
 NCBI Description
                   heat shock cognate protein 70 - tomato
                   >gi 19258 emb_CAA37971_ (X54030) heat shock protein cognate
                   70 [Lycopersicon esculentum]
                   211167
 Seq. No.
                   LIB3145-018-Q1-K1-E1
 Seq. ID
                   BLASTX
 Method
                   g3551973
 NCBI GI
                    567
 BLAST score
                    1.0e-58
 E value
                   129
 Match length
                    85
 % identity
                   (AF085068) alcohol dehydrogenase A [Gossypium hirsutum]
```

```
211168
Seq. No.
                  LIB3145-018-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g4567229
NCBI GI
                  144
BLAST score
                  6.0e-09
E value
                  54
Match length
                  52
% identity
                   (AC007119) putative pectin methylesterase [Arabidopsis
NCBI Description
                  thaliana]
                   211169
Seq. No.
                  LIB3145-018-Q1-K1-F10
Seq. ID
                  BLASTN
Method
                   g2618604
NCBI GI
                   32
BLAST score
                   1.0e-08
E value
Match length
                   48
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   211170
                   LIB3145-018-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   q4510406
NCBI GI
                   409
BLAST score
                   5.0e-40
E value
Match length
                   115
                   67
% identity
                  (AC006587) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   211171
                   LIB3145-018-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   q1173256
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
Match length
                   124
                   62
 % identity
                   40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   211172
 Seq. No.
                   LIB3145-018-Q1-K1-F6
 Seq. ID
                   BLASTX
 Method
                   g136636
 NCBI GI
                   495
 BLAST score
                   4.0e-50
 E value
                   93
 Match length
                   97
 % identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
 NCBI Description
```

29254

>gi 1076424 pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)



Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

```
211173
Seq. No.
                  LIB3145-018-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g2511689
NCBI GI
                   428
BLAST score
                   3.0e-42
E value
                   142
Match length
                   59
% identity
                  (Z99952) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
                   211174
Seq. No.
                   LIB3145-018-Q1-K1-G6
Seq. ID
                   BLASTX
Method
                   g2351580
NCBI GI
                   169
BLAST score
E value
                   6.0e-12
Match length
                   99
                   38
% identity
                   (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
Seq. No.
                   211175
                   LIB3145-018-Q1-K1-G8
Seq. ID
                   BLASTX
Method
                   g2739385
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
                   126
Match length
                   33
% identity
                   (AC002505) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   211176
Seq. No.
                   LIB3145-018-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g1136122
NCBI GI
                   313
BLAST score
                   1.0e-31
E value
                   103
Match length
                   66
% identity
                   (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                   211177
Seq. No.
                   LIB3145-018-Q1-K1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3024386
                   625
BLAST score
                   2.0e-65
E value
Match length
                   127
```

29255

NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)

94

% identity

>gi\_2129500\_pir\_\_S52006 polygalacturonase - upland cotton >gi\_606650 (U09717) polygalacturonase [Gossypium hirsutum]

211178 Seq. No. LIB3145-018-Q1-K1-H3 Seq. ID BLASTX Method g3024386 NCBI GI 259 BLAST score 1.0e-22 E value 84 Match length

67

% identity POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) NCBI Description

>gi\_2129500\_pir\_\_S52006 polygalacturonase - upland cotton >gi\_606650 (U09717) polygalacturonase [Gossypium hirsutum]

211179 Seq. No.

LIB3145-018-Q1-K1-H6 Seq. ID

BLASTX Method q4249382 NCBI GI 640 BLAST score 4.0e-67 E value 138 Match length % identity 86

(AC005966) Strong similarity to gi 3337350 F13P17.3 NCBI Description

putative permease from Arabidopsis thaliana BAC

gb\_AC004481. [Arabidopsis thaliana]

211180 Seq. No.

LIB3145-019-Q1-K1-A1 Seq. ID

BLASTX Method g2597826 NCBI GI 302 BLAST score E value 1.0e-27 97 Match length 57 % identity

(Y14590) class IV chitinase [Arabidopsis thaliana] NCBI Description

211181 Seq. No.

LIB3145-019-Q1-K1-A11 Seq. ID

BLASTX Method g2811025 NCBI GI 548 BLAST score 2.0e-56 E value 132 Match length 73 % identity

ASPARTIC PROTEINASE PRECURSOR >gi\_1944181\_dbj\_BAA19607\_ NCBI Description

(AB002695) aspartic endopeptidase [Cucurbita pepo]

211182 Seq. No.

LIB3145-019-Q1-K1-B1 Seq. ID

BLASTN Method g3702724 NCBI GI BLAST score 71 1.0e-31 E value 149 Match length 87 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:



K17N15, complete sequence [Arabidopsis thaliana]

211183 Seq. No. Seq. ID LIB3145-019-Q1-K1-B10 BLASTX Method q2119042 NCBI GI 300 BLAST score 2.0e-27 E value 69 Match length 86 % identity glycine-rich RNA-binding protein RGP-la - wood tobacco NCBI Description >gi 469070 dbj\_BAA03741\_ (D16204) RNA-binding glycine-rich protein-1 (RGP-1a) [Nicotiana sylvestris] 211184 Seq. No. LIB3145-019-Q1-K1-B2 Seq. ID BLASTX Method g4206122 NCBI GI 574 BLAST score 2.0e-59 E value Match length 127 % identity 84 (AF097667) protein phosphatase 2C homolog [Mesembryanthemum NCBI Description crystallinum] 211185 Seq. No. Seq. ID LIB3145-019-Q1-K1-B3 BLASTXMethod g114121 NCBI GI 183 BLAST score 1.0e-13 E value Match length 60 63 % identity ADP-RIBOSYLATION FACTOR 1 >gi 101185 pir\_B36167 NCBI Description ADP-ribosylation factor 1 - yeast (Saccharomyces cerevisiae) >gi 171073 (J03276) ADP-ribosylation factor [Saccharomyces cerevisiae] >gi\_1004303\_emb\_CAA58255\_ (X83276) ADP-ribosylationfactor 2 [Saccharomyces cerevisiae] >gi\_1431314\_emb\_CAA98769\_ (Z74240) ORF YDL192w [Saccharomyces cerevisiae] 211186 Seq. No. Seq. ID LIB3145-019-Q1-K1-B6 Method BLASTX q2760326 NCBI GI 416 BLAST score E value 7.0e-41140 Match length % identity (AC002130) F1N21.11 [Arabidopsis thaliana] NCBI Description Seq. No. 211187

Seq. ID LIB3145-019-Q1-K1-B7

Method BLASTX
NCBI GI g2244990
BLAST score 154
E value 2.0e-10

BLAST score

Match length

NCBI Description

% identity

E value

363 9.0e-35

125

58



```
Match length
% identity
                  (Z97340) similarity to LIM homeobox protein -
NCBI Description
                  Caenorhabditis [Arabidopsis thaliana]
                  211188
Seq. No.
                  LIB3145-019-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                  g2842487
NCBI GI
                  617
BLAST score
                  2.0e-64
E value
                  138
Match length
                  82
% identity
                  (AL021749) SOF1 protein-like protein [Arabidopsis thaliana]
NCBI Description
                  211189
Seq. No.
                  LIB3145-019-Q1-K1-C12
Seq. ID
                  BLASTN
Method
                   g2687434
NCBI GI
                   205
BLAST score
                   1.0e-112
E value
Match length
                  253
% identity
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
                   211190
Seq. No.
                   LIB3145-019-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g4454012
NCBI GI
                   421
BLAST score
                   2.0e-41
E value
                   122
Match length
                   59
% identity
                   (AL035396) Pollen-specific protein precursor like
NCBI Description
                   [Arabidopsis thaliana]
                   211191
Seq. No.
                   LIB3145-019-Q1-K1-C5
Seq. ID
                   BLASTX
Method
                   g3080370
NCBI GI
BLAST score
                   245
                   8.0e-21
E value
Match length
                   64
                   72
 % identity
                   (AL022580) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   211192
 Seq. No.
                   LIB3145-019-Q1-K1-C9
Seq. ID
                   BLASTX
Method
                   g2980784
NCBI GI
```

29258

(AL022198) puative protein [Arabidopsis thaliana]

```
211193
Seq. No.
                  LIB3145-019-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g3970689
NCBI GI
                   262
BLAST score
                   4.0e-23
E value
Match length
                   81
                   63
% identity
                  (Y18484) (+)-delta-cadinene synthase [Gossypium arboreum]
NCBI Description
                   211194
Seq. No.
                   LIB3145-019-Q1-K1-D11
Seq. ID
Method
                   BLASTN
                   g2218151
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   54
Match length
% identity
                   91
                   Vigna unguiculata type IIIa membrane protein cp-wap13 mRNA,
NCBI Description
                   complete cds
                   211195
Seq. No.
                   LIB3145-019-Q1-K1-D12
Seq. ID
Method
                   BLASTX
                   g4098129
NCBI GI
                   573
BLAST score
                   2.0e-59
E value
Match length
                   107
% identity
                   98
                   (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   211196
Seq. No.
                   LIB3145-019-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2262118
                   502
BLAST score
                   6.0e-51
E value
                   142
Match length
                   70
% identity
                   (AC002343) cell division protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   211197
Seq. No.
                   LIB3145-019-Q1-K1-D5
Seq. ID
                   BLASTN
Method
                   g662870
NCBI GI
                   39
BLAST score
```

NCBI GI g662870
BLAST score 39
E value 1.0e-12
Match length 79
% identity 87

NCBI Description A.thaliana mRNA for molybdenum cofactor biosynthesis Cnx2

protein

Seq. No. 211198

Seq. ID LIB3145-019-Q1-K1-D9

Method BLASTX NCBI GI g2546954



```
BLAST score
                  5.0e-57
E value
                  143
Match length
                  76
% identity
                  (Y15108) translation elongation factor-TU [Glycine max]
NCBI Description
Seq. No.
                  211199
                  LIB3145-019-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2738949
                  596
BLAST score
E value
                  5.0e-62
Match length
                  122
% identity
                   89
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                  ananassa]
                   211200
Seq. No.
                   LIB3145-019-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g462141
BLAST score
                   599
E value
                   3.0e-62
Match length
                   141
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)
NCBI Description
                   >gi 1085816_pir__S38570 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Atriplex nummularia
                   >gi_409575 (U02886) glyceraldehyde-3-phosphate
                   dehydrogenase [Atriplex nummularia]
                   >gi 414607_emb_CAA53269_ (X75597)
                   glyceraldehyde-3-phosphate dehydrogenase [Atriplex
                   nummularia]
Seq. No.
                   211201
                   LIB3145-019-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   q4090257
NCBI GI
BLAST score
                   460
                   5.0e-46
E value
                   91
Match length
                   96
 % identity
                   (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   211202
 Seq. No.
                   LIB3145-019-Q1-K1-E5
 Seq. ID
                   BLASTX
Method
                   g3193284
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
                   36
Match length
                   78
 % identity
                   (AF069298) No definition line found [Arabidopsis thaliana]
 NCBI Description
```

Seq. No. 211203

Seq. ID LIB3145-019-Q1-K1-E7

Method BLASTX

29260

```
q2062167
NCBI GI
                  234
BLAST score
                  1.0e-19
E value
                  73
Match length
                  62
% identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  211204
Seq. No.
                  LIB3145-019-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  g3928099
NCBI GI
                   237
BLAST score
                   7.0e-20
E value
                   104
Match length
                   25
% identity
                  (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
                   211205
Seq. No.
                   LIB3145-019-Q1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4249418
BLAST score
                   314
                   5.0e-29
E value
                   81
Match length
                   52
% identity
                   (AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H
NCBI Description
                   type domains), 5' partial [Arabidopsis thaliana]
                   211206
Seq. No.
                   LIB3145-019-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g1174600
NCBI GI
                   393
BLAST score
                   4.0e-38
E value
                   76
Match length
                   99
% identity
                   TUBULIN BETA CHAIN >gi 493710_dbj BAA06382_ (D30717)
NCBI Description
                   beta-tubulin [Oryza sativa]
                   211207
Seq. No.
Seq. ID
                   LIB3145-019-Q1-K1-F5
                   BLASTX
Method
                   g4467157
NCBI GI
BLAST score
                   255
                   5.0e-22
E value
                   120
Match length
                   47
% identity
                   (AL035540) disease resistance response like protein
NCBI Description
                   [Arabidopsis thaliana]
```

211208 Seq. No.

Seq. ID LIB3145-019-Q1-K1-F6

BLASTX Method NCBI GI q2529658 BLAST score 311 1.0e-28 E value



```
Match length
                  50
% identity
                  (AC002535) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  211209
Seq. No.
Seq. ID
                  LIB3145-019-Q1-K1-F7
                  BLASTX
Method
NCBI GI
                  q4538935
BLAST score
                  142
                  6.0e-09
E value
                  54
Match length
                  50
% identity
                  (AL049483) putative protein [Arabidopsis thaliana]
NCBI Description
                  211210
Seq. No.
                  LIB3145-019-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  g4558462
NCBI GI
BLAST score
                  187
                   5.0e-14
E value
Match length
                   90
% identity
                   43
                   (AF079404) cell cycle switch protein [Medicago sativa
NCBI Description
                  subsp. X varia]
                   211211
Seq. No.
                  LIB3145-019-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                   g3785983
NCBI GI
                   148
BLAST score
                   1.0e-09
E value
Match length
                   89
                   38
% identity
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   211212
Seq. No.
Seq. ID
                   LIB3145-019-Q1-K1-G12
                   BLASTX
Method
NCBI GI
                   g3953478
                   326
BLAST score
                   3.0e-30
E value
                   142
Match length
                   51
% identity
                   (AC002328) F2202.23 [Arabidopsis thaliana]
NCBI Description
                   211213
Seq. No.
Seq. ID
                   LIB3145-019-Q1-K1-G2
                   BLASTX
Method
                   g3292816
NCBI GI
BLAST score
                   421
                   2.0e-41
E value
Match length
                   108
% identity
                   (AL031018) putative fizzy-related protein [Arabidopsis
NCBI Description
```

29262

thaliana]

211214

Seq. No.



```
LIB3145-019-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g3649778
NCBI GI
                  161
BLAST score
                  2.0e-11
E value
                  75
Match length
                  53
% identity
NCBI Description (AJ011303) pepc2 [Vicia faba]
                  211215
Seq. No.
                  LIB3145-019-Q1-K1-G9
Seq. ID
                  BLASTN
Method
                  g18846
NCBI GI
                   43
BLAST score
                   4.0e-15
E value
                   59
Match length
                   93
% identity
NCBI Description H.japonicus RNA (Z130) for 7S (SRP) RNA
                   211216
Seq. No.
                   LIB3145-019-Q1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                  q4432817
                   362
BLAST score
                   1.0e-34
E value
                   95
Match length
                   74
% identity
                  (AC006593) unknown protein [Arabidopsis thaliana]
NCBI Description
                   211217
Seq. No.
                   LIB3145-019-Q1-K1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3763932
                   513
BLAST score
                   2.0e-52
E value
                   122
Match length
                   83
% identity
                  (AC004450) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   211218
Seq. No.
                   LIB3145-019-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g4455276
NCBI GI
BLAST score
                   143
                   7.0e-09
E value
                   61
Match length
                   48
% identity
                   (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   211219
Seq. No.
Seq. ID
                   LIB3145-019-Q1-K1-H4
Method
                   BLASTX
                   g2677828
NCBI GI
BLAST score
                   329
                   8.0e-31
E value
```

92

Match length

% identity 66

NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No.

211220

Seq. ID

LIB3145-019-Q1-K1-H5

Method NCBI GI BLASTX g119150

BLAST score E value 587 5.0e-61

Match length % identity

110 100

NCBI Description

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi\_19273\_emb\_CAA32618\_ (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>qi 295810 emb CAA37212 (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

Seq. No.

211221

Seq. ID

LIB3145-019-Q1-K1-H6

Method NCBI GI BLAST score E value BLASTX g3953471 269 7.0e-24

Match length % identity

101 58

NCBI Description

(AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No.

211222

Seq. ID Method LIB3145-019-Q1-K1-H8

Method NCBI GI BLAST score E value BLASTX g2677828 402 3.0e-39

Match length 128 % identity 62

NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No.

211223

Seq. ID Method LIB3145-020-Q1-K1-A10

Method BLASTX
NCBI GI g231504
BLAST score 722
E value 1.0e-76
Match length 148
% identity 95

NCBI Description

ACTIN 100 >gi\_100420\_pir S20092 actin - potato (fragment)

>gi 1345579 emb CAA39276 (X55746) actin [Solanum

tuberosum]

Seq. No.

211224

Seq. ID

LIB3145-020-Q1-K1-A11

Method BLASTX
NCBI GI g2982303
BLAST score 256
E value 4.0e-22
Match length 59

% identity

56

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]



```
% identity
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
Seq. No.
                  211225
Seq. ID
                  LIB3145-020-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  q4530126
BLAST score
                  312
E value
                  1.0e-28
                  93
Match length
                  59
% identity
                  (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                  211226
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-A3
                  BLASTX
Method
                  g730450
NCBI GI
                  556
BLAST score
                   3.0e-57
E value
Match length
                  139
                  77
% identity
                  60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                  >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
                   >gi 398922 emb CAA80343 (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                   211227
Seq. No.
                  LIB3145-020-Q1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4580461
BLAST score
                   168
                   8.0e-12
E value
                   67
Match length
                   57
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   211228
Seq. No.
Seq. ID
                   LIB3145-020-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   q1778149
                   160
BLAST score
                   6.0e-11
E value
                   36
Match length
% identity
                   (U66404) phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor [Zea mays]
                   211229
Seq. No.
Seq. ID
                   LIB3145-020-Q1-K1-B1
                   BLASTX
Method
NCBI GI
                   g3759184
BLAST score
                   250
                   2.0e-21
E value
Match length
                   94
```

29265



```
211230
Seq. No.
                  LIB3145-020-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                  g4490741
NCBI GI
BLAST score
                  164
                  3.0e-11
E value
                  118
Match length
% identity
                  53
                  (AL035708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211231
                  LIB3145-020-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                  g4559331
NCBI GI
                  150
BLAST score
E value
                  1.0e-09
Match length
                  31
                  87
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211232
                  LIB3145-020-Q1-K1-B5
Seq. ID
Method
                  BLASTX
                  q2465156
NCBI GI
                  140
BLAST score
                  1.0e-08
E value
                  77
Match length
                  36
% identity
                  (Z99753) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  211233
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-B6
Method
                  BLASTX
                  q128592
NCBI GI
                  379
BLAST score
E value
                  2.0e-36
                  105
Match length
                   66
% identity
                  POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                  >gi 82190 pir S22495 pollen-specific protein precursor -
                   common tobacco >gi 19902 emb CAA43454 (X61146) pollen
                   specific protein [Nicotiana tabacum]
                   211234
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-B7
                  BLASTX
Method
NCBI GI
                   q1346701
                   234
BLAST score
                   2.0e-19
E value
                   140
Match length
% identity
                   40
                  EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG)
NCBI Description
                   (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
```

29266

exopolygalacturonase [Arabidopsis thaliana]

>gi\_421831\_pir\_\_S34199 exopolygalacturonase (clone GBGe184)
- Arabidopsis thaliana >gi 313682 emb CAA51032\_ (X72291)





>gi\_3004440\_emb\_CAA76127\_ (Y16230) polygalacturonase
[Arabidopsis thaliana]

Seq. No. 211235

Seq. ID LIB3145-020-Q1-K1-C2

Method BLASTX
NCBI GI g3819164
BLAST score 659
E value 2.0e-69
Match length 137
% identity 92

NCBI Description (AJ012318) cytosolic chaperonin, delta-subunit [Glycine

max]

Seq. No. 211236

Seq. ID LIB3145-020-Q1-K1-C3

Method BLASTX
NCBI GI g4325282
BLAST score 446
E value 2.0e-44
Match length 124
% identity 72

NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

>gi\_4325286\_gb\_AAD17314\_ (AF123311) NAC domain protein NAM

٠,

[Arabidopsis thaliana]

Seq. No. 211237

Seq. ID LIB3145-020-Q1-K1-C4

Method BLASTX
NCBI GI g4105798
BLAST score 235
E value 1.0e-19
Match length 55
% identity 75

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 211238

Seq. ID LIB3145-020-Q1-K1-C9

Method BLASTX
NCBI GI g115492
BLAST score 436
E value 1.0e-43
Match length 86
% identity 50

NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)

calmodulin-related protein [Petunia hybrida]

Seq. No. 211239

Seq. ID LIB3145-020-Q1-K1-D2

Method BLASTX
NCBI GI g3746069
BLAST score 150
E value 9.0e-10
Match length 96
% identity 34

NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis

thaliana]

NCBI Description

domestica]



```
211240
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-D4
Method
                  BLASTN
NCBI GI
                  q3821780
                  34
BLAST score
                  7.0e-10
E value
                  48
Match length
                  48
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  211241
Seq. No.
                  LIB3145-020-Q1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g130172
                  649
BLAST score
                  3.0e-68
E value
                  141
Match length
                  87
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH
NCBI Description
                  PHOSPHORYLASE L) >gi_168276 (M64362) starch phosphorylase
                  [Ipomoea batatas]
                  211242
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-D6
                  BLASTX
Method
                  g515377
NCBI GI
                  388
BLAST score
                  1.0e-37
E value
                  82
Match length
                  95
% identity
                  (X79715) histone H4 [Lolium temulentum]
NCBI Description
                  211243
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-E12
                  BLASTX
Method
NCBI GI
                   g1351365
BLAST score
                   188
                   3.0e-14
E value
                   56
Match length
                   64
% identity
                   UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN
NCBI Description
                   (CR6) >gi_2130002_pir__S68969 ubiquinol--cytochrome-c
                   reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768
                   (X82325) cytochrome c reductase subunit [Solanum tuberosum]
                   211244
Seq. No.
Seq. ID
                   LIB3145-020-Q1-K1-E3
                   BLASTX
Method
                   q4138179
NCBI GI
BLAST score
                   664
                   6.0e-70
E value
Match length
                   137
                   92
% identity
```

(AJ223969) elongation factor 1 alpha subunit [Malus

```
211245
Seq. No.
                  LIB3145-020-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  q2129630
NCBI GI
BLAST score
                  406
                  1.0e-39
E value
Match length
                  105
                   66
% identity
                  lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721)
                  unknown [Arabidopsis thaliana]
                  211246
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-E6
Method
                  BLASTX
                  g4454457
NCBI GI
                   479
BLAST score
                   3.0e-48
E value
Match length
                   116
                   80
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   211247
Seq. No.
Seq. ID
                   LIB3145-020-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   q3367531
BLAST score
                   138
                   1.0e-08
E value
                   74
Match length
                   38
% identity
                   (AC004392) Strong similarity to gi_2160138 F19K23.6 gene
NCBI Description
                   product from A. thaliana BAC gb_ACO00375. [Arabidopsis
                   thaliana]
                   211248
Seq. No.
Seq. ID
                   LIB3145-020-Q1-K1-F1
                   BLASTN
Method
                   g599722
NCBI GI
BLAST score
                   32
                   8.0e-09
E value
```

Match length 72 % identity 86

C.melo mRNA for aconitase (UNI-ZAPxR) NCBI Description

>qi 2300160 emb A45787.1 A45787 Sequence 25 from Patent

WO9520046

Seq. No. 211249

LIB3145-020-Q1-K1-F12 Seq. ID

BLASTX Method NCBI GI g267082 BLAST score 633 3.0e-66 E value 122 Match length % identity 96

TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8 NCBI Description

chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

NCBI Description



```
211250
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q1370276
BLAST score
                  435
E value
                  4.0e-43
                  135
Match length
                  59
% identity
                  (X96428) MADS-box protein [Nicotiana tabacum]
NCBI Description
                  211251
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q4490292
BLAST score
                  581
                  3.0e-60
E value
                  126
Match length
                  89
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                  211252
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-F5
                  BLASTX
Method
NCBI GI
                  g2144271
BLAST score
                  253
                  9.0e-22
E value
                  54
Match length
                  91
% identity
                  trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus
NCBI Description
                  kitakamiensis (fragment) >gi 1777372 dbj BAA11578 (D82814)
                  cinnamic acid 4-hydroxylase [Populus kitakamiensis]
                   211253
Seq. No.
Seq. ID
                   LIB3145-020-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   g1856971
BLAST score
                   221
                   2.0e-25
E value
Match length
                   79
% identity
                   85
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                  periwinkle cells. [Catharanthus roseus]
Seq. No.
                   211254
                  LIB3145-020-Q1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g231574
BLAST score
                   387
E value
                   2.0e-37
Match length
                   116
% identity
                   68
```

29270

asparaginase [Lupinus arboreus]

L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi\_81837\_pir\_\_S22523 asparaginase (EC 3.5.1.1) - tree
lupine (fragment) >gi\_19137\_emb\_CAA36824\_ (X52588)



```
Seq. No.
                  211255
Seq. ID
                  LIB3145-020-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1524383
BLAST score
                  237
                  2.0e-25
E value
Match length
                  92
% identity
                  70
NCBI Description
                  (X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea
                  mays]
                  211256
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  q285286
BLAST score
                  389
E value
                  1.0e-37
Match length
                  135
% identity
                  56
                  flavonol 4'-sulfotransferase - Flaveria chloraefolia
NCBI Description
                  211257
Seq. No.
Seq. ID
                  LIB3145-020-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3738322
BLAST score
                  377
                  2.0e-36
E value
Match length
                  78
% identity
                  94
NCBI Description
                  (AC005170) putative small nuclear ribonucleoprotein
                  [Arabidopsis thaliana]
Seq. No.
                  211258
Seq. ID
                  LIB3145-020-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g4574320
BLAST score
                  156
                  2.0e-10
E value
Match length
                  54
% identity
                  59
NCBI Description
                  (AF117224) wound-induced protein WI12 [Mesembryanthemum
                  crystallinum]
Seq. No.
                  211259
Seq. ID
                  LIB3145-020-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g544250
BLAST score
                  183
E value
                  1.0e-13
Match length
                  66
                  55
% identity
                  ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)
NCBI Description
```

29271

receptor Erd2 - Arabidopsis thaliana

211260

Seq. No.

>gi\_541860\_pir A49677 endoplasmic reticulum retention



```
LIB3145-020-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3043907
BLAST score
                  233
                  1.0e-19
E value
                  73
Match length
                  63
% identity
NCBI Description
                  (AF022019) IAA8 [Lycopersicon esculentum]
Seq. No.
                  211261
                  LIB3145-021-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559334
BLAST score
                  367
                  3.0e-35
E value
Match length
                  125
% identity
                  48
NCBI Description
                 (AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.
                  211262
Seq. ID
                  LIB3145-021-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3549671
BLAST score
                  216
                  2.0e-17
E value
Match length
                  72
% identity
                  60
NCBI Description
                  (AL031394) hypothetical protein [Arabidopsis thaliana]
                  211263
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4151068
                  583
BLAST score
                  2.0e-60
E value
                  123
Match length
                  89
% identity
NCBI Description (Y10862) ribonucleotide reductase [Nicotiana tabacum]
                  211264
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3915037
BLAST score
                  647
E value
                  6.0e-68
Match length
                  136
                  91
% identity
NCBI Description
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                  >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose
                  synthase [Pisum sativum]
Seq. No.
                  211265
                  LIB3145-021-Q1-K1-A9
Seq. ID
```

Method BLASTX NCBI GI g4006878 BLAST score 373 E value 8.0e-36



Match length 49 % identity

NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

211266 Seq. No.

Seq. ID LIB3145-021-Q1-K1-B11

Method BLASTX NCBI GI q1346172 BLAST score 330 6.0e-31 E value Match length 67 91 % identity

78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) NCBI Description

(IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)

>gi\_170384 (L08830) glucose-regulated protein 78

[Lycopersicon esculentum]

211267 Seq. No.

LIB3145-021-Q1-K1-B2 Seq. ID

Method BLASTX NCBI GI g3033386 BLAST score 424 8.0e-42 E value 139 Match length 57 % identity

NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]

211268 Seq. No.

Seq. ID LIB3145-021-Q1-K1-B7

Method BLASTX NCBI GI q1346172 BLAST score 319 2.0e-29 E value Match length 67

88 % identity

NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)

(IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)

>gi 170384 (L08830) glucose-regulated protein 78

[Lycopersicon esculentum]

Seq. No. 211269

LIB3145-021-Q1-K1-B8 Seq. ID

Method BLASTX NCBI GI q2980777 BLAST score 407 8.0e-40 E value Match length 121 72 % identity

(AL022198) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 211270

LIB3145-021-Q1-K1-C10 Seq. ID

Method BLASTX NCBI GI g3600033 BLAST score 557 2.0e-57 E value Match length 138



```
% identity
                  (AF080119) contains similarity to the N terminal domain of
NCBI Description
                  the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis
                  thaliana]
                  211271
Seq. No.
                  LIB3145-021-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  q349379
NCBI GI
BLAST score
                  269
                  1.0e-23
E value
Match length
                  91
                  70
% identity
                 (L22847) HAHB-1 [Helianthus annuus]
NCBI Description
Seq. No.
                  211272
Seq. ID
                  LIB3145-021-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1263291
BLAST score
                  520
                  5.0e-53
E value
Match length
                  112
% identity
                  85
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
                  211273
Seq. No.
                  LIB3145-021-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  g1168410
NCBI GI
                  590
BLAST score
                  3.0e-61
E value
Match length
                  139
% identity
                  83
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                  >gi 2118267_pir__S58167 fructose-bisphosphate aldolase (EC
                   4.1.2.13) - garden pea >gi 927505 emb CAA61947_ (X89829)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  211274
Seq. No.
                  LIB3145-021-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g598073
NCBI GI
BLAST score
                  404
                  1.0e-39
E value
                  115
Match length
                  73
% identity
NCBI Description (L36806) GT-1 [Arabidopsis thaliana]
                  211275
Seq. No.
                  LIB3145-021-Q1-K1-D1
Seq. ID
                  BLASTX
Method
                  g1169128
NCBI GI
BLAST score
                   672
```

NCBI Description SERINE/THREONINE-PROTEIN KINASE CTR1 >gi\_166680 (L08789)

7.0e-71

140

94

E value

Match length

% identity



```
protein kinase [Arabidopsis thaliana] >gi_166682 (L08790)
                  protein kinase [Arabidopsis thaliana]
                  211276
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-D11
                  BLASTX
Method
                  g2760326
NCBI GI
                  438
BLAST score
                  2.0e-43
E value
                  143
Match length
                  57
% identity
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                  211277
Seq. No.
                  LIB3145-021-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g3925363
NCBI GI
                  597
BLAST score
                  4.0e-62
E value
                  133
Match length
                  84
% identity
                  (AF067961) homeodomain protein [Malus domestica]
NCBI Description
                  211278
Seq. No.
                  LIB3145-021-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q322577
                  670
BLAST score
                  1.0e-70
E value
                  139
Match length
                  94
% identity
NCBI Description Raf protein kinase homolog CTR1 - Arabidopsis thaliana
                  211279
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3249109
BLAST score
                  468
                  6.0e-47
E value
                  140
Match length
                  63
% identity
                  (AC003114) Contains similarity to pre-mRNA splicing factor
NCBI Description
                   (SF2), P33 subunit gb M72709 from Homo sapiens. ESTs
                   gb_T42588 and gb_R65514 come from this gene. [Arabidopsis
                   thaliana]
                  211280
```

Seq. ID LIB3145-021-Q1-K1-D5

BLASTX Method g4098129 NCBI GI BLAST score 738 E value 1.0e-78 136 Match length 99 % identity

(U73588) sucrose synthase [Gossypium hirsutum] NCBI Description

Seq. No. 211281



```
LIB3145-021-Q1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2661840
BLAST score
                  481
                  2.0e-48
E value
                  139
Match length
                  65
% identity
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                  211282
Seq. No.
                  LIB3145-021-Q1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g167367
                  528
BLAST score
                  5.0e-54
E value
Match length
                  130
% identity
                  81
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  211283
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-E1
Method
                  BLASTX
                  g4454452
NCBI GI
                  503
BLAST score
                   4.0e-51
E value
Match length
                  133
                  75
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211284
Seq. No.
                  LIB3145-021-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                   g3402711
NCBI GI
BLAST score
                   201
                   1.0e-15
E value
                   88
Match length
                   28
% identity
                  (AC004261) putative RNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   211285
Seq. No.
                  LIB3145-021-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   g1658193
NCBI GI
BLAST score
                   642
                   2.0e-67
E value
Match length
                   130
                   89
% identity
                  (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                   211286
Seq. ID
                   LIB3145-021-Q1-K1-E3
```

Method BLASTX NCBI GI q4467157 BLAST score 281

E value 5.0e-25



Match length 115 % identity 52 NCBI Description (AL

NCBI Description (AL035540) disease resistance response like protein

[Arabidopsis thaliana]

Seq. No. 211287

Seq. ID LIB3145-021-Q1-K1-E4

Method BLASTX
NCBI GI g2760320
BLAST score 322
E value 7.0e-30
Match length 109
% identity 61

NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No. 211288

Seq. ID LIB3145-021-Q1-K1-E5

Method BLASTX
NCBI GI g4455359
BLAST score 553
E value 5.0e-57
Match length 127
% identity 87

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 211289

Seq. ID LIB3145-021-Q1-K1-E6

Method BLASTX
NCBI GI g1052956
BLAST score 347
E value 8.0e-33
Match length 107
% identity 65

NCBI Description (U39747) high mobility group protein 2 HMG2 [Ipomoea nil]

Seq. No. 211290

Seq. ID LIB3145-021-Q1-K1-E7

Method BLASTN
NCBI GI g2264314
BLAST score 34
E value 1.0e-09
Match length 134
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQK4, complete sequence [Arabidopsis thaliana]

Seq. No. 211291

Seq. ID LIB3145-021-Q1-K1-E8

Method BLASTX
NCBI GI g3860274
BLAST score 209
E value 1.0e-16
Match length 53
% identity 72

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

>gi 4314397 gb AAD15607 (AC006232) putative zinc finger

protein [Arabidopsis thaliana]



```
211292
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1321627
BLAST score
                  670
                  1.0e-70
E value
Match length
                  136
                  90
% identity
                  (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
NCBI Description
                  sp.]
                  211293
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1495251
BLAST score
                  526
                  9.0e-54
E value
Match length
                  143
                  73
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211294
Seq. ID
                  LIB3145-021-Q1-K1-F11
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  33
E value
                  6.0e-09
Match length
                  33
                  58
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  211295
Seq. ID
                  LIB3145-021-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3202024
BLAST score
                  251
                  2.0e-21
E value
                  60
Match length
                  80
% identity
                  (AF069315) thylakoid-bound L-ascorbate peroxidase precursor
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                  211296
Seq. ID
                  LIB3145-021-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q927025
BLAST score
                  320
                  1.0e-29
E value
Match length
                  132
% identity
                  41
NCBI Description
                  (L44134) SPF1-like DNA-binding protein [Cucumis sativus]
```

Seq. ID LIB3145-021-Q1-K1-F8

Method BLASTX NCBI GI g3925363



BLAST score 609 E value 2.0e-63 Match length 137 % identity 84

NCBI Description (AF067961) homeodomain protein [Malus domestica]

Seq. No.

Seq. ID LIB3145-021-Q1-K1-G1

211298

Method BLASTX
NCBI GI g3785983
BLAST score 207
E value 1.0e-20
Match length 91
% identity 57

NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No. 211299

Seq. ID LIB3145-021-Q1-K1-G10

Method BLASTX
NCBI GI g4510377
BLAST score 457
E value 1.0e-45
Match length 142
% identity 65

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 211300

Seq. ID LIB3145-021-Q1-K1-G2

Method BLASTX
NCBI GI g3851636
BLAST score 130
E value 3.0e-17
Match length 102
% identity 56

NCBI Description (AF098519) unknown [Avicennia marina] >gi\_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 211301

Seq. ID LIB3145-021-Q1-K1-G4

Method BLASTX
NCBI GI g3885339
BLAST score 186
E value 6.0e-14
Match length 119
% identity 40

NCBI Description (AC005623) putative bzip protein [Arabidopsis thaliana]

Seq. No. 211302

Seq. ID LIB3145-021-Q1-K1-G5

Method BLASTX
NCBI GI g3785983
BLAST score 227
E value 9.0e-24
Match length 100
% identity 59

NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]



```
211303
Seq. No.
Seq. ID
                  LIB3145-021-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g225267
BLAST score
                  477
E value
                  5.0e-48
                  113
Match length
                  77
% identity
NCBI Description ORF 1244 [Nicotiana tabacum]
Seq. No.
                  211304
                  LIB3145-021-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3450889
                  443
BLAST score
                  5.0e-44
E value
                  136
Match length
                  66
% identity
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211305
                  LIB3145-021-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  q3413424
NCBI GI
BLAST score
                  404
                  2.0e-39
E value
                  130
Match length
                  62
% identity
                  (AJ006309) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211306
                  LIB3145-021-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2194093
BLAST score
                  629
E value
                  8.0e-66
Match length
                  134
                  87
% identity
                  Chain A, Stearoyl-Acyl Carrier Protein Desaturase From
NCBI Description
                  Castor Seeds >gi_2194094_pdb_1AFR_B Chain B, Stearoyl-Acyl
                  Carrier Protein Desaturase From Castor Seeds
                  >gi 2194095 pdb_1AFR C Chain C, Stearoyl-Acyl Carrier
                  Protein Desaturase From Castor Seeds >gi 2194096 pdb_1AFR_D
                  Chain D, Stearoyl-Acyl Carrier Protein Desaturase From
                  Castor Seeds >gi_2194097_pdb_1AFR_E Chain E, Stearoyl-Acyl
                  Carrier Protein Desaturase From Castor Seeds
                  >gi 2194098 pdb 1AFR F Chain F, Stearoyl-Acyl Carrier
                  Protein Desaturase From Castor Seeds
Seq. No.
                  211307
Seq. ID
                  LIB3145-021-Q1-K1-H11
Method
                  BLASTX
```

NCBI GI g2252836 BLAST score 364 7.0e-35 E value Match length 115 % identity 60



```
NCBI Description

(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]

Seq. No.

Seq. ID

LIB3145-021-Q1-K1-H12

Method

NCBI GI

Q1709006
```

BLAST score 226
E value 1.0e-18
Match length 67
% identity 66

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi\_726032 (U17241) S-adenosylmethionine synthetase [Actinidia

chinensis]

Seq. No. 211309

Seq. ID LIB3145-021-Q1-K1-H6

Method BLASTX
NCBI GI g2252866
BLAST score 221
E value 5.0e-18
Match length 64
% identity 66

NCBI Description (AF013294) contains region of similarity to SYT

[Arabidopsis thaliana]

Seq. No. 211310

Seq. ID LIB3145-022-Q1-K1-A1

Method BLASTX
NCBI GI g81857
BLAST score 216
E value 2.0e-17
Match length 42
% identity 93

NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa

(fragment) >gi 19658 emb CAA45349 (X63872) translationally

controlled tumor protein [Medicago sativa]

Seq. No. 211311

Seq. ID LIB3145-022-Q1-K1-A11

Method BLASTX
NCBI GI g1694976
BLAST score 343
E value 3.0e-32
Match length 74
% identity 85

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. 211312

Seg. ID LIB3145-022-Q1-K1-A4

Method BLASTX
NCBI GI g1220196
BLAST score 556
E value 3.0e-57



Match length 88 % identity

(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum] NCBI Description

Seq. No.

211313

Seq. ID

LIB3145-022-Q1-K1-A5

Method

BLASTN g3821780

NCBI GI

BLAST score

36

E value Match length 9.0e-11 37 61

% identity NCBI Description

Xenopus laevis cDNA clone 27A6-1

Seq. No.

211314

Seq. ID

LIB3145-022-Q1-K1-B11

Method NCBI GI BLASTX g1488255

BLAST score

531 3.0e-54

E value Match length % identity

156 57

NCBI Description

(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]

>gi\_2961381\_emb\_CAA18128\_ (AL022141) ferulate-5-hydroxylase

(FAH1) [Arabidopsis thaliana] >gi\_3925365 (AF068574)

ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No.

211315

58

Seq. ID

LIB3145-022-Q1-K1-B4

 ${\tt BLASTX}$ Method NCBI GI g3913185 BLAST score 405 1.0e-39 E value 130

Match length % identity

CINNAMYL ALCOHOL DEHYDROGENASE (CAD) >qi 2984653 (AF038561) NCBI Description cinnamyl alcohol dehydrogenase; CAD [Eucalyptus globulus]

211316 Seq. No.

Seq. ID LIB3145-022-Q1-K1-B7

BLASTX Method NCBI GI g4102861 BLAST score 411 3.0e-40 E value Match length 80 93 % identity

(AF016893) copper/zinc-superoxide dismutase [Populus NCBI Description

tremuloides]

Seq. No.

211317

Seq. ID

LIB3145-022-Q1-K1-B9

Method BLASTX NCBI GI q1946359 BLAST score 371 E value 1.0e-35 Match length 119 % identity 59

NCBI Description



```
(U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211318
Seq. No.
Seq. ID
                  LIB3145-022-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  g231509
BLAST score
                  564
                  4.0e-58
E value
                  133
Match length
                  77
% identity
                  ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809_pir__S30935
NCBI Description
                  actin-depolymerizing factor - trumpet lily
                  >gi 22748 emb CAA78483 (Z14110) actin depolymerizing
                  factor [Lilium longiflorum]
                  211319
Seq. No.
Seq. ID
                  LIB3145-022-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2833386
BLAST score
                  564
E value
                  3.0e-58
Match length
                  133
                  86
% identity
                  RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR
NCBI Description
                   (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E)
                  >gi 2129493 pir S62724 ribulose-phosphate 3-epimerase (EC
                   5.1.3.1) precursor - spinach >gi 1162980 (L42328)
                  ribulose-5-phosphate 3-epimerase [Spinacia oleracea]
                   >gi 3264788 (AF070941) ribulose-phosphate 3-epimerase
                   [Spinacia oleracea] >gi_1587969_prf__2207382A
                  D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]
                  211320
Seq. No.
                  LIB3145-022-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3641837
BLAST score
                   400
                   5.0e-39
E value
Match length
                   111
% identity
                   74
NCBI Description
                  (AL023094) Nonclathrin coat protein gamma - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   211321
                   LIB3145-022-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464707
BLAST score
                   303
                   1.0e-27
E value
Match length
                   96
                   67
% identity
```

40S RIBOSOMAL PROTEIN S18 >gi\_480908\_pir\_\_S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein



[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

211322 Seq. No. Seq. ID LIB3145-022-Q1-K1-D12 Method BLASTX NCBI GI g1055161 BLAST score 152 8.0e-10 E value Match length 112 35 % identity

NCBI Description (U40029) similar to human 100 kDa coactivator (U22055)

[Caenorhabditis elegans]

 Seq. No.
 211323

 Seq. ID
 LIB3145-022-Q1-K1-D2

 Method
 BLASTN

 NCBI GI
 g3869069

 BLAST score
 44

BLAST score 44
E value 2.0e-15
Match length 128
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 211324

Seq. ID LIB3145-022-Q1-K1-D3

Method BLASTX
NCBI GI g4467146
BLAST score 480
E value 2.0e-48
Match length 127
% identity 68

NCBI Description (AL035540) galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 211325

Seq. ID LIB3145-022-Q1-K1-D4

Method BLASTN
NCBI GI g3869069
BLAST score 33
E value 6.0e-09
Match length 190
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 211326

Seq. ID LIB3145-022-Q1-K1-D6

Method BLASTX

```
NCBI GI
                   q3850816
BLAST score
                  436
                  3.0e-43
E value
Match length
                  89
                  87
% identity
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                  sativa]
Seq. No.
                  211327
Seq. ID
                  LIB3145-022-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2462756
BLAST score
                  331
                  7.0e-37
E value
Match length
                  127
                  67
% identity
                  (AC002292) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                  211328
Seq. No.
Seq. ID
                  LIB3145-022-Q1-K1-E1
Method
                  BLASTN
NCBI GI
                  g2656030
BLAST score
                  33
                  6.0e-09
E value
Match length
                  215
                  82
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUL8
Seq. No.
                  211329
Seq. ID
                  LIB3145-022-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4191789
BLAST score
                  270
                  2.0e-27
E value
Match length
                  122
% identity
                  59
                   (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  211330
Seq. ID
                  LIB3145-022-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g625990
BLAST score
                  342
                  3.0e-32
E value
Match length
                  129
                  50
% identity
NCBI Description porin, plastid - garden pea
Seq. No.
                  211331
Seq. ID
                  LIB3145-022-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2281093
BLAST score
                  228
```

29285

5.0e-19

76

E value Match length

```
% identity
                  (AC002333) beta transducin isolog [Arabidopsis thaliana]
NCBI Description
                  211332
Seq. No.
Seq. ID
                  LIB3145-022-Q1-K1-E7
Method
                  BLASTX
                  g2191175
NCBI GI
                  195
BLAST score
                  6.0e-15
E value
Match length
                  48
                  77
% identity
                  (AF007270) A IG002P16.24 gene product [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  211333
                  LIB3145-022-Q1-K1-E8
Seq. ID
Method
                  BLASTX
                  g2146731
NCBI GI
BLAST score
                  243
                  8.0e-21
E value
                  79
Match length
% identity
                  31
                  FK506-binding protein - Arabidopsis thaliana >gi_1354207
NCBI Description
                  (U49453) rof1 [Arabidopsis thaliana]
                  211334
Seq. No.
                  LIB3145-022-Q1-K1-E9
Seq. ID
Method
                  BLASTN
                  g623524
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
Match length
                  186
% identity
                  82
NCBI Description Pisolithus tinctorius (F00015) mRNA, EST0145
                  211335
Seq. No.
Seq. ID
                  LIB3145-022-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  613
                  6.0e-64
E value
Match length
                  140
                  82
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. ID LIB3145-022-Q1-K1-F12

Method BLASTX
NCBI GI g3757523
BLAST score 472
E value 3.0e-48
Match length 122
% identity 79

NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]

Seq. No. 211337

Seq. ID LIB3145-022-Q1-K1-F2

```
BLASTX
Method
                   q3548815
NCBI GI
BLAST score
                   273
                   4.0e-24
E value
                   62
Match length
                   85
% identity
                   (AC005313) similar to axoneme-associated protein mst101
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   211338
                  LIB3145-022-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                   q2505872
```

NCBI GI 272 BLAST score 5.0e-24 E value 140 Match length 48

% identity

(Y12227) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 211339 Seq. ID LIB3145-022-Q1-K1-F6 BLASTX Method NCBI GI q2661840 BLAST score 382

5.0e-37 E value Match length 116 % identity 60

(Y15430) adenosine kinase [Physcomitrella patens] NCBI Description

Seq. No. 211340

Seq. ID LIB3145-022-Q1-K1-G1

Method BLASTN g2760168 NCBI GI 50 BLAST score 4.0e-19 E value Match length 148 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 211341

Seq. ID LIB3145-022-Q1-K1-G2

Method BLASTN NCBI GI q531832 BLAST score 39 1.0e-12 E value Match length 91 86 % identity

NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 211342

LIB3145-022-Q1-K1-G4 Seq. ID

Method BLASTX NCBI GI g4337175 439 BLAST score 1.0e-43 E value Match length 142



```
% identity
                    (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                    gb_T04111, gb_R841\overline{8}0, gb_R654\overline{2}8, gb_T444\overline{3}9, gb_T76570,
                    gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and
                    gb_AA720210 come from this gene. [Arabidopsis thaliana]
 Seq. No.
                    211343
                   LIB3145-022-Q1-K1-G6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    q3482971
 BLAST score
                    346
 E value
                    1.0e-32
                    73
 Match length
                    79
 % identity
                   (AL031369) putative protein [Arabidopsis thaliana]
 NCBI Description
                    211344
 Seq. No.
                    LIB3145-022-Q1-K1-G9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2160166
 BLAST score
                    362
                    2.0e-34
 E value
 Match length
                    140
 % identity
                    51
                   (AC000132) No definition line found [Arabidopsis thaliana]
 NCBI Description
                    211345
 Seq. No.
                    LIB3145-022-Q1-K1-H1
 Seq. ID
 Method
                    BLASTX
                    g2832643
 NCBI GI
 BLAST score
                    195
                    1.0e-15
 E value
 Match length
                    54
                    72
 % identity
                   (AL021710) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    211346
 Seq. No.
                    LIB3145-022-Q1-K1-H2
 Seq. ID
                    BLASTX
 Method
                    g1345642
 NCBI GI
                    223
 BLAST score
                    2.0e-18
 E value
                    49
 Match length
                    80
 % identity
                    FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450
 NCBI Description
                    75A1) (CYPLXXVA1) >gi_629710_pir__S38985 flavonoid
                    3',5'-hydroxylase Hf1 - garden petunia
                    >gi_311656_emb_CAA80266_ (Z22545) flavonoid
                    3',5'-hydroxylase [Petunia x hybrida]
                    >qi 1853972 dbj BAA03438 (D14588)
                    flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi_3426337
                    (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida]
                    >qi 738772 prf 2001426B flavonoid 3',5'-hydroxylase
                    [Petunia x hybrida]
```

Seq. ID LIB3145-022-Q1-K1-H5

211347

Seq. No.

```
BLASTX
Method
                  g3435196
NCBI GI
BLAST score
                  615
                  3.0e-64
E value
                  136
Match length
                  81
% identity
                  (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  211348
Seq. No.
                  LIB3145-022-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  q2245020
NCBI GI
BLAST score
                  257
                  3.0e-22
E value
                  128
Match length
                  45
% identity
                  (Z97341) growth regulator homolog [Arabidopsis thaliana]
NCBI Description
                  211349
Seq. No.
Seq. ID
                  LIB3145-023-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g2144271
                  640
BLAST score
                  4.0e-67
E value
                  135
Match length
                  90
% identity
                  trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus
NCBI Description
                  kitakamiensis (fragment) >gi_1777372_dbj_BAA11578_ (D82814)
                  cinnamic acid 4-hydroxylase [Populus kitakamiensis]
                  211350
Seq. No.
Seq. ID
                  LIB3145-023-Q1-K1-A8
                  BLASTX
Method
NCBI GI
                  g3928142
BLAST score
                   693
                  2.0e-73
E value
                  140
Match length
                  20
% identity
                  (AJ131045) protein phosphatase [Cicer arietinum]
NCBI Description
                  211351
Seq. No.
Seq. ID
                  LIB3145-023-Q1-K1-B10
                  BLASTX
Method
                   g2791896
NCBI GI
BLAST score
                   635
                   1.0e-66
E value
                  136
Match length
% identity
                   93
                  (Y08997) 146kDa nuclear protein [Xenopus laevis]
NCBI Description
                   211352
Seq. No.
```

Seq. ID LIB3145-023-Q1-K1-B12 Method BLASTX NCBI GI g132944

NCBI GI g132944
BLAST score 606
E value 4.0e-63
Match length 118



```
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >qi 806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
                  211353
Seq. No.
Seq. ID
                  LIB3145-023-Q1-K1-B4
                  BLASTX
Method
                  g1703089
NCBI GI
                  258
BLAST score
                  2.0e-22
E value
                  94
Match length
                  48
% identity
```

NCBI Description

ACYLAMINO-ACID-RELEASING ENZYME (ACYL-PEPTIDE HYDROLASE)

(APH) (ACYLAMINOACYL-PEPTIDASE) (DNF15S2 PROTEIN) >gi 2118063 pir JC4655 acylaminoacyl-peptidase (EC 3.4.19.1) - human >gi\_556514\_dbj\_BAA07476\_ (D38441) acylamino acid-releasing enzyme [Homo sapiens]

211354 Seq. No. LIB3145-023-Q1-K1-B5 Seq. ID Method BLASTX NCBI GI q2117725 719 BLAST score 2.0e-76 E value

145 Match length % identity 87

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform NCBI Description

SBE2.2 precursor - Arabidopsis thaliana (fragment) >gi 726490 (U22428) starch branching enzyme class II

[Arabidopsis thaliana]

Seq. No. 211355

LIB3145-023-Q1-K1-B7 Seq. ID

Method BLASTX g1174599 NCBI GI BLAST score 758 6.0e-81 E value 146 Match length 98 % identity

TUBULIN BETA-2 CHAIN >gi\_1076659\_pir\_\_S50748 beta-tubulin -NCBI Description

potato >gi 609270\_emb CAA83853\_ (Z33402) beta-tubulin

[Solanum tuberosum]

211356 Seq. No.

LIB3145-023-Q1-K1-B9 Seq. ID

BLASTX Method NCBI GI q3287683 317 BLAST score 3.0e-29 E value 121 Match length 19 % identity

(AC003979) Similar to apoptosis protein MA-3 gb D50465 from NCBI Description

Mus musculus. [Arabidopsis thaliana]

211357 Seq. No.

LIB3145-023-Q1-K1-C1 Seq. ID



Method BLASTX
NCBI GI g100069
BLAST score 181
E value 2.0e-13
Match length 97
% identity 41

NCBI Description cysteine proteinase tpp (EC 3.4.22.-) - garden pea

>gi\_3980198\_emb\_CAA46863\_ (X66061) thiolprotease [Pisum

sativum]

Seq. No. 211358

Seq. ID LIB3145-023-Q1-K1-C10

Method BLASTX
NCBI GI g1352681
BLAST score 340
E value 6.0e-32
Match length 115
% identity 60

NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi 1076391 pir\_\_S55457

phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis

thaliana >gi\_633028\_dbj\_BAA07287\_ (D38109) protein

phosphatase 2C [Arabidopsis thaliana]

Seq. No. 211359

Seq. ID LIB3145-023-Q1-K1-C2

Method BLASTX
NCBI GI g729506
BLAST score 597
E value 4.0e-62
Match length 131
% identity 83

NCBI Description NARINGENIN, 2-OXOGLUTARATE 3-DIOXYGENASE

(FLAVONONE-3-HYDROXYLASE) (FHT) >gi\_481216\_pir\_\_S38338

naringenin 3-dioxygenase - common stock

>gi 288107 emb CAA51192 (X72594) naringenin,2-oxoglutarate

3-dioxygenase [Matthiola incana]

Seq. No. 211360

Seq. ID LIB3145-023-Q1-K1-C3

Method BLASTX
NCBI GI g3913416
BLAST score 470
E value 3.0e-47
Match length 124
% identity 73

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi\_2129920\_pir\_\_S68990 adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle

>gi\_758695 (U12573) S-adenosyl-L-methionine decarboxylase
proenzyme [Catharanthus roseus] >gi\_1094441\_prf\_\_2106177A

Met(S-adenosyl) decarboxylase [Catharanthus roseus]

Seq. No. 211361

Seq. ID LIB3145-023-Q1-K1-C6

Method BLASTN NCBI GI g439653 BLAST score 59



E value 3.0e-25 Match length 59 % identity 100

NCBI Description G.hirsutum mRNA for ribosomal protein 16, small subunit

Seq. No.

211362

Seq. ID

LIB3145-023-Q1-K1-D1

Method NCBI GI BLAST score BLASTX g3915165 249 1.0e-21

E value Match length

58

% identity
NCBI Description

86

NCBI Description

TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi\_2792520 (AF042320) tryptophan synthase beta subunit [Camptotheca acuminata] >gi\_2801771 (AF042321) tryptophan synthase beta

[Camptotheca acuminata]

Seq. No.

211363

Seq. ID

LIB3145-023-Q1-K1-D10

Method BLASTX
NCBI GI g417103
BLAST score 623
E value 4.0e-65
Match length 124
% identity 100

NCBI Description

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]
>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa]

rabacum; >g1\_5665690 (AF093655) Histone H3 [Oryza sativa]
>gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 211364

Seq. ID LIB3145-023-Q1-K1-D12

Method BLASTX
NCBI GI g2911075
BLAST score 407
E value 8.0e-40
Match length 134
% identity 57

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 211365



```
LIB3145-023-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760326
                  166
BLAST score
E value
                  4.0e-12
Match length
                  46
% identity
                  65
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                  211366
Seq. No.
Seq. ID
                  LIB3145-023-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  q2119042
BLAST score
                  275
                  2.0e-24
E value
                  60
Match length
                  87
% identity
                  glycine-rich RNA-binding protein RGP-la - wood tobacco
NCBI Description
                  >gi 469070 dbj BAA03741 (D16204) RNA-binding glycine-rich
                  protein-1 (RGP-1a) [Nicotiana sylvestris]
Seq. No.
                  211367
Seq. ID
                  LIB3145-023-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2760326
BLAST score
                  381
                  9.0e-37
E value
                  117
Match length
                  59
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
Seq. No.
                  211368
Seq. ID
                  LIB3145-023-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3024020
BLAST score
                  662
E value
                  1.0e-69
Match length
                  131
                  95
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
                  211369
Seq. No.
                  LIB3145-023-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220524
BLAST score
                  281
                  5.0e-25
E value
Match length
                  95
% identity
                  61
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
```

Seq. ID LIB3145-023-Q1-K1-E1

Method BLASTX NCBI GI g4006875



```
BLAST score
                  9.0e-18
E value
                  53
Match length
% identity
                  83
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                  211371
Seq. No.
Seq. ID
                  LIB3145-023-Q1-K1-E6
                  BLASTX
Method
                  g2982466
NCBI GI
BLAST score
                  253
                  9.0e-22
E value
                  98
Match length
                   46
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                  211372
Seq. No.
                  LIB3145-023-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                   q2662343
NCBI GI
                   238
BLAST score
E value
                   5.0e-20
Match length
                   47
% identity
                   98
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   211373
Seq. No.
                   LIB3145-023-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   g4115925
NCBI GI
BLAST score
                   597
                   4.0e-62
E value
Match length
                   134
                   49
% identity
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >qi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
                   211374
Seq. No.
Seq. ID
                   LIB3145-023-Q1-K1-F4
                   {\tt BLASTX}
Method
NCBI GI
                   g3023197
BLAST score
                   593
                   1.0e-61
E value
                   139
Match length
                   82
% identity
                   14-3-3-LIKE PROTEIN D (SGF14D) >gi_1575731 (U70536) SGF14D
NCBI Description
                   [Glycine max]
                   211375
Seq. No.
```

Seq. ID LIB3145-023-Q1-K1-F8

Method BLASTX
NCBI GI g1729860
BLAST score 619
E value 1.0e-64
Match length 124



% identity 99 NCBI Description 268

26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1) (LEMA-1) >gi\_1362099\_pir\_\_S56672 probable 26S proteinase chain MA-1 - tomato >gi\_732815\_emb\_CAA52445\_ (X74426) Mg-dependent ATPase 1 [Lycopersicon esculentum]

Seq. No. 211376

Seq. ID LIB3145-023-Q1-K1-G11

Method BLASTX
NCBI GI g1169200
BLAST score 335
E value 2.0e-31
Match length 119
% identity 58

% identity !

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR

>gi\_421829\_pir\_\_S33706 DNA-damage resistance protein Arabidopsis thaliana >gi\_166694 (M98455) [Arabidopsis
thaliana recombination and DNA-damage resistance protein
(DRT111) mRNA, complete cds.], gene product [Arabidopsis

thaliana]

Seq. No. 211377

Seq. ID LIB3145-023-Q1-K1-G2

Method BLASTX
NCBI GI g2982331
BLAST score 470
E value 2.0e-47
Match length 98
% identity 96

NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No. 211378

Seq. ID LIB3145-023-Q1-K1-G3

Method BLASTX
NCBI GI g1498053
BLAST score 496
E value 3.0e-50
Match length 136
% identity 73

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 211379

Seq. ID LIB3145-023-Q1-K1-G4

Method BLASTX
NCBI GI g3420906
BLAST score 270
E value 9.0e-24
Match length 107
% identity 38

NCBI Description (AF080595) zinc finger protein; WRKY1 [Pimpinella

brachycarpa]

Seq. No. 211380

Seq. ID LIB3145-023-Q1-K1-G5

Method BLASTX NCBI GI g1350956



```
BLAST score 492
E value 9.0e-50
Match length 104
% identity 93
NCRI Description 405 RIBO
```

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 211381

Seq. ID LIB3145-023-Q1-K1-G7

Method BLASTX
NCBI GI g2511574
BLAST score 426
E value 4.0e-42
Match length 100
% identity 83

NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis

thaliana] >gi 3421075 (AF043520) 20S proteasome subunit

PAB1 [Arabidopsis thaliana]

Seq. No. 211382

Seq. ID LIB3145-023-Q1-K1-H12

Method BLASTX
NCBI GI g2642446
BLAST score 222
E value 3.0e-18
Match length 122
% identity 45

NCBI Description (AC002391) similar to auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 211383

Seq. ID LIB3145-023-Q1-K1-H2

Method BLASTX
NCBI GI g119150
BLAST score 736
E value 2.0e-78
Match length 139
% identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi\_19273 emb CAA32618\_ (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi\_295810\_emb\_CAA37212\_ (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

Seq. No. 211384

Seq. ID LIB3145-024-Q1-K1-A11

Method BLASTX
NCBI GI g4544404
BLAST score 153
E value 6.0e-10
Match length 64
% identity 52

NCBI Description (AC007047) unknown protein [Arabidopsis thaliana]

Seq. No. 211385

Seq. ID LIB3145-024-Q1-K1-A3

Method BLASTX

```
g2618705
NCBI GI
                  271
BLAST score
                  3.0e-24
E value
                  76
Match length
                  70
% identity
                   (AC002510) putative ABC transporter, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                  211386
Seq. No.
                  LIB3145-024-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g349379
BLAST score
                   466
                   1.0e-46
E value
                   138
Match length
                   74
% identity
NCBI Description (L22847) HAHB-1 [Helianthus annuus]
                   211387
Seq. No.
                   LIB3145-024-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   q3924597
NCBI GI
BLAST score
                   203
E value
                   7.0e-16
                   137
Match length
% identity
                   40
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                   211388
Seq. No.
                   LIB3145-024-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g542157
BLAST score
                   558
                   2.0e-57
E value
Match length
                   126
% identity
                   82
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                   211389
                   LIB3145-024-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g3335375
NCBI GI
                   327
BLAST score
                   1.0e-30
E value
                   98
Match length
                   68
 % identity
                   (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
                   211390
 Seq. No.
                   LIB3145-024-Q1-K1-B7
 Seq. ID
                   BLASTX
 Method
                   g3176874
 NCBI GI
 BLAST score
                   281
                   2.0e-25
 E value
                   83
Match length
                   66
 % identity
 NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis
```



## thaliana]

```
211391
Seq. No.
                  LIB3145-024-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262140
BLAST score
                  192
E value
                  4.0e-15
                  37
Match length
                  89
% identity
NCBI Description (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
Seq. No.
                  211392
                  LIB3145-024-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                   369
E value
                   1.0e-35
                  78
Match length
                  87
% identity
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                   211393
                   LIB3145-024-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                   g1173256
NCBI GI
BLAST score
                   256
                   5.0e-22
E value
                   78
Match length
                   73
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   211394
Seq. No.
                   LIB3145-024-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   q3451075
NCBI GI
                   386
BLAST score
                   2.0e-37
E value
                   118
Match length
                   63
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   211395
Seq. No.
                   LIB3145-024-Q1-K1-D9
Seq. ID
                   BLASTX
Method
                   q1174592
NCBI GI
                   706
BLAST score
                   7.0e-75
E value
                   137
Match length
                   97
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 2119270_pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
```

sativum]

Seq. ID

211401

LIB3145-024-Q1-K1-F11

```
211396
Seq. No.
                  LIB3145-024-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g3152606
NCBI GI
                  303
BLAST score
                  6.0e-28
E value
                  54
Match length
                  91
% identity
                  (AC004482) putative ring zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  211397
Seq. No.
Seq. ID
                  LIB3145-024-Q1-K1-E6
                  BLASTX
Method
                  g4469020
NCBI GI
                  254
BLAST score
                  2.0e-22
E value
                  67
Match length
                  78
% identity
                   (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  211398
Seq. No.
                  LIB3145-024-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  q730450
NCBI GI
BLAST score
                   258
                   6.0e-23
E value
                   60
Match length
                   80
% identity
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
                   >qi 398922 emb CAA80343 (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                   211399
Seq. No.
Seq. ID
                   LIB3145-024-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   g2317910
BLAST score
                   403
                   3.0e-39
E value
                   120
Match length
                   58
% identity
NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]
                   211400
Seq. No.
Seq. ID
                   LIB3145-024-Q1-K1-F1
Method
                   BLASTX
                   q4097547
NCBI GI
BLAST score
                   205
                   2.0e-16
E value
Match length
                   88
                   28
% identity
NCBI Description
                  (U64906) ATFP3 [Arabidopsis thaliana]
```

NCBI GI

BLAST score



```
BLASTX
Method
                   g2384671
NCBI GI
                   323
BLAST score
                   6.0e-30
E value
                   144
Match length
                   54
% identity
                   (AF012657) putative potassium transporter AtKT2p
NCBI Description
                   [Arabidopsis thaliana]
                   211402
Seq. No.
                   LIB3145-024-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g1350720
NCBI GI
                   346
BLAST score
                   4.0e-33
E value
                   77
Match length
                   83
% identity
                   60S RIBOSOMAL PROTEIN L32
NCBI Description
                   211403
Seq. No.
                   LIB3145-024-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   g3334286
NCBI GI
                   238
BLAST score
                   2.0e-20
E value
                   75
Match length
                   68
% identity
                   PHENYLALANINE AMMONIA-LYASE >gi 2631995 emb CAA05251
NCBI Description
                   (AJ002221) phenylalanine ammonia lyase [Digitalis lanata]
                   211404
Seq. No.
Seq. ID
                   LIB3145-024-Q1-K1-F9
                   BLASTX
Method
                   q2351374
NCBI GI
                   242
BLAST score
                   2.0e-26
E value
                   76
Match length
                   76
% identity
                   (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                   [Arabidopsis thaliana]
                   211405
Seq. No.
Seq. ID
                   LIB3145-024-Q1-K1-G12
                   BLASTN
Method
                   q3985931
NCBI GI
BLAST score
                   44
                   2.0e-15
E value
                   100
Match length
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21H1, complete sequence [Arabidopsis thaliana]
                   211406
 Seq. No.
                   LIB3145-024-Q1-K1-G4
 Seq. ID
Method
                   BLASTX
```

29300

g2213600

Match length

% identity

56

64



```
2.0e-15
E value
                   62
Match length
% identity
                   (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   211407
                   LIB3145-024-Q1-K1-G6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g289919
BLAST score
                   90
                   1.0e-43
E value
Match length
                   110
                   95
% identity
                   Gossypium hirsutum chloroplast photosystem II chlorophyll
NCBI Description
                   A/B-binding protein gene, complete cds
                   211408
Seq. No.
                   LIB3145-024-Q1-K1-G8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1762113
BLAST score
                   33
E value
                   6.0e-09
Match length
                   53
                   91
% identity
                   Coccoid stramenopile CCMP1144 nuclear 18S ribosomal RNA
NCBI Description
Seq. No.
                   211409
                   LIB3145-024-Q1-K1-H12
Seq. ID
Method
                   BLASTX
                   g730512
NCBI GI
                   529
BLAST score
E value
                   4.0e-54
                   119
Match length
                   88
% identity
                   RAS-RELATED PROTEIN RIC2 >gi_481506_pir__S38741 GTP-binding
NCBI Description
                   protein ric2 - rice >gi_2182\overline{2}8_dbj_\overline{B}AA0\overline{29}04 (D13758)
                   ras-related GTP binding protein [Oryza sativa]
                   211410
Seq. No.
                   LIB3145-024-Q1-K1-H9
Seq. ID
                   BLASTX
Method
                   g4490323
NCBI GI
BLAST score
                   408
                   5.0e-40
E value
                   127
Match length
% identity
                   64
                   (AJ131464) nitrate transporter [Arabidopsis thaliana]
NCBI Description
                   211411
Seq. No.
Seq. ID
                   LIB3145-025-Q1-K1-A10
                   BLASTX
Method
                   q4490737
NCBI GI
                    185
BLAST score
                    7.0e-14
E value
```



```
(AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                  211412
Seq. No.
                  LIB3145-025-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1694976
BLAST score
                  401
                  4.0e-39
E value
                  115
Match length
                  65
% identity
                   (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                  thaliana]
                  211413
Seq. No.
                  LIB3145-025-Q1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3924596
BLAST score
                   489
                   1.0e-49
E value
Match length
                   109
                   86
% identity
NCBI Description
                   (AF069442) putative phospho-ser/thr phosphatase
                   [Arabidopsis thaliana]
                   211414
Seq. No.
                   LIB3145-025-Q1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4455214
BLAST score
                   542
E value
                   9.0e-56
Match length
                   117
                   88
% identity
                   (AL035440) putative dihydrolipoamide succinyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   211415
                   LIB3145-025-Q1-K1-A7
Seq. ID
Method
                   BLASTX
                   g3402683
NCBI GI
BLAST score
                   140
                   1.0e-08
E value
                   88
Match length
                   45
% identity
                  (AC004697) patatin-like protein [Arabidopsis thaliana]
NCBI Description
```

LIB3145-025-Q1-K1-A8 Seq. ID

w ,

BLASTX Method g3236238 NCBI GI 252 BLAST score 1.0e-21 E value Match length 127 50 % identity

(AC004684) putative ARF1 GTPase activating protein NCBI Description [Arabidopsis thaliana] >gi 4519792\_dbj BAA75744.1\_

(AB017876) Asp1 [Arabidopsis thaliana]

NCBI Description



```
211417
Seq. No.
                  LIB3145-025-Q1-K1-B1
Seq. ID
                  BLASTX
Method
                  g549706
NCBI GI
                  178
BLAST score
                  5.0e-13
E value
                  106
Match length
                  41
% identity
                  KTI12 PROTEIN >gi 539197_pir S37937 KTI12 protein - yeast
NCBI Description
                  (Saccharomyces cerevisiae) >gi 486185 emb CAA81950
                  (Z28110) ORF YKL110c [Saccharomyces cerevisiae]
                  >qi 536816 emb CAA54646 (X77511) KTI12 [Saccharomyces
                  cerevisiae]
                  211418
Seq. No.
                  LIB3145-025-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g2244956
NCBI GI
                  196
BLAST score
                  4.0e-15
E value
Match length
                  116
% identity
                  34
                   (Z97340) strong similarity to pectinesterase [Arabidopsis
NCBI Description
                  thaliana]
                  211419
Seq. No.
                  LIB3145-025-Q1-K1-B12
Seq. ID
                  BLASTN
Method
                  g3236234
NCBI GI
                   44
BLAST score
                   1.0e-15
E value
Match length
                   84
                   88
% identity
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   211420
Seq. No.
                   LIB3145-025-Q1-K1-B2
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
                   7.0e-11
E value
Match length
                   48
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   211421
Seq. ID
                   LIB3145-025-Q1-K1-B3
                   BLASTX
Method
                   q2661179
NCBI GI
BLAST score
                   287
                   7.0e-26
E value
                   111
Match length
% identity
```

(U80984) AtZW10 [Arabidopsis thaliana]

BLAST score



```
211422
Seq. No.
                     LIB3145-025-Q1-K1-B5
   Seq. ID
                     BLASTX
   Method
                     g3822036
   NCBI GI
                      221
   BLAST score
                      4.0e-18
   E value
                     115
   Match length
   % identity
                      46
                     (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
   NCBI Description
   Seq. No.
                      211423
                      LIB3145-025-Q1-K1-B6
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      q3928083
   BLAST score
                      531
                      2.0e-54
   E value
   Match length
                      118
   % identity
                      80
                     (AC005770) unknown protein [Arabidopsis thaliana]
   NCBI Description
                      211424
   Seq. No.
                      LIB3145-025-Q1-K1-B7
   Seq. ID
   Method
                      BLASTX
                      g3702121
   NCBI GI
   BLAST score
                      417
                      4.0e-41
   E value
   Match length
                      121
   % identity
                      74
                      (AJ011681) retinoblastoma-related protein [Chenopodium
   NCBI Description
                      rubrum]
                      211425
   Seq. No.
                      LIB3145-025-Q1-K1-B9
   Seq. ID
                      BLASTN
   Method
                      g3128137
   NCBI GI
                      52
   BLAST score
                      3.0e-20
   E value
                      128
   Match length
                      85
   % identity
                      Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
   NCBI Description
                      K9I9, complete sequence [Arabidopsis thaliana]
                      211426
   Seq. No.
                      LIB3145-025-Q1-K1-C10
   Seq. ID
                      BLASTX
   Method
                      q1931653
   NCBI GI
   BLAST score
                      201
                      9.0e-16
   E value
                      75
   Match length
                      35
   % identity
                     (U95973) unknown protein [Arabidopsis thaliana]
   NCBI Description
   Seq. No.
                      211427
                      LIB3145-025-Q1-K1-C2
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      q3169725
```

```
3.0e-44
```

E value 3.0e-44 Match length 108 % identity 71

NCBI Description (AF007569) succinate dehydrogenase iron-sulfur protein

subunit [Bradyrhizobium japonicum]

Seq. No. 211428

Seq. ID LIB3145-025-Q1-K1-C5

Method BLASTX
NCBI GI g3492803
BLAST score 354
E value 9.0e-34
Match length 106
% identity 58

NCBI Description (AJ002479) ENBP1 [Medicago truncatula]

Seq. No. 211429

Seq. ID LIB3145-025-Q1-K1-C6

Method BLASTN
NCBI GI g2687434
BLAST score 234
E value 1.0e-129
Match length 274
% identity 96

NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 211430

Seq. ID LIB3145-025-Q1-K1-C7

Method BLASTX
NCBI GI g2642158
BLAST score 482
E value 1.0e-48
Match length 128
% identity 73

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 211431

Seq. ID LIB3145-025-Q1-K1-C8

Method BLASTX
NCBI GI g4126401
BLAST score 446
E value 2.0e-44
Match length 109
% identity 81

NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis]

Seq. No. 211432

Seq. ID LIB3145-025-Q1-K1-C9

Method BLASTX
NCBI GI g1916292
BLAST score 151
E value 5.0e-10
Match length 92
% identity 36

NCBI Description (U89793) allergen Amb a VI [Ambrosia artemisiifolia]



47

% identity

NCBI Description

```
Seq. No.
                  211433
                  LIB3145-025-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122265
                  217
BLAST score
                  1.0e-17
E value
Match length
                  56
                   68
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                   (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)
                   (EIF-4F P26 SUBUNIT) >gi_2288883_emb_CAA71580_ (Y10548)
                   eIF4E protein [Arabidopsis thaliana]
                   211434
Seq. No.
                   LIB3145-025-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                   g2760839
NCBI GI
BLAST score
                   306
                   5.0e-28
E value
                   123
Match length
                   52
% identity
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   211435
                   LIB3145-025-Q1-K1-D12
Seq. ID
                   BLASTX
Method
                   q1172633
NCBI GI
                   377
BLAST score
E value
                   2.0e-36
                   83
Match length
                   87
% identity
                   PROLIFERA PROTEIN >gi_675491 (L39954) contains MCM2/3/5
NCBI Description
                   family signature; PROSITE; PS00847; disruption leads to
                   early lethal phenotype; similar to MCM2/3/5 family, most
                   similar to YBR1441 [Arabidopsis thaliana]
                   211436
Seq. No.
                   LIB3145-025-Q1-K1-D4
Seq. ID
Method
                   BLASTX
                   g1732511
NCBI GI
                   291
BLAST score
                   1.0e-26
E value
Match length
                   61
                   90
% identity
                   (U62742) Ran binding protein 1 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   211437
 Seq. No.
                   LIB3145-025-Q1-K1-D5
 Seq. ID
                   BLASTX
Method
                   g4105772
NCBI GI
                   399
 BLAST score
                   4.0e-39
 E value
                   81
Match length
```

(AF049917) PGP9B [Petunia x hybrida]

```
211438
Seq. No.
                  LIB3145-025-Q1-K1-D6
Seq. ID
                  BLASTN
Method
                  g2264304
NCBI GI
                  68
BLAST score
                  7.0e-30
E value
Match length
                  144
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBG8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   211439
                   LIB3145-025-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   q19611
NCBI GI
                   220
BLAST score
                   6.0e-18
E value
Match length
                   62
                   73
% identity
                   (X13675) histone H3 (AA 1-123) [Medicago sativa]
NCBI Description
                   >gi 2916748_emb_CAA05554_ (AJ002555) histone H3 [Pisum
                 🌉 satīvum]
Seq. No.
                   211440
                   LIB3145-025-Q1-K1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2642434
                   418
BLAST score
E value
                   4.0e-41
                   110
Match length
% identity
                   73
                   (ACO02391) putative Rerl protein [Arabidopsis thaliana]
NCBI Description
                   211441
Seq. No.
                   LIB3145-025-Q1-K1-E1
Seq. ID
Method
                   BLASTX
                   q4510364
NCBI GI
                   236
BLAST score
                   8.0e-20
E value
                   101
Match length
                   52
 % identity
                   (AC007017) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   211442
 Seq. No.
                   LIB3145-025-Q1-K1-E11
 Seq. ID
                   BLASTX
Method
                   g4559398
 NCBI GI
                   213
 BLAST score
                   4.0e-17
 E value
                   55
Match length
                   71
 % identity
                   (AC006526) putative mitochondrial carrier protein
 NCBI Description
```

Seq. ID LIB3145-025-Q1-K1-E12

[Arabidopsis thaliana]

Method BLASTX

Method

NCBI GI

BLASTX q1220196



```
NCBI GI
                   g2529229
                   368
BLAST score
                   1.0e-35
E value
                   86
Match length
                   86
% identity
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                   211444
Seq. No.
                   LIB3145-025-Q1-K1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g730125
                   526
BLAST score
                   8.0e-54
E value
                   122
Match length
                   81
% identity
                   NADPH-CYTOCHROME P450 REDUCTASE >gi 322739 pir S31502
NCBI Description
                   NADPH--ferrihemoprotein reductase (\overline{EC}\ 1.6.\overline{2.4})^{-} Madagascar
                   periwinkle >gi 18139_emb_CAA49446_ (X69791)
                   NADPH--ferrihemoprotein reductase [Catharanthus roseus]
                   211445
Seq. No.
                   LIB3145-025-Q1-K1-E7
Seq. ID
Method
                   BLASTX
                   g3309082
NCBI GI
                   215
BLAST score
                   2.0e-17
E value
                   80
Match length
                   56
% identity
                   (AF076251) calcineurin B-like protein 1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   211446
                   LIB3145-025-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   q1076746
NCBI GI
                   493
BLAST score
                   7.0e-50
E value
                   119
Match length
                   82
% identity
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160 emb CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   211447
Seq. ID
                   LIB3145-025-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   q3243274
                   205
BLAST score
                   3.0e-16
E value
                   52
Match length
% identity
NCBI Description
                   (AF072134) TCP3 [Arabidopsis thaliana]
                   211448
Seq. No.
Seq. ID
                   LIB3145-025-Q1-K1-F3
```



```
BLAST score
                  3.0e-56
E value
                  115
Match length
                  89
% identity
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                  211449
Seq. No.
                  LIB3145-025-Q1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4126473
                   498
BLAST score
                  2.0e-50
E value
                  137
Match length
                  72
% identity
                   (AB014884) adenylyl cyclase associated protein [Gossypium
NCBI Description
                  hirsutum]
                   211450
Seq. No.
                   LIB3145-025-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                   g1076269
NCBI GI
BLAST score
                   304
E value
                   5.0e-28
                   98
Match length
                   58
% identity
                   pullulanase - spinach >gi_634093_emb_CAA58803_ (X83969)
NCBI Description
                   pullulanase [Spinacia oleracea]
Seq. No.
                   211451
                   LIB3145-025-Q1-K1-G10
Seq. ID
                   BLASTX
Method
                   g3080420
NCBI GI
BLAST score
                   380
                   1.0e-36
E value
                   122
Match length
                   65
% identity
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   211452
Seq. No.
                   LIB3145-025-Q1-K1-G11
Seq. ID
                   BLASTX
Method
                   g2961377
NCBI GI
BLAST score
                   152
                   4.0e-10
E value
                   49
Match length
% identity
                   (AL022141) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   211453
Seq. No.
Seq. ID
                   LIB3145-025-Q1-K1-G2
```

BLASTX Method NCBI GI q4580398 BLAST score 218 3.0e-20 E value Match length 116



93

78

9.0e-35

BLAST score

Match length

% identity

E value

```
% identity
                  (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                  thaliana]
                  211454
Seq. No.
                  LIB3145-025-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539343
BLAST score
                  488
                  2.0e-49
E value
                  126
Match length
% identity
                  75
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                  211455
Seq. No.
                  LIB3145-025-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006924
                   388
BLAST score
                   1.0e-37
E value
                  88
Match length
                   78
% identity
                   (Z99708) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   211456
                   LIB3145-025-Q1-K1-G8 **
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1173209
                   568
BLAST score
E value
                   1.0e-58
Match length
                   114
                   98
% identity
                   40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
NCBI Description
                   protein S16 protein - upland cotton
                   >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
                   211457
Seq. No.
                   LIB3145-025-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   g4049401
NCBI GI
                   160
BLAST score
                   6.0e-11
E value
                   48
Match length
                   67
% identity
                   (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
NCBI Description
                   thaliana]
                   211458
Seq. No.
                   LIB3145-025-Q1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g133867
```

40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal NCBI Description protein S11 - maize >gi\_22470\_emb\_CAA39438\_ (X55967) ribosomal protein S11 [Zea mays]

211459 Seq. No.

LIB3145-025-Q1-K1-H11 Seq. ID

Method BLASTX g2388564 NCBI GI 141 BLAST score 9.0e-09 E value Match length 104 % identity 38

(AC000098) ESTs gb\_AA042402,gb\_ATTS1380 come from this NCBI Description

gene. [Arabidopsis thaliana]

211460 Seq. No.

LIB3145-025-Q1-K1-H12 Seq. ID

Method BLASTX q135406 NCBI GI 503 BLAST score 3.0e-51 E value 98 Match length 96 % identity

TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi\_99768\_pir\_\_A32712 tubulin NCBI Description

alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi\_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

211461 Seq. No.

LIB3145-025-Q1-K1-H3 Seq. ID

BLASTX Method g462013 NCBI GI 380 BLAST score 9.0e-37 E value 85 Match length % identity 85

ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description

>gi 542022\_pir\_\_S39558 HSP90 homolog - Madagascar periwinkle >gi 348696 (L14594) heat shock protein 90

[Catharanthus roseus]

211462 Seq. No.

LIB3145-025-Q1-K1-H5 Seq. ID

Method BLASTN NCBI GI q2804257 45 BLAST score 3.0e-16 E value Match length 125 % identity 84

Arabidopsis thaliana DNA for phosphoglycerate NCBI Description

dehydrogenase, complete cds

211463 Seq. No.

LIB3145-025-Q1-K1-H8 Seq. ID

BLASTX Method g3309583 NCBI GI 561 BLAST score



```
5.0e-58
E value
                  113
Match length
                  96
% identity
                  (AF073830) fructose-6-phosphate
NCBI Description
                  2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]
                  211464
Seq. No.
                  LIB3145-025-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  g927575
NCBI GI
                  341
BLAST score
                  4.0e-32
E value
                  76
Match length
                  75
% identity
NCBI Description (U12926) alpha galactosidase [Glycine max]
                  211465
Seq. No.
                   LIB3145-026-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1747294
BLAST score
                   560
                   7.0e-58
E value
Match length
                   117
% identity
                   95
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
                   211466
Seq. No.
                   LIB3145-026-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g4033469
NCBI GI
                   152
BLAST score
                   6.0e-10
E value
Match length
                   107
                   12
% identity
                   ARGININE/SERINE-RICH SPLICING FACTOR RSP41
NCBI Description
                   >gi 1707370_emb_CAA67799_ (X99436) splicing factor
                   [Arabidopsis thaliana]
                   211467
Seq. No.
                   LIB3145-026-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   g3334138
NCBI GI
                   447
BLAST score
                   1.0e-44
E value
                   134
Match length
                   67
% identity
                   CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin
NCBI Description
                   [Glycine max]
                   211468
Seq. No.
                   LIB3145-026-Q1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4406809
BLAST score
                   157
                   1.0e-10
E value
```

62

Match length

% identity



```
(AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211469
Seq. No.
                  LIB3145-026-Q1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3980413
                  174
BLAST score
                  1.0e-12
E value
                  38
Match length
% identity
                  92
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                  211470
                  LIB3145-026-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135265
BLAST score
                  370
                  2.0e-35
E value
Match length
                  89
                  74
% identity
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]
                  211471
Seq. No.
                  LIB3145-026-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                   g3913439
NCBI GI
                   312
BLAST score
                   1.0e-28
E value
Match length
                   116
                   58
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1498080 (U64927) S-adenosylmethionine
                   decarboxylase [Ipomoea nil]
                   211472
Seq. No.
                   LIB3145-026-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   q2981475
NCBI GI
BLAST score
                   470
                   3.0e-47
E value
                   109
Match length
                   82
% identity
                   (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
NCBI Description
                   domestica]
                   211473
Seq. No.
                   LIB3145-026-Q1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4510345
                   227
BLAST score
                   9.0e-19
E value
                   44
Match length
                   86
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. LIB3145-026-Q1-K1-B4 Seq. ID

211474

```
Method
                  g441457
NCBI GI
                  598
BLAST score
                  2.0e-62
E value
                  121
Match length
                  98
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                   esculentum]
                   211475
Seq. No.
                  LIB3145-026-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                   q2827554
NCBI GI
                   424
BLAST score
                   8.0e-42
E value
Match length
                   109
                   78
% identity
                   (AL021635) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   211476
Seq. No.
                   LIB3145-026-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2660677
BLAST score
                   200
                   9.0e-16
E value
                   58
Match length
% identity
                   62
                   (AC002342) unknown protein [Arabidopsis thaliana]
NCBI Description
                   211477
Seq. No.
                   LIB3145-026-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   q1084415
NCBI GI
BLAST score
                   399
                   7.0e-39
E value
                   119
Match length
                   66
% identity
                   RNA-binding protein - Wood tobacco >gi 624925 dbj BAA05170
NCBI Description
                    (D26182) RNA-binding glycine rich protein (RGP-2)
                    [Nicotiana sylvestris]
                   211478
Seq. No.
                   LIB3145-026-Q1-K1-D1
Seq. ID
                   {\tt BLASTX}
Method
                   g4235430
NCBI GI
                   408
BLAST score
                   4.0e-40
E value
                   105
Match length
                   79
 % identity
                   (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
                   211479
 Seq. No.
                   LIB3145-026-Q1-K1-D3
 Seq. ID
```

BLASTX

241

q3065835

Method NCBI GI

BLAST score



```
E value
                  117
Match length
                  48
% identity
                   (AF058800) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  211480
Seq. No.
                  LIB3145-026-Q1-K1-D4
Seq. ID
                  BLASTX
Method
                  g4263787
NCBI GI
                  190
BLAST score
                  2.0e-14
E value
                   89
Match length
                   62
% identity
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   211481
                   LIB3145-026-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                   g4455800
NCBI GI
BLAST score
                   354
                   1.0e-33
E value
Match length
                   128
% identity
                   57
NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]
                   211482
Seq. No.
                   LIB3145-026-Q1-K1-D7
Seq. ID
                   BLASTN
Method
                   g167312
NCBI GI
                   96
BLAST score
                   7.0e-47
E value
Match length
                   96
                   100
% identity
                   Gossypium hirsutum vacuolar H+-ATPase catalytic subunit
NCBI Description
                   mRNA, complete cds
                   211483
Seq. No.
Seq. ID
                   LIB3145-026-Q1-K1-D9
                   BLASTX
Method
                   g1174592
NCBI GI
                   718
BLAST score
                   3.0e-76
E value
                   141
Match length
                   100
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   211484
Seq. No.
Seq. ID
                   LIB3145-026-Q1-K1-E2
                   BLASTN
Method
                   q2275090
NCBI GI
```

Method BLASTN
NCBI GI g2275090
BLAST score 152
E value 6.0e-80
Match length 223
% identity 96



```
NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)
                  211485
Seq. No.
                  LIB3145-026-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                  q1888485
NCBI GI
                   494
BLAST score
                  5.0e-50
E value
                  107
Match length
                  86
% identity
                  (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
NCBI Description
                   211486
Seq. No.
                   LIB3145-026-Q1-K1-E4
Seq. ID
Method
                   BLASTX
                   q3128209
NCBI GI
BLAST score
                   543
                   9.0e-56
E value
                   139
Match length
                   43
% identity
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]
Seq. No.
                   211487
                   LIB3145-026-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   q924951
NCBI GI
                   331
BLAST score
                   7.0e-31
E value
Match length
                   138
                   46
% identity
NCBI Description (U30324) class I chitinase [Theobroma cacao]
                   211488
Seq. No.
                   LIB3145-026-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   q4063743
NCBI GI
                   208
BLAST score
                   2.0e-16
E value
                   120
Match length
                   54
% identity
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   211489
Seq. No.
                   LIB3145-026-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g2244734
NCBI GI
                   644
BLAST score
                   1.0e-67
E value
                   130
Match length
                   98
 % identity
                  (D88414) actin [Gossypium hirsutum]
NCBI Description
                   211490
 Seq. No.
                   LIB3145-026-Q1-K1-F2
 Seq. ID
```

BLASTX

582

g122087

Method

NCBI GI BLAST score



2.0e-60 E value 136 Match length 87 % identity HISTONE H3 >gi\_81849\_pir\_\_S04520 histone H3 (clone pH3c-1) NCBI Description - alfalfa >gi\_82609\_pir\_A26014 histone H3 - wheat >gi\_19607\_emb\_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi\_19609\_emb\_CAA31965\_ (X13674) histone H3 (AA 1-136) [Medicago satīva] >gi\_21797\_emb\_CAA25451 (X00937) H3 histone [Triticum aestivum]  $>gi_488565$  (U09459) histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803) histone H3 [Onobrychis viciifolia] Seq. No. 211491 LIB3145-026-Q1-K1-F3 Seq. ID BLASTN Method q3123514 NCBI GI 42 BLAST score E value 2.0e-14 62 Match length 92 % identity NCBI Description E.lagascae mRNA for Mago Nashi-like protein 211492 Seq. No. LIB3145-026-Q1-K1-F4 Seq. ID BLASTX Method q2213595 NCBI GI 324 BLAST score 3.0e - 30E value Match length 95 64 % identity NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana] 211493 Seq. No. LIB3145-026-Q1-K1-G2 Seq. ID Method BLASTX NCBI GI q4314388 255 BLAST score 5.0e-22 E value Match length 72 62 % identity NCBI Description (AC006232) hypothetical protein [Arabidopsis thaliana] 211494 Seq. No. LIB3145-026-Q1-K1-G9 Seq. ID BLASTX Method g1199467 NCBI GI 377 BLAST score 3.0e-36 E value 137 Match length 53 % identity (D64155) possible aldehyde decarbonylase [Arabidopsis NCBI Description thaliana]

Seq. No. LIB3145-026-Q1-K1-H1 Seq. ID

211495

BLASTX Method NCBI GI g1199467



```
BLAST score
                  8.0e-38
E value
                  137
Match length
                  55
% identity
                   (D64155) possible aldehyde decarbonylase [Arabidopsis
NCBI Description
                  thaliana]
                   211496
Seq. No.
                   LIB3145-026-Q1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1710530
BLAST score
                   577
E value
                   8.0e-60
                   112
Match length
% identity
                   60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
NCBI Description
                   ribosomal protein L27a - Arabidopsis thaliana
                   >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
                   211497
Seq. No.
                   LIB3145-027-Q1-K1-B1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1200001
                   35
BLAST score
                   4.0e-10
E value
                   99
Match length
                   84
% identity
                   B.thuringiensis crylBa2 gene >gi_2467598_gb_I42103_I42103
NCBI Description
                   Sequence 1 from patent US
                   211498
Seq. No.
                   LIB3145-027-Q1-K1-B11
Seq. ID
Method
                   BLASTX
                   g168695
NCBI GI
                   244
BLAST score
                   1.0e-20
E value
                   102
Match length
                   53
 % identity
                    (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                   zein gamma [Zea mays]
                   211499
 Seq. No.
                   LIB3145-027-Q1-K1-C9
 Seq. ID
                   BLASTX
 Method
                   g168695
 NCBI GI
                   229
 BLAST score
                   2.0e-19
 E value
                   58
Match length
                   74
 % identity
                    (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
 NCBI Description
                    zein gamma [Zea mays]
                    211500
 Seq. No.
                    LIB3145-027-Q1-K1-D10
 Seq. ID
```

BLASTX

g2668744

Method

NCBI GI

```
BLAST score
                  3.0e-41
E value
                  78
Match length
% identity
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                  211501
Seq. No.
                  LIB3145-027-Q1-K1-E1
Seq. ID
                  BLASTX
Method
                  q4090435
NCBI GI
BLAST score
                  183
                   4.0e-14
E value
                  72
Match length
                   53
% identity
                  (U63372) truncated CrylAc [synthetic construct]
NCBI Description
                   211502
Seq. No.
                  LIB3145-027-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g143126
NCBI GI
                   154
BLAST score
                   5.0e-18
E value
                   83
Match length
                   65
% identity
                  (M73249) [Bacillus thuringiensis gene, complete CDS.], gene
NCBI Description
                   product [Bacillus thuringiensis]
                   211503
Seq. No.
                   LIB3145-027-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   q2414156
NCBI GI
                   465
BLAST score
                   1.0e-46
E value
                   138
Match length
                   73
% identity
                   (Y09787) delta-endotoxin [Bacillus thuringiensis]
NCBI Description
```

Seq. No. 211504

Seq. ID LIB3145-027-Q1-K1-G1

Method BLASTX
NCBI GI g2414156
BLAST score 718
E value 3.0e-76
Match length 141
% identity 96

NCBI Description (Y09787) delta-endotoxin [Bacillus thuringiensis]

Seq. No. 211505

Seq. ID LIB3145-027-Q1-K1-G2

Method BLASTX
NCBI GI g117543
BLAST score 364
E value 1.0e-35
Match length 108
% identity 73

NCBI Description 130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL PROTOXIN) >gi 98531 pir A26513 parasporal

29319

.



crystal protein - Bacillus thuringiensis (strain aizawai)
>gi\_143099 (M16463) insecticidal protein [Bacillus
thuringiensis]

Seq. No. 211506 LIB3145-027-Q1-K1-G4 Seq. ID Method BLASTX NCBI GI q2414156 BLAST score 528 5.0e-54 E value Match length 135 78 % identity (Y09787) delta-endotoxin [Bacillus thuringiensis] NCBI Description Seq. No. 211507 LIB3145-028-Q1-K1-A10 Seq. ID Method BLASTX NCBI GI g799177 BLAST score 273 3.0e-24 E value Match length 118 25 % identity NCBI Description (U22055) 100 kDa coactivator [Homo sapiens] Seq. No. 211508 LIB3145-028-Q1-K1-A2 Seq. ID Method BLASTX NCBI GI g3063696 BLAST score 245 4.0e-21 E value Match length 82 % identity 66 NCBI Description (AL022537) putative protein [Arabidopsis thaliana] Seq. No. 211509 Seq. ID LIB3145-028-Q1-K1-A5 Method BLASTX NCBI GI g4490308 BLAST score 194 E value 6.0e-15 Match length 61 % identity 64 NCBI Description (AL035678) putative protein [Arabidopsis thaliana] Seq. No. 211510 LIB3145-028-Q1-K1-A9 Seq. ID Method BLASTX NCBI GI g3228664 BLAST score 375 E value 5.0e-36 Match length 141 53 % identity NCBI Description (AF069986) nitrilase and fragile histidine triad fusion

Seq. No. 211511

Seq. ID LIB3145-028-Q1-K1-B1

protein NitFhit [Caenorhabditis elegans]



```
BLASTX
Method
NCBI GI
                  g3822225
BLAST score
                  438
                  2.0e-43
E value
                  144
Match length
                  60
% identity
                  (AF079183) RING-H2 finger protein RHG1a [Arabidopsis
NCBI Description
                  thaliana]
                  211512
Seq. No.
                  LIB3145-028-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129538
BLAST score
                  758
E value
                  6.0e-81
Match length
                  144
                  97
% identity
NCBI Description
                  AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                  211513
Seq. ID
                  LIB3145-028-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  q1946367
BLAST score
                  218
E value
                  3.0e-18
                  54
Match length
                  78
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  211514
Seq. ID
                  LIB3145-028-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3608495
BLAST score
                  495
E value
                  4.0e-50
                  133
Match length
                  77
% identity
NCBI Description
                  (AF089738) plastid division protein FtsZ [Arabidopsis
                  thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid
                  division protein FtsZ [Arabidopsis Thaliana]
Seq. No.
                  211515
Seq. ID
                  LIB3145-028-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q2811029
BLAST score
                  153
E value
                  4.0e-10
Match length
                  102
% identity
                  37
NCBI Description ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)
                  (ACETYLORNITHINE TRANSAMINASE) (AOTA)
                  >gi 1944511 emb CAA69936 (Y08680) acetylornithine
```

aminotransferase [Alnus glutinosa]

Seq. No. 211516

Seq. ID LIB3145-028-Q1-K1-C2

BLAST score

183



```
BLASTX
Method
                  q1707017
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
                   39
Match length
                  79
% identity
                  (U78721) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
                   211517
Seq. No.
                   LIB3145-028-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1778376
BLAST score
                   501
                   7.0e-51
E value
                   130
Match length
                   72
% identity
                  (U81288) PsRT17-1 [Pisum sativum]
NCBI Description
                   211518
Seq. No.
                   LIB3145-028-Q1-K1-C9
Seq. ID
                   BLASTN
Method
                   q2623911
NCBI GI
BLAST score
                   74
E value
                   2.0e-33
                   100
Match length
                   95
% identity
                   Gossypium barbadense ATPase B subunit (atpB) and ribulose
NCBI Description
                   1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL)
                   genes, chloroplast genes encoding chloroplast proteins,
                   partial cds, and atpB-rbcL intergenic spacer
                   211519
Seq. No.
                   LIB3145-028-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   g4001803
NCBI GI
BLAST score
                   105
                   5.0e-09
E value
                   43
Match length
                   74
% identity
                   (AF041474) BAF53a [Homo sapiens] >gi 4218064 dbj BAA74577
NCBI Description
                   (AB015907) actin-related protein [Homo sapiens]
                   211520
Seq. No.
                   LIB3145-028-Q1-K1-D12
Seq. ID
                   BLASTX
Method
                   g1350548
NCBI GI
                   224
BLAST score
                   2.0e-18
E value
                   65
Match length
                   60
 % identity
                   (L47609) heat shock-like protein [Picea glauca]
NCBI Description
                   211521
 Seq. No.
                   LIB3145-028-Q1-K1-D2
 Seq. ID
                   BLASTX
Method
                   g4580389
NCBI GI
```



```
0e-13
E value
                  40
Match length
                  80
% identity
                  (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211522
Seq. No.
                  LIB3145-028-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                  g2924792
NCBI GI
                  155
BLAST score
E value
                  1.0e-16
Match length
                  65
% identity
                  71
NCBI Description (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
                  211523
Seq. No.
                  LIB3145-028-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                  q4090884
NCBI GI
                  280
BLAST score
                  7.0e-25
E value
                  87
Match length
% identity
                  (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                  synaptobrevin 7B [Arabidopsis thaliana]
                  211524
Seq. No.
                  LIB3145-028-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4163997
BLAST score
                   284
                   1.0e-25
E value
Match length
                   94
                   57
% identity
                   (AF087483) alpha-xylosidase precursor [Arabidopsis
NCBI Description
                   thaliana]
                   211525
Seq. No.
                   LIB3145-028-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g1709446
NCBI GI
                   616
BLAST score
                   3.0e-64
E value
                   135
Match length
                   85
% identity
                   PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
NCBI Description
                   PRECURSOR (PDHE1-A) >gi 2117533 pir__JC4358 pyruvate
                   dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha
                   chain - Arabidopsis thaliana mitochondrion >gi_710400
                   (U21214) pyruvate dehydrogenase E1 alpha subunit
```

[Arabidopsis thaliana]

211526 Seq. No.

Seq. ID LIB3145-028-Q1-K1-E4

BLASTX Method NCBI GI q2982297 456 BLAST score



```
E value
                   2.0e-45
Match length
                   101
% identity
                   (AF051233) KIAA0107-like protein [Picea mariana]
NCBI Description
                   211527
Seq. No.
                   LIB3145-028-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   q3395435
NCBI GI
BLAST score
                   219
                   7.0e-18
E value
                   115
Match length
% identity
                   (AC004683) myosin heavy chain-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   211528
Seq. No.
                   LIB3145-028-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   g1747310
NCBI GI
                   167
BLAST score
                   3.0e-12
E value
Match length
                   67
% identity
                   52
                   (D58424) Myb-like DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   211529
Seq. No.
                   LIB3145-028-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   g3128168
NCBI GI
                   400
BLAST score
                   4.0e-39
E value
Match length
                   94
                   74
% identity
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   211530
                   LIB3145-028-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   g2738248
NCBI GI
                   267
BLAST score
E value
                   1.0e-23
                   99
Match length
                   60
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   211531
Seq. No.
                   LIB3145-028-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g129941
NCBI GI
BLAST score
                   530
                   3.0e-54
E value
```

136

68

Match length

% identity



EXOPOLYGALACTURONASE (EXOPG) (PECTINASE) (GALACTURAN NCBI Description 1,4-ALPHA-GALACTURONIDASE) >gi\_82020\_pir\_\_JQ0992 polygalacturonase (EC 3.2.1.15) P22 - evening primrose >gi\_256552\_bbs\_114659 polygalacturonase homolog {clone P22} [Oenothera organensis, pollen, Peptide, 362 aa] 211532 Seq. No. LIB3145-028-Q1-K1-G1 Seq. ID Method BLASTX NCBI GI q974782 BLAST score 109 1.0e-12 E value Match length 79 % identity 59 (Z49150) cobalamine-independent methionine synthase NCBI Description [Solenostemon scutellarioides] 211533 Seq. No. LIB3145-028-Q1-K1-G2 Seq. ID BLASTX Method g3860258 NCBI GI 161 BLAST score 5.0e-11 E value . 52 Match length % identity 60 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana] 211534 Seq. No. LIB3145-028-Q1-K1-G3 Seq. ID BLASTX Method g2244841 NCBI GI BLAST score 291 3.0e-26 E value 87 Match length % identity 67 (Z97337) hypothetical protein [Arabidopsis thaliana] NCBI Description 211535 Seq. No. LIB3145-028-Q1-K1-G4 Seq. ID Method BLASTX g1351135 NCBI GI BLAST score 545 E value 8.0e-64 Match length 138 86 % identity SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) NCBI Description >gi\_436792\_emb\_CAA50317\_ (X70990) sucrose synthase [Arabidopsis thaliana] 211536 Seq. No.

Seq. ID LIB3145-028-Q1-K1-G9

BLASTX Method NCBI GI q3873807 252 BLAST score 1.0e-21 E value Match length 115 % identity 50



NCBI Description (Z49907) B0491.1 [Caenorhabditis elegans] 211537 Seq. No. LIB3145-028-Q1-K1-H1 Seq. ID Method BLASTN g4454587 NCBI GI BLAST score 33 E value 5.0e-09 107 Match length 89 % identity Arabidopsis thaliana BAC F21A20 from chromosome V near 61 NCBI Description cM, complete sequence [Arabidopsis thaliana] 211538 Seq. No. LIB3145-028-Q1-K1-H10 Seq. ID BLASTX Method NCBI GI q2815246 BLAST score 218 1.0e-17 E value 55 Match length 71 % identity (X95709) class I type 2 metallothionein [Cicer arietinum] NCBI Description 211539 Seq. No. LIB3145-028-Q1-K1-H11 Seq. ID Method BLASTX a119354 NCBI GI 529 BLAST score 4.0e-54 E value Match length 113 88 % identity ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_82082\_pir\_\_JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi 19281 emb CAA41115 (X58108) enolase [Lycopersicon esculentum] 211540 Seq. No. Seq. ID LIB3145-028-Q1-K1-H3 Method BLASTX q1430907 NCBI GI 200 BLAST score E value 5.0e-16 74 Match length % identity 55 (Z49144) multidrug resistance-associated protein 2 NCBI Description [Oryctolagus cuniculus]

Seq. No. 211541

LIB3145-028-Q1-K1-H5 Seq. ID

Method BLASTX NCBI GI g437327 BLAST score 303 4.0e-28 E value 77 Match length % identity 81

NCBI Description (L04497) MYB A; putative [Gossypium hirsutum]

NCBI Description



```
211542
Seq. No.
                  LIB3145-028-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g3337361
NCBI GI
                  337
BLAST score
                  1.0e-31
E value
                  84
Match length
                  71
% identity
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
Seq. No.
                  211543
                  LIB3145-028-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119354
BLAST score
                  230
                  2.0e-40
E value
Match length
                  101
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir JQ1185
                  phosphopyruvate hydratase (EC 4.2.1.11) - tomato
                  >qi 19281 emb CAA41115 (X58108) enolase [Lycopersicon
                   esculentum]
                  211544
Seq. No.
                  LIB3145-028-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076414
BLAST score
                   457
E value
                   1.0e-45
Match length
                   136
% identity
                   subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
NCBI Description
                   thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)
                   subtilisin-like protease [Arabidopsis thaliana]
                   211545
Seq. No.
                   LIB3145-029-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g1350720
NCBI GI
                   340
BLAST score
                   5.0e-32
E value
Match length
                   105
                   63
% identity
                  60S RIBOSOMAL PROTEIN L32
NCBI Description
                   211546
Seq. No.
Seq. ID
                   LIB3145-029-Q1-K1-A12
Method
                   BLASTX
                   g1173223
NCBI GI
                   338
BLAST score
                   3.0e-32
E value
                   70
Match length
                   90
% identity
                   40S RIBOSOMAL PROTEIN S11 >gi 454848 (L28831) ribosomal
```

29327

protein S11 [Glycine max]



```
Seq. No.
                   211547
Seq. ID
                   LIB3145-029-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1350720
BLAST score
                   186
E value
                   5.0e-14
Match length
                   61
% identity
                   62
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                   211548
Seq. ID
                  LIB3145-029-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1589778
BLAST score
                   369
E value
                  7.0e-58
Match length
                  125
% identity
                  83
NCBI Description
                 (U62135) SPINDLY [Arabidopsis thaliana]
Seq. No.
                  211549
Seq. ID
                  LIB3145-029-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g1730108
BLAST score
                  195
E value
                  1.0e-29
Match length
                  113
% identity
                  63
NCBI Description
                  LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
                  HYDROXYLASE) >gi_486848 pir S36233 flavanone 3-hydroxylase
                  homolog - garden petunia
Seq. No.
                  211550
Seq. ID
                  LIB3145-029-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2911058
BLAST score
                  98
E value
                  7.0e-11
Match length
                  65
% identity
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  211551
Seq. ID
                  LIB3145-029-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  q2738949
BLAST score
                  458
E value
                  7.0e-46
Match length
                  104
% identity
NCBI Description
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
```

Seq. No. 211552 Seq. ID LIB3145-029-Q1-K1-B2

Method BLASTX



```
g3152587
NCBI GI
BLAST score
                  213
                  2.0e-32
E value
Match length
                  88
                  77
% identity
                  (AC002986) Similar to CREB-binding protein homolog
NCBI Description
                  gb_U88570 from D. melanogaster and contains similarity to
                  callus-associated protein gb U01961 from Nicotiana tabacum.
                  EST gb W43427 comes from this gene. [Arabidopsis thaliana]
Seq. No.
                  211553
Seq. ID
                  LIB3145-029-Q1-K1-B3
                  {\tt BLASTX}
Method
NCBI GI
                  q4510342
BLAST score
                  151
                  8.0e-23
E value
                  99
Match length
                  65
% identity
                  (AC006921) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  211554
Seq. ID
                  LIB3145-029-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4106413
BLAST score
                  251
E value
                  3.0e-29
                  112
Match length
                  57
% identity
                  (AF082991) beta-D-glucosidase beta subunit precursor [Avena
NCBI Description
                  sativa]
Seq. No.
                  211555
Seq. ID
                  LIB3145-029-Q1-K1-C10
                  BLASTX
Method
NCBI GI
                  g4457221
BLAST score
                  234
E value
                  7.0e-20
                  82
Match length
                  66
% identity
                  (AF127797) putative bZIP DNA-binding protein [Capsicum
NCBI Description
                  chinense]
Seq. No.
                  211556
Seq. ID
                  LIB3145-029-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  g1130683
                  252
BLAST score
                  1.0e-140
E value
                  274
Match length
```

% identity 99

NCBI Description G.hirsutum gene for acetohydroxyacid synthase (2381 bp)

Seq. No. 211557

Seq. ID LIB3145-029-Q1-K1-C9

Method BLASTX NCBI GI g3142301



```
BLAST score
                  7.0e-29
E value
                  80
Match length
                  71
% identity
                  (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                  molecule 2, large isoform precursor gb_M76710 from Xenopus
                  laevis, and beta transducin from S. cerevisiae gb_Q05946.
                  ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101,
                  gb H3630
                  211558
Seq. No.
Seq. ID
                  LIB3145-029-Q1-K1-D10
                  BLASTX
Method
                  q3176668
NCBI GI
BLAST score
                  349
                  2.0e-33
E value
                  75
Match length
                  91
% identity
                  (ACO04393) Similar to ribosomal protein L17 gb_X62724 from
NCBI Description
                  Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and
                  gb_Z33937 come from this gene. [Arabidopsis thaliana]
                  211559
Seq. No.
Seq. ID
                  LIB3145-029-Q1-K1-D2
                  BLASTX
Method
                  g130172
NCBI GI
BLAST score
                  212
                  3.0e-44
E value
                  110
Match length
                  86
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH
NCBI Description
                  PHOSPHORYLASE L) >gi_168276 (M64362) starch phosphorylase
                  [Ipomoea batatas]
                  211560
Seq. No.
                  LIB3145-029-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  q2507281
NCBI GI
BLAST score
                  390
                  3.0e-46
E value
                  100
Match length
                  89
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb_CAA66048_
NCBI Description
                   (X97380) atran2 [Arabidopsis thaliana]
Seq. No.
                  211561
Seq. ID
                  LIB3145-029-Q1-K1-D6
```

BLASTX Method NCBI GI g1370194 BLAST score 353 3.0e-52E value 116 Match length 93 % identity

(Z73946) RAB8C [Lotus japonicus] NCBI Description

211562 Seq. No.

LIB3145-029-Q1-K1-D8 Seq. ID

```
ASTN
Method
                  q4539331
NCBI GI
                  35
BLAST score
                  4.0e-10
E value
                  59
Match length
                  90
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13
NCBI Description
                   (ESSA project)
                  211563
Seq. No.
                  LIB3145-029-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  q3776005
NCBI GI
                   366
BLAST score
E value
                   2.0e-35
                   77
Match length
                   95
% identity
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   211564
Seq. No.
                   LIB3145-029-Q1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3004565
BLAST score
                   325
                   3.0e - 30
E value
                   139
Match length
% identity
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   211565
Seq. No.
                   LIB3145-029-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4049341
                   173
BLAST score
                   1.0e-12
E value
Match length
                   80
% identity
                   54
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                   211566
Seq. No.
                   LIB3145-029-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g4455300
NCBI GI
                   152
BLAST score
                   3.0e-10
E value
                   29
Match length
 % identity
                   83
                   (AL035528) putative pectate lyase All (fragment)
 NCBI Description
                    [Arabidopsis thaliana]
                   211567
 Seq. No.
                   LIB3145-029-Q1-K1-F2
 Seq. ID
                   BLASTX
 Method
                   g3452551
 NCBI GI
                   175
 BLAST score
                    5.0e-27
 E value
```

Match length



```
% identity
NCBI Description (AJ007743) cysteine proteinase precursor [Vicia sativa]
                  211568
Seq. No.
Seq. ID
                  LIB3145-029-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2407802
BLAST score
                  240
                  2.0e-20
E value
Match length
                  68
% identity
                  75
NCBI Description (Y12576) histone H2B [Arabidopsis thaliana]
                  211569
Seq. No.
Seq. ID
                  LIB3145-029-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  211570
Seq. ID
                  LIB3145-029-Q1-K1-G12
Method
                  BLASTX
                  g464985
NCBI GI
BLAST score
                  167
E value
                  3.0e-12
Match length
                  32
                  100
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)
                  >gi 398699 emb CAA78713 (Z14989) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana]
Seq. No.
                  211571
                  LIB3145-029-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4033429
BLAST score
                  153
                  2.0e-19
E value
Match length
                  86
% identity
                  63
NCBI Description PYRUVATE KINASE (PK) >gi 2854033 (AF043910) pyruvate kinase
                  [Eimeria tenella]
Seq. No.
                  211572
Seq. ID
                  LIB3145-029-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g130172
BLAST score
                  373
                                                           1300
                  2.0e-55
E value
Match length
                  131
% identity
```

PHOSPHORYLASE L) >gi 168276 (M64362) starch phosphorylase

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH



## [Ipomoea batatas]

```
Seq. No.
                  211573
Seq. ID
                  LIB3145-029-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g228210
BLAST score
                  142
                  4.0e-09
E value
Match length
                  68
                  47
% identity
NCBI Description granule-bound starch synthase [Solanum tuberosum]
                  211574
Seq. No.
Seq. ID
                  LIB3145-029-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4098129
BLAST score
                  337
E value
                  3.0e-32
                  67
Match length
                  97
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                  211575
Seq. ID
                  LIB3145-029-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q4325342
BLAST score
                  358
                  5.0e-40
E value
                  123
Match length
                  75
% identity
NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]
Seq. No.
                  211576
Seq. ID
                  LIB3145-029-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g136644
BLAST score
                  154
E value
                  4.0e-10
Match length
                  32
                  91
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_100765_pir__A34506
                  23K ubiquitin carrier protein E2 - wheat >gi 170782
                   (M28059) ubiquitin carrier protein [Triticum vulgare]
Seq. No.
                  211577
Seq. ID
                  LIB3145-030-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1781348
BLAST score
                  551
E value
                  7.0e-57
Match length
                  110
                  96
% identity
NCBI Description (Y10380) homologous to plastidic aldolases [Solanum
```

tuberosum]

211578

Seq. No.

Method

NCBI GI

E value

BLAST score

BLASTX

609 2.0e-63

g1136793

```
LIB3145-030-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3461820
BLAST score
                  243
                  1.0e-20
E value
Match length
                  80
% identity
                  57
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                  211579
                  LIB3145-030-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g421929
NCBI GI
BLAST score
                  254
E value
                  6.0e-31
                  108
Match length
% identity
                  11
NCBI Description ubiquitin - tomato >gi 312160 emb CAA51679 (X73156)
                  ubiquitin [Lycopersicon esculentum]
Seq. No.
                  211580
Seq. ID
                  LIB3145-030-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  37
                  2.0e-11
E value
Match length
                  39
% identity
                  39
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  211581
                  LIB3145-030-Q1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4510363
BLAST score
                  434
E value
                  4.0e-43
Match length
                  91
                  90
% identity
NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  211582
Seq. ID
                  LIB3145-030-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g533256
BLAST score
                  239
E value
                  2.0e-20
Match length
                  88
                  52
% identity
NCBI Description (L27101) pectinesterase [Petunia inflata]
Seq. No.
                  211583
Seq. ID
                  LIB3145-030-Q1-K1-B9
```

```
Match length 140 % identity 80
```

NCBI Description (X91486) PMSR protein [Brassica napus]

Seq. No. 211584

Seq. ID LIB3145-030-Q1-K1-C1

Method BLASTX
NCBI GI g4510339
BLAST score 531
E value 2.0e-54
Match length 125
% identity 41

NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis

thaliana]

Seq. No. 211585

Seq. ID LIB3145-030-Q1-K1-C12

Method BLASTX
NCBI GI g1854386
BLAST score 513
E value 3.0e-52
Match length 132
% identity 73

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No. 211586

Seq. ID LIB3145-030-Q1-K1-C2

Method BLASTX
NCBI GI g4490737
BLAST score 353
E value 2.0e-33
Match length 100
% identity 43

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 211587

Seq. ID LIB3145-030-Q1-K1-C3

Method BLASTX
NCBI GI g542020
BLAST score 579
E value 5.0e-60
Match length 134
% identity 81

NCBI Description sucrose transport protein - castor bean

>gi 468562 emb\_CAA83436\_ (Z31561) sucrose carrier [Ricinus

communis]

Seq. No. 211588

Seq. ID LIB3145-030-Q1-K1-C4

Method BLASTX
NCBI GI g2739375
BLAST score 220
E value 6.0e-18
Match length 99
% identity 55

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

NCBI Description



```
211589
Seq. No.
                  LIB3145-030-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  q2252871
NCBI GI
                  209
BLAST score
                  7.0e-17
E value
                  72
Match length
% identity
                  (AF013294) No definition line found [Arabidopsis thaliana]
NCBI Description
                  211590
Seq. No.
                  LIB3145-030-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  q2507421
NCBI GI
                  355
BLAST score
                  7.0e-34
E value
                  73
Match length
                  90
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                   211591
Seq. No.
                  LIB3145-030-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g3242077
NCBI GI
                   222
BLAST score
                   3.0e-18
E value
                   95
Match length
                   52
% identity
                  (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
                   211592
Seq. No.
                   LIB3145-030-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   q4337175
NCBI GI
                   263
BLAST score
E value
                   5.0e-23
                   92
Match length
                   60
% identity
                   (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb_AA720210 come from this gene. [Arabidopsis thaliana]
                   211593
Seq. No.
                   LIB3145-030-Q1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4538911
BLAST score
                   287
                   9.0e-26
E value
                   134
Match length
 % identity
                   (AL049482) hypothetical protein [Arabidopsis thaliana]
```



```
Seq. No.
Seq. ID
                  LIB3145-030-Q1-K1-D11
Method
                  BLASTX
                  g115492
NCBI GI
                  692
BLAST score
                  3.0e-73
E value
                  135
Match length
% identity
                  58
NCBI Description CALMODULIN-RELATED PROTEIN >gi_169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
                  211595
Seq. No.
                  LIB3145-030-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g2618686
NCBI GI
                  343
BLAST score
                  2.0e-32
E value
                  127
Match length
                  53
% identity
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]
                  211596
Seq. No.
                  LIB3145-030-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3201632
NCBI GI
BLAST score
                   324
                   4.0e-30
E value
                  131
Match length
                   47
% identity
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]
                   211597
Seq. No.
                   LIB3145-030-Q1-K1-E12
Seq. ID
Method
                   BLASTX
                   q1345787
NCBI GI
BLAST score
                   434
E value
                   4.0e-43
                   97
Match length
                   82
% identity
                   CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)
NCBI Description
                   >qi 567937 dbj BAA05641 (D26594) chalcone synthase
                   [Camellia sinensis]
                   211598
Seq. No.
                   LIB3145-030-Q1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2738949
BLAST score
                   499
                   1.0e-50
E value
Match length
                   109
% identity
                   86
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                   ananassa]
```

Seq. No. 211599

Seq. ID LIB3145-030-Q1-K1-E5

Method BLASTX



```
q2335106
NCBI GI
                  287
BLAST score
                  6.0e-26
E value
                  98
Match length
                  24
% identity
                  (AC002339) salt inducible protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  211600
Seq. No.
                  LIB3145-030-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g3786004
NCBI GI
                  428
BLAST score
                  3.0e-42
E value
                  105
Match length
                   75
% identity
NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]
                   211601
Seq. No.
                  LIB3145-030-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g553107
NCBI GI
                   364
BLAST score
                   8.0e-35
E value
                   108
Match length
% identity
                   67
NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]
                   211602
Seq. No.
                   LIB3145-030-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g1351279
NCBI GI
                   120
BLAST score
                   2.0e-13
E value
                   71
Match length
                   64
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi 602590 emb_CAA58230_ (X83227) triosephosphate isomerase
                   [Petunia x hybrida]
                   211603
Seq. No.
                   LIB3145-030-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q4432857
NCBI GI
BLAST score
                   147
E value
                   2.0e-09
                   56
Match length
                   52
 % identity
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   211604
                   LIB3145-030-Q1-K1-F9
 Seq. ID
 Method
                   BLASTX
                   q3157934
 NCBI GI
 BLAST score
                   159
                   8.0e-11
 E value
```

Match length

% identity (AC002131) Similar to hypothetical protein F09E5.8 NCBI Description gb\_U37429 from C. elegans. ESTs gb\_T42019 and gb\_N97000 come from this gene. [Arabidopsis thaliana] 211605 Seq. No. LIB3145-030-Q1-K1-G1 Seq. ID BLASTX Method g3834316 NCBI GI 291 BLAST score 2.0e-26 E value 103 Match length 52 % identity (AC005679) Similar to gb\_X16648 pathogenesis related NCBI Description protein from Hordeum vulgare. EST gb\_Z18206 comes from this gene. [Arabidopsis thaliana] 211606 Seq. No. LIB3145-030-Q1-K1-G10 Seq. ID BLASTX Method g3600054 NCBI GI 412 BLAST score 2.0e-40 E value 133 Match length 54 % identity

(AF080120) No definition line found [Arabidopsis thaliana] NCBI Description

211607 Seq. No.

LIB3145-030-Q1-K1-G3 Seq. ID

BLASTX Method g4490747 NCBI GI 386 BLAST score 1.0e-37 E value 104 Match length 74 % identity

(AL035708) DnaJ-like protein [Arabidopsis thaliana] NCBI Description

211608 Seq. No.

LIB3145-030-Q1-K1-G7 Seq. ID

BLASTX Method q2879811 NCBI GI 197 BLAST score 2.0e-15 E value 41 Match length 98 % identity

(AJ223316) ribosomal protein L30 [Lupinus luteus] NCBI Description

211609 Seq. No.

LIB3145-030-Q1-K1-H7 Seq. ID

BLASTN Method NCBI GI g2687434 341 BLAST score 0.0e+00E value 403 Match length 96 % identity

Eucryphia lucida large subunit 26S ribosomal RNA gene, NCBI Description

partial sequence



```
211610
Seq. No.
Seq. ID
                  LIB3145-030-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  q2760326
BLAST score
                  228
E value
                  6.0e-19
Match length
                  123
% identity
                  43
NCBI Description
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
                  211611
Seq. No.
                  LIB3145-030-Q1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1840425
BLAST score
                  166
                  1.0e-11
E value *
Match length
                  44
% identity
                  68
                  (U36586) alcohol dehydrogenase [Vitis vinifera]
NCBI Description
                  211612
Seq. No.
Seq. ID
                  LIB3145-031-Q1-K1-A1
Method
                  BLASTX
                  g1408471
NCBI GI
BLAST score
                  535
E value
                  8.0e-55
Match length
                  120
% identity
                  82
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                  thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
Seq. No.
                  211613
Seq. ID
                  LIB3145-031-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4098129
BLAST score
                  331
                  2.0e-31
E value
Match length
                  64
% identity
                  95
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                  211614
                  LIB3145-031-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245113
BLAST score
                  251
E value
                  2.0e-21
                  133
Match length
% identity
                  43
NCBI Description
                  (Z97343) glycerol-3-phosphate permease homolog [Arabidopsis
                  thaliana]
```

Seq. No. 211615

Seq. ID LIB3145-031-Q1-K1-A4

Method BLASTX

```
q136636
NCBI GI
BLAST score
                   401
                   4.0e-39
E value
                   75
Match length
% identity
                   96
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi 1076424 pir __S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                   Conjugating Enzyme (E.C.\overline{6}.3.2.1\overline{9}) >\overline{g}i_29\overline{8}1894_pdb_2AAK_
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
                   211616
Seq. No.
                   LIB3145-031-Q1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q136057
                   472
BLAST score
                   2.0e-47
E value
                   123
Match length
                   76
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi 556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
                   211617
Seq. No.
                   LIB3145-031-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   q100226
NCBI GI
BLAST score
                    359
E value
                    3.0e - 34
                    141
Match length
% identity
                   hypothetical protein - tomato >gi_19275_emb_CAA78112_
NCBI Description
                    (Z12127) protein of unknown function [Lycopersicon
                    esculentum] >gi_445619_prf__1909366A Leu zipper protein
                    [Lycopersicon esculentum]
Seq. No.
                    211618
                    LIB3145-031-Q1-K1-A7
Seq. ID
                    BLASTX
Method
```

NCBI GI g2369766
BLAST score 696
E value 1.0e-73
Match length 133
% identity 95

NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No. 211619

Seq. ID LIB3145-031-Q1-K1-A8

MethodBLASTXNCBI GIg2245070BLAST score481E value2.0e-48



```
Match length
% identity
                  66
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  211620
Seq. ID
                  LIB3145-031-Q1-K1-B12
                  BLASTX
Method
NCBI GI
                  q3355626
BLAST score
                  532
E value
                  2.0e-54
Match length
                  120
% identity
                  82
                 (Y09204) histidinol-phosphate aminotransferase [Nicotiana
NCBI Description
                  tabacum]
                  211621
Seq. No.
                  LIB3145-031-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g1905785
NCBI GI
BLAST score
                  157
E value
                  1.0e-10
Match length
                  143
                  34
% identity
NCBI Description (Y10685) G/HBF-1 [Glycine max]
                  211622
Seq. No.
Seq. ID
                  LIB3145-031-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2842757
                  220
BLAST score
                  7.0e-18
E value
Match length
                  144
% identity
                  47
NCBI Description LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi 1806261 emb CAA41453
                  (X58577) DNA-binding protein; bZIP type [Petroselinum
                  crispum]
Seq. No.
                  211623
Seq. ID
                  LIB3145-031-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3702327
BLAST score
                  382
                  7.0e-37
E value
                  97
Match length
% identity
                  72
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  211624
Seq. No.
Seq. ID
                  LIB3145-031-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g3461835
```

Method BLASTX
NCBI GI g3461835
BLAST score 171
E value 4.0e-12
Match length 48
% identity 67

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana] >gi\_3927840 (AC005727) putative protein kinase [Arabidopsis



## thaliana]

```
211625
Seq. No.
                  LIB3145-031-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                  g2224933
NCBI GI
                  271
BLAST score
                  7.0e-24
E value
                  80
Match length
                  69
% identity
                  (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
NCBI Description
                  >gi_2224935 (AF004217) ethylene-insensitive3 [Arabidopsis
                  thaliana]
                   211626
Seq. No.
                  LIB3145-031-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                   g4559358
NCBI GI
                   355
BLAST score
                   8.0e-34
E value
                   84
Match length
                   80
% identity
                   (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   211627
Seq. No.
                   LIB3145-031-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g4150974
NCBI GI
                   347
BLAST score
                   5.0e-33
E value
                   92
Match length
                   68
% identity
                   (AJ224331) cystatin [Castanea sativa]
NCBI Description
                   211628
Seq. No.
                   LIB3145-031-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g3901014
NCBI GI
                   234
BLAST score
                   1.0e-19
E value
                   55
Match length
                   76
 % identity
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   211629
 Seq. No.
                   LIB3145-031-Q1-K1-C7
 Seq. ID
                   BLASTX
 Method
                   q3193292
 NCBI GI
 BLAST score
                    484
                   8.0e-49
 E value
                   139
 Match length
                    65
 % identity
                    (AF069298) similar to ATPases associated with various
 NCBI Description
                    cellular activites (Pfam: AAA.hmm, score: 230.91)
```

[Arabidopsis thaliana]

Seq. ID

Method



```
211630
Seq. No.
                  LIB3145-031-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g3264767
NCBI GI
                  291
BLAST score
                  3.0e-26
E value
                  120
Match length
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                  211631
Seq. No.
                  LIB3145-031-Q1-K1-D1
Seq. ID
                  BLASTX
Method
                  g2264369
NCBI GI
                  187
BLAST score
                  5.0e-14
E value
                  143
Match length
                   33
% identity
                  (AC002354) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   211632
Seq. No.
                  LIB3145-031-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g586797
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
                   107
Match length
                   33
% identity
NCBI Description HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III
                   211633
Seq. No.
                   LIB3145-031-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   g531829
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
                   78
Match length
                   42
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   211634
Seq. No.
                   LIB3145-031-Q1-K1-D6
 Seq. ID
                   BLASTX
Method
                   q3821280
NCBI GI
                   385
 BLAST score
                   9.0e-38
 E value
                   76
 Match length
 % identity
                    (AJ009952) asparagine synthetase type II [Phaseolus
 NCBI Description
                   vulgaris]
                   211635
 Seq. No.
```

29344

LIB3145-031-Q1-K1-D8

BLASTX



NCBI GI g1707015 BLAST score 255 E value 5.0e-22 Match length 59 % identity 92

NCBI Description (U78721) protein phosphatase 2C isolog [Arabidopsis

thaliana]

Seq. No. 211636

Seq. ID LIB3145-031-Q1-K1-E1

Method BLASTX
NCBI GI g3377797
BLAST score 501
E value 8.0e-51
Match length 125
% identity 78

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 211637

Seq. ID LIB3145-031-Q1-K1-E11

Method BLASTX
NCBI GI g3341694
BLAST score 591
E value 2.0e-61
Match length 140
% identity 81

NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No. 211638

Seq. ID LIB3145-031-Q1-K1-E2

Method BLASTX
NCBI GI g1170747
BLAST score 222
E value 2.0e-18
Match length 47
% identity 96

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >qi 167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >qi 167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 211639

Seq. ID LIB3145-031-Q1-K1-E5

Method BLASTN
NCBI GI g1053062
BLAST score 52
E value 3.0e-20
Match length 84
% identity 90

NCBI Description Solanum lycopersicum small GTP-binding protein (LeRab1A)

mRNA, complete cds

Seq. No. 211640



```
Seq. ID
                  LIB3145-031-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2213600
BLAST score
                  187
E value
                  5.0e-14
Match length
                  49
% identity
                  65
                  (AC000348) T7N9.20 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211641
                  LIB3145-031-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979553
BLAST score
                  212
E value
                  6.0e-17
Match length
                  113
% identity
                  42
NCBI Description
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  211642
                  LIB3145-031-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529686
BLAST score
                  250
E value
                  2.0e-21
Match length
                  95
% identity
                  52
NCBI Description
                  (AC002535) putative G-beta-repeat containing protein, 5'
                  partial [Arabidopsis thaliana]
Seq. No.
                  211643
                  LIB3145-031-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q128592
BLAST score
                  316
E value
                  4.0e-29
Match length
                  93
% identity
                  63
                  POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                  >gi 82190 pir S22495 pollen-specific protein precursor -
                  common tobacco >gi 19902 emb CAA43454 (X61146) pollen
                  specific protein [Nicotiana tabacum]
Seq. No.
                  211644
                  LIB3145-031-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263791
BLAST score
                  317
E value
                  3.0e-29
Match length
                  117
% identity
NCBI Description
                  (AC006068) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  211645
Seq. ID
                  LIB3145-031-Q1-K1-F8
Method
                  BLASTX
```

NCBI GI g3327957
BLAST score 155
E value 3.0e-10
Match length 52
% identity 54

NCBI Description (AF060490) TLS-associated protein TASR-2 [Mus musculus]

>gi 3327976 (AF067730) TLS-associated protein TASR-2 [Homo

sapiens]

Seq. No. 211646

Seq. ID LIB3145-031-Q1-K1-F9

Method BLASTX
NCBI GI g1916292
BLAST score 188
E value 4.0e-14
Match length 94
% identity 41

NCBI Description (U89793) allergen Amb a VI [Ambrosia artemisiifolia]

Seq. No. 211647

Seq. ID LIB3145-031-Q1-K1-G1

Method BLASTX
NCBI GI g3182981
BLAST score 271
E value 6.0e-24
Match length 72
% identity 75

NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj BAA13096

(D86494) diminuto [Pisum sativum]

Seq. No. 211648

Seq. ID LIB3145-031-Q1-K1-G11

Method BLASTX
NCBI GI g218157
BLAST score 368
E value 2.0e-54
Match length 134
% identity 85

NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 211649

Seq. ID LIB3145-031-Q1-K1-G2

Method BLASTX
NCBI GI g1729927
BLAST score 152
E value 2.0e-10
Match length 57
% identity 49

NCBI Description QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE

TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi\_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No. 211650

Seq. ID LIB3145-031-Q1-K1-G3

Method BLASTX NCBI GI g267069 BLAST score 611

```
E value
Match length
                  113
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  211651
Seq. No.
                  LIB3145-031-Q1-K1-G4
```

Seq. ID BLASTX Method g1170567 NCBI GI BLAST score 358 2.0e-34 E value 88 Match length 82

% identity

NCBI Description

Seq. No.

>gi\_602565\_emb\_CAA83565\_ (Z32632) INO1 [Citrus x paradisi]

211652

LIB3145-031-Q1-K1-G5 Seq. ID BLASTX Method g2253583 NCBI GI BLAST score 220 7.0e-18 E value

84 Match length 61 % identity

(U78721) hypothetical protein [Arabidopsis thaliana] NCBI Description

MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi\_1085960\_pir\_\_S52648 INO1 protein - Citrus paradisi

211653 Seq. No.

LIB3145-031-Q1-K1-G7 Seq. ID BLASTN

Method g3449334 NCBI GI BLAST score 56 1.0e-22 E value 140 Match length % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MYH9, complete sequence [Arabidopsis thaliana]

211654 Seq. No.

LIB3145-031-Q1-K1-G8 Seq. ID BLASTX Method

NCBI GI g1351271 557 BLAST score E value 2.0e-57 133 Match length % identity

TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) NCBI Description >gi 1084309\_pir\_\_S52032 triose-phosphate isomerase (EC

5.3.1.1) precursor, chloroplast - spinach >gi 806312 (L36387) triosephosphate isomerase, chloroplast isozyme

[Spinacia oleracea]

211655 Seq. No.

LIB3145-031-Q1-K1-H1 Seq. ID

```
Method BLASTX
NCBI GI g2959370
BLAST score 225
E value 2.0e-18
Match length 96
```

% identity 42
NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.

Seq. ID LIB3145-031-Q1-K1-H5

211656

Method BLASTX
NCBI GI g1702986
BLAST score 509
E value 9.0e-52
Match length 130
% identity 83

NCBI Description 14-3-3-LIKE PROTEIN GF14 CHI >gi\_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi\_1256534 (L09112) GF14

chi chain [Arabidopsis thaliana]

Seq. No. 211657

Seq. ID LIB3145-031-Q1-K1-H8

Method BLASTX
NCBI GI g461942
BLAST score 358
E value 3.0e-34
Match length 119
% identity 60

NCBI Description DNAJ PROTEIN HOMOLOG 1 (DNAJ-1) >gi\_479277\_pir\_\_S33312 dnaJ

protein - leek (fragment) >gi\_16087\_emb\_CAA49211\_ (X69436)
DNA J protein [Allium porrum] >gi\_447267\_prf\_\_1914140A DnaJ

protein [Allium porrum]

Seq. No. 211658

Seq. ID LIB3145-032-Q1-K1-A6

Method BLASTX
NCBI GI g505100
BLAST score 240
E value 2.0e-20
Match length 77
% identity 58

NCBI Description (D31886) KIAA0066 [Homo sapiens]

Seq. No. 211659

Seq. ID LIB3145-032-Q1-K1-A7

Method BLASTN
NCBI GI g1217627
BLAST score 102
E value 1.0e-50
Match length 113
% identity 98

NCBI Description G.hinsutum mRNA for stearoyl-acyl-carrier protein

desaturase

Seq. No. 211660

Seq. ID LIB3145-032-Q1-K1-B11

Method BLASTX

```
g320596
NCBI GI
BLAST score
                  314
                  5.0e-29
E value
                  76
Match length
                  86
% identity
NCBI Description floral binding protein 2 - garden petunia
                  211661
Seq. No.
                  LIB3145-032-Q1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3746940
                  408
BLAST score
                   3.0e-40
E value
                   90
Match length
% identity
NCBI Description (AF091810) actin 3 [Anemia phyllitidis]
                   211662
Seq. No.
                   LIB3145-032-Q1-K1-B6
Seq. ID
                   BLASTX
Method
                   q2695925
NCBI GI
                   206
BLAST score
                   2.0e-16
E value
                   48
Match length
                   77
% identity
                   (AJ222776) hypothetical protein [Hordeum vulgare]
NCBI Description
                   211663
Seq. No.
                   LIB3145-032-Q1-K1-B8
Seq. ID
                   BLASTX
Method
                   g4115377
NCBI GI
                   430
BLAST score
                   1.0e-42
E value
Match length
                   104
                   78
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   211664
Seq. No.
                   LIB3145-032-Q1-K1-B9
Seq. ID
Method
                   BLASTX
                   q4580461
NCBI GI
                   357
BLAST score
                   5.0e-34
E value
                   122
Match length
 % identity
                   (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   211665
 Seq. No.
                   LIB3145-032-Q1-K1-C11
 Seq. ID
 Method
                   BLASTX
                   q3142297
 NCBI GI
                   356
 BLAST score
                   6.0e-34
 E value
                   111
 Match length
 % identity
                    64
                    (AC002411) Contains similarity to serine/threonine protein
 NCBI Description
                   phosphatase gb_X83099 from S. cerevisiae. [Arabidopsis
```



```
thaliana]
                  211666
Seq. No.
                  LIB3145-032-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122070
BLAST score
                  160
E value
                   5.0e-11
                  93
Match length
                   34
% identity
                  ELONGATION FACTOR 1-ALPHA 2 (EF-1-ALPHA-2) >gi_886061
NCBI Description
                   (U26267) translation elongation factor EF-lalpha [Euplotes
                   crassus]
                   211667
Seq. No.
                  LIB3145-032-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3056595
BLAST score
                   251
E value
                   1.0e-21
Match length
                   62
                   82
% identity
NCBI Description
                  (AC004255) T1F9.16 [Arabidopsis thaliana]
Seq. No.
                   211668
Seq. ID
                   LIB3145-032-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   g3540196
BLAST score
                   439
                   1.0e-43
E value
Match length
                   115
% identity
                   64
                   (AC004260) Putative amp-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   211669
Seq. ID
                   LIB3145-032-Q1-K1-C9
Method
                   BLASTX
```

NCBI GI q224293 BLAST score 392 4.0e-38 E value Match length 83 94 % identity

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 211670

LIB3145-032-Q1-K1-D10 Seq. ID

Method BLASTX NCBI GI g3522943 BLAST score 165 5.0e-17 E value Match length 108 17 % identity

(AC004411) putative p-glycoprotein [Arabidopsis thaliana] NCBI Description

Seq. No. 211671

LIB3145-032-Q1-K1-D2 Seq. ID

Seq. No.

Seq. ID

211676

LIB3145-032-Q1-K1-E9



```
Method
NCBI GI
                  g3687243
BLAST score
                  245
E value
                   6.0e-21
Match length
                  61
                  79
% identity
                  (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
Seq. No.
                  211672
                  LIB3145-032-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3901014
BLAST score
                  214
                  2.0e-17
E value
Match length
                  53
% identity
                  66
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
Seq. No.
                  211673
                  LIB3145-032-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4090259
BLAST score
                  180
E value
                  3.0e-13
Match length
                  46
% identity
                  72
                  (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga
NCBI Description
                  menziesii]
Seq. No.
                  211674
Seq. ID
                  LIB3145-032-Q1-K1-E11
Method
                  BLASTX
                  q3746059
NCBI GI
BLAST score
                  290
E value
                  8.0e-30
Match length
                  109
% identity
                   67
NCBI Description
                  (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
                  thaliana] >gi 4432812 gb AAD20662 (AC006593) putative
                  cysteinyl-tRNA synthetase [Arabidopsis thaliana]
                  211675
Seq. No.
                  LIB3145-032-Q1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g542200
BLAST score
                  361
E value
                  1.0e-34
Match length
                  110
% identity
NCBI Description
                  hypothetical protein - garden asparagus
                  >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
```

```
Method
                  q3912988
NCBI GI
                  468
BLAST score
                  4.0e-47
E value
                  105
Match length
                  90
% identity
NCBI Description FLORAL HOMEOTIC PROTEIN AGL9 >gi_2345158 (AF015552) AGL9
                  [Arabidopsis thaliana] >gi_2829878 (AC002396) AGL9
                  [Arabidopsis thaliana]
                  211677
Seq. No.
                  LIB3145-032-Q1-K1-F2
Seq. ID
                  BLASTX
```

Method BLASTX
NCBI GI g2827641
BLAST score 205
E value 3.0e-16
Match length 97
% identity 43

NCBI Description (AL021636) Cytochrome P450-like protein [Arabidopsis

thaliana]

 Seq. No.
 211678

 Seq. ID
 LIB3145-032-Q1-K1-F3

 Method
 BLASTN

 NCBI GI
 g3821780

 BLAST score
 33

BLAST score 33 E value 4.0e-09 Match length 33 % identity 58

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 211679 Seq. ID LIB3145-032-Q1-K1-F7

Method BLASTX
NCBI GI G1220196

NCBI GI g1220196 BLAST score 526 E value 7.0e-54 Match length 117 % identity 81

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 211680

Seq. ID LIB3145-032-Q1-K1-F9

Method BLASTX
NCBI GI g4510342
BLAST score 465
E value 8.0e-47
Match length 102
% identity 83

NCBI Description (AC006921) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 211681

Seq. ID LIB3145-032-Q1-K1-G2

Method BLASTX
NCBI GI g3281853
BLAST score 336



```
1.0e-31
E value
Match length
                   104
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  211682
Seq. No.
                  LIB3145-032-Q1-K1-G9
Seq. ID
                   BLASTX
Method
                   q4263695
NCBI GI
                   197
BLAST score
                   2.0e-15
E value
                   103
Match length
% identity
                  (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                   thaliana]
                   211683
Seq. No.
                   LIB3145-032-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   g2244749
NCBI GI
                   389
BLAST score
                   6.0e-38
E value
                   98
Match length
                   79
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                   211684
Seq. No.
                   LIB3145-032-Q1-K1-H4
Seq. ID
                   BLASTX
Method
                   q3264769
NCBI GI
                   378
BLAST score
                   4.0e-51
E value
                   123
Match length
                   56
% identity
                   (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                   armeniaca]
                   211685
 Seq. No.
                   LIB3145-032-Q1-K1-H5
 Seq. ID
 Method
                   BLASTX
                   q3810596
NCBI GI
                   97
BLAST score
                   3.0e-10
 E value
                   114
Match length
 % identity
                   (AC005398) reverse-transcriptase-like protein [Arabidopsis
 NCBI Description
                   thaliana]
                    211686
 Seq. No.
                   LIB3145-032-Q1-K1-H9
 Seq. ID
 Method
                   BLASTX
                    g3668089
 NCBI GI
 BLAST score
                    174
                    1.0e-12
 E value
 Match length
                    71
                    45
 % identity
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
```



```
211687
Seq. No.
                  LIB3145-033-Q1-K1-A1
Seq. ID
                  BLASTX
Method
                  q1420887
NCBI GI
                  148
BLAST score
                  2.0e-09
E value
                  65
Match length
                  43
% identity
                  (U34334) non-specific lipid transfer-like protein
NCBI Description
                  [Phaseolus vulgaris]
                  211688
Seq. No.
                  LIB3145-033-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                  q4417271
NCBI GI
                  654
BLAST score
                  8.0e-69
E value
                  132
Match length
                   89
% identity
NCBI Description (AC007019) putative cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
                   211689
Seq. No.
                   LIB3145-033-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   q2506275
NCBI GI
                   331
BLAST score
                   5.0e-31
E value
                   94
Match length
                   69
% identity
NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
                   211690
Seq. No.
                   LIB3145-033-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                   q2511586
NCBI GI
                   458
BLAST score
                   6.0e - 46
E value
Match length
                   97
                   89
 % identity
                   (Y13182) multicatalytic endopeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   211691
 Seq. No.
                   LIB3145-033-Q1-K1-B8
 Seq. ID
                   BLASTX
 Method
                   q3513727
 NCBI GI
 BLAST score
                   203
                    6.0e-16
 E value
 Match length
                   55
                   73
 % identity
                    (AF080118) contains similarity to TPR domains (Pfam:
 NCBI Description
                    TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                    kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                    thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
```

protein [Arabidopsis thaliana]



```
Seq. No.
                  211692
Seq. ID
                  LIB3145-033-Q1-K1-C1
                  BLASTX
Method
NCBI GI
                  g1477428
BLAST score
                  466
                  8.0e-47
E value
                  90
Match length
% identity
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
                  211693
Seq. No.
Seq. ID
                  LIB3145-033-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q829290
BLAST score
                  236
E value
                  6.0e-20
Match length
                  90
% identity
                  59
                  (X14315) chalcone synthase [Sinapis alba]
NCBI Description
                  >gi_226869_prf__1609233B chalcone synthase 1 [Sinapis alba]
Seq. No.
                  211694
                  LIB3145-033-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g4096662
NCBI GI
BLAST score
                  408
E value
                  4.0e-40
Match length
                  89
% identity
                  91
                  (U35026) Rab1-like small GTP-binding protein [Petunia x
NCBI Description
                  hybrida]
Seq. No.
                  211695
Seq. ID
                  LIB3145-033-Q1-K1-C12
Method
                  BLASTN
NCBI GI
                  g2687434
BLAST score
                   90
E value
                  1.0e-43
Match length
                  118
                   94
% identity
NCBI Description
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
                  partial sequence
Seq. No.
                   211696
Seq. ID
                  LIB3145-033-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2495155
BLAST score
                  239
                   2.0e-20
E value
Match length
                  80
                   62
% identity
                  GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR)
NCBI Description
                  >gi_1694926_dbj_BAA08910_ (D50407) glutamyl-tRNA reductase
```

Seq. No. 211697

[Cucumis sativus]

```
LIB3145-033-Q1-K1-D11
Seq. ID
Method
                  BLASTX
                  g3152613
NCBI GI
BLAST score
                  198
E value
                  2.0e-15
Match length
                  105
% identity
                  43
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211698
                  LIB3145-033-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g4454032
NCBI GI
BLAST score
                  248
E value
                  3.0e-21
Match length
                  115
% identity
                  45
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
                  211699
Seq. No.
                  LIB3145-033-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703143
BLAST score
                  289
                  1.0e-31
E value
Match length
                  112
% identity
                  65
NCBI Description
                  ACTIN-LIKE PROTEIN 3 > gi 881635 (U29610) Arp3 [Acanthamoeba
                  castellanii]
                  211700
Seq. No.
Seq. ID
                  LIB3145-033-Q1-K1-E12
Method
                  BLASTX
                  g3860247
NCBI GI
BLAST score
                  586
                  7.0e-61
E value
Match length
                  130
% identity
                  86
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211701
Seq. ID
                  LIB3145-033-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2351097
BLAST score
                  187
E value
                  5.0e-14
Match length
                  44
                  80
% identity
NCBI Description
                 (AB006810) ATMRK1 [Arabidopsis thaliana]
```

Seq. No. 211702

Seq. ID LIB3145-033-Q1-K1-F10

Method BLASTX
NCBI GI g3426038
BLAST score 375
E value 3.0e-36
Match length 99

Match length

47



```
% identity
NCBI Description
                  (AC005168) unknown protein [Arabidopsis thaliana]
                  211703
Seq. No.
Seq. ID
                  LIB3145-033-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q2244910
BLAST score
                  153
                  2.0e-10
E value
Match length
                  34
% identity
NCBI Description
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                  211704
Seq. ID
                  LIB3145-033-Q1-K1-F12
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  38
                  5.0e-12
E value
Match length
                  230
                  79
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  211705
                  LIB3145-033-Q1-K1-F2
Seq. ID
Method
                  BLASTX
                  g2464880
NCBI GI
BLAST score
                  210
                  8.0e-17
E value
Match length
                  82
                  49
% identity
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                  211706
Seq. ID
                  LIB3145-033-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g82426
BLAST score
                  580
E value
                  4.0e-60
Match length
                  117
% identity
                  46
NCBI Description
                  ubiquitin precursor - barley (fragment)
                  >gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
Seq. No.
                  211707
Seq. ID
                  LIB3145-033-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3915089
BLAST score
                  221
                  5.0e-18
E value
```

% identity 89
NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi\_2144269\_pir\_\_JC5129 trans-cinnamate 4-monooxygenase (EC



1.14.13.11) A - Populus kitækamiensis >gi\_1139561\_dbj\_BAA11579\_ (D82815) cinnamic acid 4-hydroxylase [Populus kitakamiensis] >gi\_1777370\_dbj\_BAA11576 (D82812) cinnamic acid

4-hydroxylase [Populus kitakamiensis]

Seq. No. 211708

Seq. ID LIB3145-033-Q1-K1-G10

Method BLASTX
NCBI GI g3096935
BLAST score 199
E value 1.0e-15
Match length 55
% identity 75

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 211709

Seq. ID LIB3145-033-Q1-K1-H5

Method BLASTX
NCBI GI g167367
BLAST score 382
E value 5.0e-37
Match length 92
% identity 80

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 211710

Seq. ID LIB3145-034-Q1-K1-A11

Method BLASTX
NCBI GI g4105772
BLAST score 282
E value 4.0e-25
Match length 64
% identity 38

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 211711

Seq. ID LIB3145-034-Q1-K1-A3

Method BLASTX
NCBI GI g114193
BLAST score 641
E value 3.0e-67
Match length 126
% identity 96

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP

SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 1) >gi 170225 (M64261)

3-deoxy-D-arabino-heptulosonate 7-phosphate synthase

[Nicotiana tabacum] >gi\_228697\_prf\_\_1808327A

deoxyheptulosonate phosphate synthase [Nicotiana tabacum]

Seq. No. 211712

Seq. ID LIB3145-034-Q1-K1-A4

Method BLASTX NCBI GI g3021483 BLAST score 147

```
E value 1.0e-09 Match length 42 74
```

NCBI Description (AJ224931) histone H2B-2 [Lycopersicon esculentum]

Seq. No. 211713

Seq. ID LIB3145-034-Q1-K1-A8

Method BLASTX
NCBI GI g531829
BLAST score 205
E value 4.0e-16
Match length 67
% identity 60

NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector

pSport1]

Seq. No. 211714

Seq. ID LIB3145-034-Q1-K1-A9

Method BLASTX
NCBI GI g2832643
BLAST score 263
E value 6.0e-23
Match length 112
% identity 52

NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No. 211715

Seq. ID LIB3145-034-Q1-K1-B1

Method BLASTX
NCBI GI g1814403
BLAST score 303
E value 1.0e-27
Match length 107
% identity 62

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 211716

Seq. ID LIB3145-034-Q1-K1-B2

Method BLASTX
NCBI GI g2738248
BLAST score 587
E value 5.0e-61
Match length 133
% identity 87

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No. 211717

Seq. ID LIB3145-034-Q1-K1-B3

Method BLASTX
NCBI GI g464621
BLAST score 429
E value 2.0e-42
Match length 117
% identity 71

NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi\_280374\_pir\_\_S28586



ribosomal protein ML16 - common ice plant >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 211718

Seq. ID LIB3145-034-Q1-K1-B7

Method BLASTX
NCBI GI g1168192
BLAST score 257
E value 2.0e-22
Match length 79
% identity 67

NCBI Description 14-3-3-LIKE PROTEIN B (VFA-1433B) >gi 1076543\_pir\_\_S52900

14-3-3 brain protein homolog - fava bean

>gi 695767 emb CAA88416 (Z48505) 14-3-3 brain protein

homolog [Vicia faba]

Seq. No. 211719

Seq. ID LIB3145-034-Q1-K1-B8

Method BLASTX
NCBI GI g1488647
BLAST score 293
E value 6.0e-37
Match length 114
% identity 71

NCBI Description (X99937) RNA helicase [Spinacia oleracea]

Seq. No. 211720

Seq. ID LIB3145-034-Q1-K1-B9

Method BLASTX
NCBI GI g4490937
BLAST score 271
E value 7.0e-24
Match length 131
% identity 31

NCBI Description (AJ132261) hypothetical helicase K12H4.8-like protein [Homo

sapiens]

Seq. No. 211721

Seq. ID LIB3145-034-Q1-K1-C1

Method BLASTX
NCBI GI g4263712
BLAST score 282
E value 4.0e-25
Match length 72
% identity 71

NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis

thaliana]

Seq. No. 211722

Seq. ID LIB3145-034-Q1-K1-C10

Method BLASTX
NCBI GI g2245125
BLAST score 305
E value 6.0e-28
Match length 95
% identity 63



```
(Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  211723
Seq. No.
Seq. ID
                  LIB3145-034-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3763932
BLAST score
                  227
E value
                  6.0e-19
Match length
                  85
% identity
                  55
                  (AC004450) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  211724
Seq. No.
                  LIB3145-034-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2995990
BLAST score
                  264
                  3.0e-23
E value
Match length
                  102
                  57
% identity
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
Seq. No.
                  211725
Seq. ID
                  LIB3145-034-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q3702327
BLAST score
                  323
E value
                  4.0e-30
                  102
Match length
                  59
% identity
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
                  211726
Seq. No.
Seq. ID
                  LIB3145-034-Q1-K1-C7
Method
                  BLASTX
                  g4263712
NCBI GI
BLAST score
                 291
                  3.0e-26
E value
Match length
                  72
                  72
% identity
NCBI Description
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
                  thaliana]
Seq. No.
                  211727
                  LIB3145-034-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708423
BLAST score
                  268
                  2.0e-23
E value
Match length
                  122
% identity
                  41
NCBI Description
                  ISOFLAVONE REDUCTASE HOMOLOG A622 >qi 507823 dbj BAA05866
```

Seq. No. 211728

(D28505) A622 [Nicotiana tabacum]

```
LIB3145-034-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583130
BLAST score
                  157
E value
                  2.0e-10
Match length
                  107
% identity
                   (AC002387) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  211729
Seq. No.
                  LIB3145-034-Q1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  38
                  6.0e-12
E value
Match length
                  102
                  84
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  211730
Seq. ID
                  LIB3145-034-Q1-K1-D8
Method
                  BLASTN
NCBI GI
                  g2687434
BLAST score
                  188
E value
                  1.0e-101
Match length
                  271
% identity
                   92
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  211731
Seq. ID
                  LIB3145-034-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1729927
BLAST score
                  354
E value
                  1.0e-33
Match length
                  126
                  54
% identity
NCBI Description
                  QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi 940182
                   (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]
                  211732
Seq. No.
Seq. ID
                  LIB3145-034-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1170714
BLAST score
                  295
```

1.0e-26 E value Match length 65 82 % identity

NCBI Description SHAGGY RELATED PROTEIN KINASE ASK-GAMMA

>gi\_541850\_pir\_\_S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi 456509 emb CAA53180 (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi\_2059329\_emb\_CAA73247\_ (Y12710)

Seq. No.

211738



## shaggy-like kinase gamma [Arabidopsis thaliana]

```
211733
Seq. No.
Seq. ID
                  LIB3145-034-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q218157
BLAST score
                  475
E value
                  2.0e-54
Match length
                  129
% identity
                  84
                  (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
                  211734
Seq. No.
Seq. ID
                  LIB3145-034-Q1-K1-E4
Method
                  BLASTX
                  g2829894
NCBI GI
BLAST score
                  362
E value
                  1.0e-34
Match length
                  91
                  75
% identity
NCBI Description
                  (AC002311) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  211735
Seq. ID
                  LIB3145-034-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  q3024386
BLAST score
                  370
E value
                  2.0e-35
Match length
                  124
% identity
                  60
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                  >gi_2129500_pir__S52006 polygalacturonase - upland cotton
                  >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  211736
Seq. ID
                  LIB3145-034-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3281869
BLAST score
                  321
E value
                  9.0e-30
Match length
                  102
                  65
% identity
                  (AL031004) RSZp22 splicing factor [Arabidopsis thaliana]
NCBI Description
                  >gi 3435094 (AF033586) 9G8-like SR protein [Arabidopsis
                  thaliana]
                  211737
Seq. No.
Seq. ID
                  LIB3145-034-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q2584806
BLAST score
                  597
E value
                  4.0e-62
Match length
                  129
% identity
                  81
NCBI Description
                  (Y15253) phospholipase C [Pisum sativum]
```

```
LIB3145-034-Q1-K1-F2
Seq. ID
                  BLASTX
Method
                  a2760326
NCBI GI
                  320
BLAST score
                  1.0e-29
E value
                  125
Match length
                  50
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                  211739
Seq. No.
                  LIB3145-034-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  q3912988
NCBI GI
                  253
BLAST score
                  8.0e-22
E value
                  82
Match length
                   66
% identity
NCBI Description FLORAL HOMEOTIC PROTEIN AGL9 >gi_2345158 (AF015552) AGL9
                   [Arabidopsis thaliana] >gi_2829878 (AC002396) AGL9
                   [Arabidopsis thaliana]
                   211740
Sea. No.
                   LIB3145-034-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                   g3912988
NCBI GI
                   418
BLAST score
                   4.0e-41
E value
                   84
Match length
                   96
% identity
                   FLORAL HOMEOTIC PROTEIN AGL9 >gi_2345158 (AF015552) AGL9
NCBI Description
                   [Arabidopsis thaliana] >gi 2829878 (AC002396) AGL9
                   [Arabidopsis thaliana]
                   211741
Seq. No.
                   LIB3145-034-Q1-K1-F7
 Seq. ID
                   BLASTX
Method
                   g133872
NCBI GI
                   414
 BLAST score
                   1.0e-40
 E value
                   122
 Match length
                   67
 % identity
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
 NCBI Description
                   >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                   spinach >gi 322404 pir A44121 small subunit ribosomal
                   protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                    (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi_170143 (M82923) chloroplast ribosomal protein S1
                    [Spinacia oleracea]
                   211742
 Seq. No.
                   LIB3145-034-Q1-K1-F9
 Seq. ID
```

Method BLASTX
NCBI GI g4467125
BLAST score 369
E value 2.0e-35
Match length 106
% identity 53

29365

.



(AL035538) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 211743

Seq. ID LIB3145-034-Q1-K1-G2

Method BLASTX NCBI GI g4415916 BLAST score 145 E value 4.0e-09 103 Match length % identity 30

(AC006282) putative pectin methylesterase [Arabidopsis NCBI Description

thaliana]

Seq. No. 211744

LIB3145-034-Q1-K1-G3 Seq. ID

Method BLASTX g729011 NCBI GI BLAST score 310 E value 2.0e-28 Match length 115 % identity 34

NCBI Description

CALMODULIN >gi\_1360745\_pir\_\_S58709 calmodulin - Neurospora crassa >gi\_5542\_emb\_CAA50271\_ (X70923) calmodulin [Neurospora crassa] >gi\_168767 (L02964) calmodulin [Neurospora crassa] >gi\_562117 (U15993) calmodulin [Neurospora crassa] >gi\_562117 (U15993) calmodulin [Colletotrichum trifolii] >qi 2654183 (AF034964)

calmodulin; CgCaM [Glomerella cingulata]

Seq. No. 211745

Seq. ID LIB3145-034-Q1-K1-G4

Method BLASTX NCBI GI g3183321 BLAST score 358 E value 4.0e - 34Match length 122 % identity 57

HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I NCBI Description

>gi 2330820 emb CAB11050 (Z98530) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 211746

Seq. ID LIB3145-034-Q1-K1-H3

Method BLASTX NCBI GI g1297359 BLAST score 483 E value 9.0e-49 Match length 131 % identity 71

NCBI Description (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]

Seq. No. 211747

Seq. ID LIB3145-034-Q1-K1-H6

Method BLASTX NCBI GI g3241945 BLAST score 376 E value 3.0e-36 Match length 95



% identity 65
NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 211748

Seq. ID LIB3145-035-Q1-K1-A1

Method BLASTX
NCBI GI g3184285
BLAST score 229
E value 5.0e-19
Match length 66
% identity 65

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No. 211749

Seq. ID LIB3145-035-Q1-K1-A2

Method BLASTX
NCBI GI g2244939
BLAST score 253
E value 7.0e-22
Match length 122
% identity 44

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 211750

Seq. ID LIB3145-035-Q1-K1-A4

Method BLASTX
NCBI GI g2924512
BLAST score 302
E value 1.0e-27
Match length 98
% identity 55

NCBI Description (AL022023) beta-galactosidase - like protein [Arabidopsis

thaliana]

Seq. No. 211751

Seq. ID LIB3145-035-Q1-K1-A8

Method BLASTX
NCBI GI g2262173
BLAST score 379
E value 1.0e-36
Match length 134
% identity 58

NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis

thaliana]

Seq. No. 211752

Seq. ID LIB3145-035-Q1-K1-B1

Method BLASTX
NCBI GI g3043430
BLAST score 188
E value 3.0e-14
Match length 91
% identity 49

NCBI Description (AJ005347) annexin [Cicer arietinum]

Seq. No. 211753

Seq. ID LIB3145-035-Q1-K1-B11



Method BLASTX NCBI GI g1169238 BLAST score 176 E value 1.0e-12 Match length 85 % identity 46

GLUTAMATE DECARBOXYLASE (GAD) >gi 1076648 pir A48767 NCBI Description qlutamate decarboxylase (EC 4.1.1.15), calmodulin-binding garden petunia >qi 294112 (L16797) glutamate decarboxylase

[Petunia hybrida] >gi 309680 (L16977) glutamate

decarboxylase [Petunia hybrida]

Seq. No.

211754 LIB3145-035-Q1-K1-B6 Seq. ID

Method BLASTX NCBI GI q401322 BLAST score 646 E value 8.0e-68 132 Match length % identity 97

VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description

SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic

subunit [Gossypium hirsutum]

Seq. No. 211755

LIB3145-035-Q1-K1-B7 Seq. ID

BLASTX Method NCBI GI g2244970 BLAST score 587 7.0e-61 E value 146 Match length 71 % identity

(Z97340) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi 2326365 emb CAA74765 (Y14423) putative cell wall

protein [Arabidopsis thaliana]

211756 Seq. No.

LIB3145-035-Q1-K1-C2 Seq. ID

BLASTN Method NCBI GI g1777666 BLAST score 71 E value 5.0e - 32Match length 135 88 % identity

NCBI Description Dudleya viscida 18S ribosomal RNA gene, partial sequence

211757 Seq. No.

LIB3145-035-Q1-K1-C3 Seq. ID

Method BLASTX NCBI GI g1345933 BLAST score 562 E value 5.0e-58 Match length 114 % identity 92

CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS) NCBI Description

>gi\_1084323\_pir\_\_S53007 citrate synthase - cucurbit >gi\_975633\_dbj\_BAA07328\_ (D38132) glyoxysomal citrate

% identity

NCBI Description

82



## synthase [Cucurbita sp.]

```
Seq. No.
                  211758
                  LIB3145-035-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024386
BLAST score
                  777
E value
                  4.0e-83
Match length
                  147
                  99
% identity
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                  >gi_2129500_pir__S52006 polygalacturonase - upland cotton
                  >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
                  211759
Seq. No.
                  LIB3145-035-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2959767
BLAST score
                  139
                  9.0e-09
E value
Match length
                  78
                  46
% identity
NCBI Description
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
                  211760
Seq. No.
Seq. ID
                  LIB3145-035-Q1-K1-D3
                  BLASTX
Method
NCBI GI
                  g3549672
BLAST score
                  362
E value
                  2.0e-34
                  133
Match length
                  58
% identity
                  (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
                  211761
Seq. No.
Seq. ID
                  LIB3145-035-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                  q2465434
BLAST score
                  478
E value
                  4.0e-48
                  109
Match length
                  83
% identity
NCBI Description
                  (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
                  211762
Seq. No.
                  LIB3145-035-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708236
BLAST score
                  579
E value
                  1.0e-60
Match length
                  136
```

HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)

>gi\_2129617\_pir\_\_JC4567 hydroxymethylglutaryl-CoA synthase



(EC 4.1.3.5) - Arabidopsis thaliana >gi 1143390 emb CAA58763\_ (X83882)

hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi\_1586548\_prf\_\_2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No. 211763

Seq. ID LIB3145-035-Q1-K1-E3

Méthod BLASTX
NCBI GI g1572681
BLAST score 290
E value 3.0e-26
Match length 108
% identity 53

NCBI Description (U69897) oligopeptidase B [Trypanosoma cruzi]

Seq. No. 211764

Seq. ID LIB3145-035-Q1-K1-E4

Method BLASTX
NCBI GI g2144271
BLAST score 492
E value 6.0e-50
Match length 102
% identity 92

NCBI Description trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus

kitakamiensis (fragment) >gi 1777372 dbj BAA11578 (D82814)

cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No. 211765

Seq. ID LIB3145-035-Q1-K1-E7

Method BLASTX
NCBI GI g401322
BLAST score 730
E value 1.0e-77
Match length 142
% identity 99

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic

subunit [Gossypium hirsutum]

Seq. No. 211766

Seq. ID LIB3145-035-Q1-K1-E8

Method BLASTX
NCBI GI g1710112
BLAST score 642
E value 2.0e-67
Match length 129
% identity 93

NCBI Description (U53864) PRH19 [Arabidopsis thaliana]

Seq. No. 211767

Seq. ID LIB3145-035-Q1-K1-E9

Method BLASTX
NCBI GI g2244785
BLAST score 174
E value 6.0e-13
Match length 49



% identity NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

211768 Seq. No.

Seq. ID LIB3145-035-Q1-K1-F1

Method BLASTX g2129826 NCBI GI BLAST score 580 4.0e-60 E value Match length 128 % identity 88

dynamin-like protein phragmoplastin 5 - soybean >gi\_1218004 NCBI Description

(U36430) SDL5A [Glycine max]

Seq. No. 211769

LIB3145-035-Q1-K1-F2 Seq. ID

BLASTX Method NCBI GI g2498464 BLAST score 176 1.0e-12 E value 60 Match length 60 % identity

28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF NCBI Description

ASSOCIATED PROTEIN) >gi\_1136584 (U41745) PDGF associated

protein [Homo sapiens] >gi\_1589642\_prf\_\_2211382B

platelet-derived growth factor-associated protein [Homo

sapiens]

Seq. No. 211770

LIB3145-035-Q1-K1-F7 Seq. ID

Method BLASTX NCBI GI g1703108 BLAST score 482 E value 1.0e-48 Match length 95 94 % identity

NCBI Description

ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis

thaliana]

211771 Seq. No.

Seq. ID LIB3145-035-Q1-K1-F8

Method BLASTX q3688123 NCBI GI BLAST score 526 9.0e-54E value Match length 123 % identity 80

NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum

Seq. No. 211772

LIB3145-035-Q1-K1-G1 Seq. ID

Method BLASTX NCBI GI g3915096

```
BLAST score
E value
                   4.0e-64
Match length
                   124
% identity
                   91
NCBI Description
                  211773
```

TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)

>gi 1574976 (U47293) trans-cinnamate 4-hydroxylase [Populus

tremuloides]

Seq. No. Seq. ID LIB3145-035-Q1-K1-G2 Method BLASTX NCBI GI g1657621 BLAST score 535 8.0e-55 E value

Match length 127 % identity 78

NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)

putative acyl-coA dehydrogenase [Arabidopsis thaliana]

211774 Seq. No.

LIB3145-035-Q1-K1-G4 Seq. ID

Method BLASTX NCBI GI g289920 BLAST score 635 E value 2.0e-66 Match length 130 % identity 93

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

Seq. No. 211775

Seq. ID LIB3145-035-Q1-K1-G5

Method BLASTX NCBI GI q3024126 BLAST score 502 6.0e-51 E value Match length 98 % identity 97

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_1655576\_emb\_CAA95856\_ (Z71271) S-adenosyl-L-methionine

synthetase I [Catharanthus roseus]

Seq. No. 211776

Seq. ID LIB3145-035-Q1-K1-H2

Method BLASTX NCBI GI g2944446 BLAST score 347 E value 7.0e-33 85 Match length % identity

NCBI Description (AF050756) cysteine endopeptidase precursor [Ricinus

communis]

Seq. No. 211777

LIB3145-035-Q1-K1-H3 Seq. ID



```
Method
                   BLASTX
NCBI GI
                   g2104681
BLAST score
                   207
                   1.0e-17
E value
Match length
                   118
% identity
                   54
NCBI Description
                  (X97907) transcription factor [Vicia faba]
Seq. No.
                   211778
Seq. ID
                   LIB3145-035-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3885515
BLAST score
                   427
E value
                   3.0e-42
Match length
                   99
% identity
                   81
                   (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                   sativa]
                   211779
Seq. No.
                   LIB3145-037-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406789
BLAST score
                   431
E value
                   1.0e-42
                   130
Match length
% identity
                   65
NCBI Description
                   (AC006532) putative glutamate decarboxylase [Arabidopsis
                   thalianal
                   211780
Seq. No.
Seq. ID
                   LIB3145-037-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3551245
BLAST score
                   155
E value
                   2.0e-10
Match length
                   66
                   48
% identity
                  (AB012702) P40-like protein [Daucus carota]
NCBI Description
Seq. No.
                   211781
Seq. ID
                   LIB3145-037-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g2244910
BLAST score
                   246
                   6.0e-21
E value
                   118
Match length
                   45
% identity
NCBI Description
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                   211782
Seq. ID
                   LIB3145-037-Q1-K1-A6
```

Method BLASTX NCBI GI q2290532 BLAST score 248 E value 3.0e-21Match length 90



```
% identity
NCBI Description
                  (U94748) AN11 [Petunia x hybrida]
Seq. No.
                  211783
Seq. ID
                  LIB3145-037-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q4455169
BLAST score
                  369
                  2.0e-35
E value
Match length
                  132
% identity
                  55
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  211784
                  LIB3145-037-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063396
BLAST score
                  504
                  3.0e-51
E value
Match length
                  113
% identity
                  83
NCBI Description (AB012947) vcCyP [Vicia faba]
                  211785
Seq. No.
                  LIB3145-037-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827992
BLAST score
                  406
E value
                  9.0e-40
Match length
                  119
% identity
                  60
NCBI Description (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
                  211786
Seq. No.
Seq. ID
                  LIB3145-037-Q1-K1-B2
Method
                  BLASTX
                  g3319343
NCBI GI
BLAST score
                  332
                  3.0e - 31
E value
Match length
                  82
% identity
                  68
NCBI Description
                  (AF077407) contains similarity to sugar transporters (Pfam:
                  sugar tr.hmm, score: 395.91) [Arabidopsis thaliana]
Seq. No.
                  211787
                  LIB3145-037-Q1-K1-B4
Seq. ID
Method
                  BLASTX
```

NCBI GI g4510363 BLAST score 539 E value 2.0e-55 Match length 112 % identity 86

NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 211788



```
LIB3145-037-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  q2880043
NCBI GI
                  379
BLAST score
                  1.0e-36
E value
                  132
Match length
                  55
% identity
                  (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                  hydrolase [Arabidopsis thaliana]
                  211789
Seq. No.
                  LIB3145-037-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                  g2832698
NCBI GI
                   275
BLAST score
                  2.0e-24
E value
                   98
Match length
                   58
% identity
                  (AL021713) starch synthase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   211790
Seq. No.
                   LIB3145-037-Q1-K1-C10
Seq. ID
                   BLASTX
Method
                   g4539351
NCBI GI
                   243
BLAST score
                   1.0e-20
E value
                   124
Match length
% identity
                   50
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   211791
Seq. No.
                   LIB3145-037-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g4574320
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
                   56
Match length
                   64
% identity
                   (AF117224) wound-induced protein WI12 [Mesembryanthemum
NCBI Description
                   crystallinum]
                   211792
 Seq. No.
                   LIB3145-037-Q1-K1-C7
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q3024386
 BLAST score
                   515
                   2.0e-52
 E value
                   132
 Match length
 % identity
                   POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
 NCBI Description
                   >gi 2129500 pir__S52006 polygalacturonase - upland cotton
                   >gi_606650 (U09717) polygalacturonase [Gossypium hirsutum]
                   211793
 Seq. No.
                   LIB3145-037-Q1-K1-C9
 Seq. ID
```

29375

BLASTX

Method

Seq. No.

Seq. ID



```
q3063396
NCBI GI
                  501
BLAST score
                  6.0e-51
E value
                  115
Match length
                  82
% identity
                 (AB012947) vcCyP [Vicia faba]
NCBI Description
                  211794
Seq. No.
                  LIB3145-037-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  g3834325
NCBI GI
                  408
BLAST score
                  3.0e-43
E value
                  130
Match length
% identity
                   (AC005679) Strong similarity to gb_AF067141 gamma-glutamyl
NCBI Description
                  hydrolase from Arabidopsis thaliana. ESTs gb_R83955,
                   gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and
                   gb AI00672 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   211795
                   LIB3145-037-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g1708995
NCBI GI
                   248
BLAST score
                   3.0e-21
E value
                   57
Match length
                   82
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_726030
                   (U17240) S-adenosylmethionine synthetase [Actinidia
                   chinensis]
                   211796
Seq. No.
                   LIB3145-037-Q1-K1-D3
Seq. ID
                   BLASTX
Method
                   g3915866
NCBI GI
                   607
BLAST score
                   3.0e-63
E value
                   138
Match length
                   80
 % identity
                   GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
NCBI Description
                   >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine
                   synthetase [Lupinus luteus]
                   211797
 Seq. No.
                   LIB3145-037-Q1-K1-D4
 Seq. ID
                   BLASTX
Method
                   g100200
 NCBI GI
                   361
 BLAST score
                   2.0e-34
 E value
                   101
Match length
 % identity
                   chlorophyll a/b-binding protein type I precursor - tomato
 NCBI Description
                   211798
```

LIB3145-037-Q1-K1-D5

```
Method
                   BLASTX
NCBI GI
                   g3257556
BLAST score
                   202
E value
                   8.0e-16
Match length
                   99
% identity
                   46
```

(AP000005) 494aa long hypothetical protein [Pyrococcus NCBI Description

horikoshii]

Seq. No. 211799

Seq. ID LIB3145-037-Q1-K1-D6

Method BLASTX NCBI GI q462195 BLAST score 369 E value 2.0e-35 Match length 78 % identity 91

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi 100682 pir S21636 GOS2 protein - rice

>gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]

>gi 3789950 (AF094774) translation initiation factor [Oryza

satīva]

Seq. No. 211800

LIB3145-037-Q1-K1-D9 Seq. ID

Method BLASTX NCBI GI g2367392 BLAST score 270 E value 9.0e-24 Match length 136 % identity 40

(U82513) random slug cDNA25 protein [Dictyostelium NCBI Description

discoideum]

Seq. No. 211801

Seq. ID LIB3145-037-Q1-K1-E10

Method BLASTX NCBI GI g4138583 BLAST score 458 E value 6.0e-46Match length 117 % identity 80

NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No.

211802

LIB3145-037-Q1-K1-E11 Seq. ID Method

BLASTX NCBI GI g2494244 BLAST score 179 E value 4.0e-13 Match length 127 % identity 32

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (ELONGATION FACTOR

TU) (EF-TU) >gi\_2119923\_pir\_\_D64340 translation elongation factor, EF-1 alpha - Methanococcus jannaschii >gi 1591042 (U67486) translation elongation factor EF-1, subunit alpha

[Methanococcus jannaschii]



```
211803
Seq. No.
Seq. ID
                  LIB3145-037-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q1931647
BLAST score
                  509
E value
                  8.0e-52
Match length
                  133
% identity
                  71
NCBI Description
                  (U95973) endomembrane protein EMP70 precusor isolog
                  [Arabidopsis thaliana]
                  211804
Seq. No.
Seq. ID
                  LIB3145-037-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2388689
BLAST score
                  213
E value
                  4.0e-17
Match length
                  75
% identity
                  65
NCBI Description (AF016633) GH1 protein [Glycine max]
Seq. No.
                  211805
Seq. ID
                  LIB3145-037-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3643602
BLAST score
                  307
E value
                  4.0e-28
Match length
                  112
% identity
                  58
                  (AC005395) putative tonoplast intrinsic protein
NCBI Description
                  [Arabidopsis thaliana]
                  211806
Seq. No.
Seq. ID
                  LIB3145-037-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1168518
BLAST score
                  551
E value
                  1.0e-56
Match length
                  135
% identity
                  73
NCBI Description
                  APURINIC ENDONUCLEASE-REDOX PROTEIN (DNA-(APURINIC OR
                  APYRIMIDINIC SITE) LYASE) >gi 472869 emb CAA54234 (X76912)
                  ARP protein [Arabidopsis thaliana]
Seq. No.
                  211807
                  LIB3145-037-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462762
BLAST score
                  294
```

Method BLASTX
NCBI GI g2462762
BLAST score 294
E value 1.0e-26
Match length 100
% identity 60

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 211808

```
Seq. ID
                  LIB3145-037-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  q974782
BLAST score
                  546
E value
                  3.0e-56
Match length
                  106
% identity
                  92
NCBI Description
                 (Z49150) cobalamine-independent methionine synthase
                  [Solenostemon scutellarioides]
Seq. No.
                  211809
Seq. ID
                  LIB3145-037-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3914131
BLAST score
                  169
E value
                  6.0e-12
Match length
                  95
% identity
                  37
NCBI Description
                 PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR
                  (LTP 2) (MAJOR POLLEN ALLERGEN PAR J 2.0102) (PAR J II) (P8
                  PROTEIN) >gi 1532056 emb CAA65122 (X95866) P8 protein
                  [Parietaria judaica]
Seq. No.
                  211810
Seq. ID
                  LIB3145-037-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2880049
BLAST score
                  296
E value
                  8.0e-27
Match length
                  118
% identity
                  55
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  211811
Seq. ID
                  LIB3145-037-Q1-K1-F9
                  BLASTX
Method
NCBI GI
                  g4580523
BLAST score
                  468
E value
                  5.0e-47
                  127
Match length
% identity
NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
Seq. No.
                  211812
                  LIB3145-037-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2465923
                  393
BLAST score
E value
                  3.0e-38
Match length
                  124
% identity
                  (AF024648) receptor-like serine/threonine kinase
NCBI Description
```

[Arabidopsis thaliana]

Seq. No. 211813

Seq. ID LIB3145-037-Q1-K1-G6

Method BLASTX

```
q4309727
NCBI GI
                  157
BLAST score
                  4.0e-11
E value
                  33
Match length
                  88
% identity
                 (AC006439) putative mitochondrial 60S ribosomal protein L6
NCBI Description
                  [Arabidopsis thaliana]
                  211814
Seq. No.
                  LIB3145-037-Q1-K1-G8
Seq. ID
                  BLASTX
Method
                  g548852
NCBI GI
                  349
BLAST score
                  5.0e-33
E value
                  82
Match length
                  78
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
```

 Seq. No.
 211815

 Seq. ID
 LIB3145-037-Q1-K1-G9

 Method
 BLASTX

 NCBI GI
 g2290532

 BLAST score
 257

 E value
 3.0e-22

Match length 90 % identity 59

NCBI Description (U94748) AN11 [Petunia x hybrida]

Seq. No. 211816

Seq. ID LIB3145-037-Q1-K1-H12

Method BLASTX
NCBI GI g3970652
BLAST score 390
E value 3.0e-44
Match length 114
% identity 78

NCBI Description (X77499) amino acid permease [Arabidopsis thaliana]

Seq. No. 211817

Seq. ID LIB3145-037-Q1-K1-H3

Method BLASTX
NCBI GI g3915826
BLAST score 415
E value 8.0e-41
Match length 124
% identity 61

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 211818

Seq. ID LIB3145-037-Q1-K1-H4

Method BLASTX
NCBI GI g2218152
BLAST score 653
E value 1.0e-68
Match length 130



% identity 91

NCBI Description (AF005279) type IIIa membrane protein cp-wap13 [Vigna

unguiculata]

Seq. No. 211819

Seq. ID LIB3145-037-Q1-K1-H6

Method BLASTX
NCBI GI 9730463
BLAST score 319
E value 2.0e-29
Match length 105
% identity 58

NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)

>gi\_630323\_pir\_\_S44069 ribosomal protein L35a.e.c15 - yeast

(Saccharomyces cerevisiae) >gi\_484241 (L23923) ribosomal

protein L37 [Saccharomyces cerevisiae]

>gi\_1420537\_emb\_CAA99454\_ (Z75142) ORF YOR234c

[Saccharomyces cerevisiae]

Seq. No. 211820

Seq. ID LIB3145-037-Q1-K1-H9

Method BLASTX
NCBI GI g322750
BLAST score 654
E value 8.0e-69
Match length 128
% identity 98

NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco

>gi\_170217 (M74100) ubiquitin fusion protein [Nicotiana

sylvestris]

Seq. No. 211821

Seq. ID LIB3145-038-Q1-K1-A1

Method BLASTX
NCBI GI g3126969
BLAST score 143
E value 6.0e-09
Match length 61
% identity 51

NCBI Description (AF061808) chalcone isomerase [Elaeagnus umbellata]

Seq. No. 211822

Seq. ID LIB3145-038-Q1-K1-A11

Method BLASTX
NCBI GI g3650033
BLAST score 167
E value 1.0e-11
Match length 128
% identity 38

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 211823

Seq. ID LIB3145-038-Q1-K1-A12

Method BLASTX
NCBI GI g1142619
BLAST score 310
E value 2.0e-28



Match length 74 % identity 86

NCBI Description (U18348) phaseolin G-box binding protein PG1 [Phaseolus

vulgaris]

Seq. No. 211824

Seq. ID LIB3145-038-Q1-K1-A3

Method BLASTX
NCBI GI g167367
BLAST score 291
E value 3.0e-26
Match length 56
% identity 100

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 211825

Seq. ID LIB3145-038-Q1-K1-A4

Method BLASTX
NCBI GI g1362003
BLAST score 532
E value 2.0e-54
Match length 136
% identity 81

NCBI Description protein phosphatase 2A B regulatory chain 55K - Arabidopsis

thaliana >gi\_710330 (U18129) 55 kDa B regulatory subunit of

phosphatase 2A [Arabidopsis thaliana]

Seg. No. 211826

Seq. ID LIB3145-038-Q1-K1-A6

Method BLASTX
NCBI GI g3552003
BLAST score 712
E value 1.0e-75
Match length 134
% identity 99

NCBI Description (AF085083) alcohol dehydrogenase A [Gossypium hirsutum]

>gi\_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi 3552007 (AF085085) alcohol dehydrogenase A

[Gossypium hirsutum] >gi 4140632 (AF090165) alcohol

dehydrogenase A [Gossypium hirsutum] >gi\_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140638 (AF090168) alcohol dehydrogenase A [Gossypium

hirsutum]

Seq. No. 211827

Seq. ID LIB3145-038-Q1-K1-A8

Method BLASTX
NCBI GI g2497486
BLAST score 186
E value 4.0e-25
Match length 68
% identity 93

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP

KINASE) >gi\_2121275 (AF000147) UMP/CMP kinase [Arabidopsis

thaliana]



```
Seq. No.
                  211828
                  LIB3145-038-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2497486
BLAST score
                  135
                  3.0e-17
E value
                  67
Match length
                  75
% identity
                  URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                  KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                  thaliana]
                  211829
Seq. No.
Seq. ID
                  LIB3145-038-Q1-K1-B1
Method
                  BLASTX
                  g2281330
NCBI GI
BLAST score
                  121
                  2.0e-11
E value
Match length
                  86
                  52
% identity
                  (U85646) putative pectate lyase Nt59 [Nicotiana tabacum]
NCBI Description
Seq. No.
                  211830
Seq. ID
                  LIB3145-038-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3218550
BLAST score
                   448
E value
                  1.0e-44
Match length
                  122
% identity
                  71
                  (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211831
Seq. ID
                  LIB3145-038-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4415915
BLAST score
                   228
                   8.0e-19
E value
Match length
                  111
                   40
% identity
NCBI Description
                   (AC006282) putative pectin methylesterase [Arabidopsis
                   thaliana]
Seq. No.
                   211832
                  LIB3145-038-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3738339
```

BLAST score 522 3.0e-53E value 118 Match length % identity 86

(AC005170) putative kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 211833

LIB3145-038-Q1-K1-B3 Seq. ID

Method BLASTX NCBI GI g461729

Seq. ID

Method

NCBI GI

BLASTX

g3334144



```
BLAST score
                  7.0e-40
E value
                  97
Match length
                  76
% identity
                  10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)
NCBI Description
                  >qi 2146744 pir__S65597 probable chaperonin, 10K -
                  Arabidopsis thaliana >gi_166662 (L02843) 10 kDa chaperonin
                  [Arabidopsis thaliana]
                  211834
Seq. No.
                  LIB3145-038-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q70644
                  521
BLAST score
                  3.0e-53
E value
                  104
Match length
                  19
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
                  211835
Seq. No.
                  LIB3145-038-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g3218550
NCBI GI
BLAST score
                   180
                   3.0e-13
E value
Match length
                   54
                   63
% identity
                   (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
NCBI Description
                   211836
Seq. No.
                   LIB3145-038-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   q732248
NCBI GI
BLAST score
                   173
E value
                   2.0e-12
Match length
                   75
% identity
                   47
                   HYPOTHETICAL PROTEIN IN PTB 5'REGION (ORF1)
NCBI Description
                   >gi 484992_pir__PN0619 hypothetical protein 100 -
                   Clostridium acetobutylicum (strain NCIMB 8052) (fragment)
                   >gi 144891 (L04468) putative; ORF1 [Clostridium
                   acetobutylicum]
                   211837
 Seq. No.
                   LIB3145-038-Q1-K1-B9
 Seq. ID
 Method
                   BLASTX
                   g2765366
 NCBI GI
                   197
 BLAST score
                   3.0e-15
E value
                   92
Match length
 % identity
                   47
                   (Y14038) putative Ole e 1 protein [Betula pendula]
 NCBI Description
                   211838
 Seq. No.
                   LIB3145-038-Q1-K1-C1
```



BLAST score 2.0e-56 E value Match length 133 80 % identity NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >gi\_1695698\_dbj\_BAA13181\_ (D86925) C-type cyclin [Oryza sativa] 211839 Seq. No. LIB3145-038-Q1-K1-C10 Seq. ID BLASTX Method g3914007 NCBI GI 625 BLAST score 2.0e-65 E value 132 Match length % identity 90 MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1848291 NCBI Description (U88087) LON protease homolog [Arabidopsis thaliana] 211840 Seq. No. LIB3145-038-Q1-K1-C4 Seq. ID BLASTX Method g4115925 NCBI GI 462 BLAST score 3.0e-46E value 102 Match length 45 % identity (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] NCBI Description >gi\_4539439\_emb\_CAB40027.1\_ (AL049523) RNA-binding protein [Arabidopsis thaliana] 211841 Seq. No. LIB3145-038-Q1-K1-C6 Seq. ID BLASTX Method g4559372 NCBI GI 348 BLAST score 6.0e-33 E value 86 Match length 76 % identity (AC006585) putative CONSTANS protein [Arabidopsis thaliana] NCBI Description 211842 Seq. No. LIB3145-038-Q1-K1-C7 Seq. ID BLASTX Method q3738297 NCBI GI BLAST score 225 2.0e-18 E value

115 Match length % identity

(AC005309) unknown protein [Arabidopsis thaliana] NCBI Description

211843 Seq. No.

LIB3145-038-Q1-K1-C8 Seq. ID

BLASTX Method g4249418 NCBI GI BLAST score 199 2.0e-15 E value

```
94
```

Match length 94 % identity 27

NCBI Description (AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H type domains), 5' partial [Arabidopsis thaliana]

Seq. No. 211844

Seq. ID LIB3145-038-Q1-K1-D1

Method BLASTX
NCBI GI g3859560
BLAST score 203
E value 6.0e-16
Match length 112
% identity 38

NCBI Description (AF098668) acyl-protein thioesterase [Homo sapiens]

Seq. No. 211845

Seq. ID LIB3145-038-Q1-K1-D11

Method BLASTX
NCBI GI g4454042
BLAST score 388
E value 1.0e-37
Match length 111
% identity 63

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 211846

Seq. ID LIB3145-038-Q1-K1-D6

Method BLASTX
NCBI GI g3182981
BLAST score 644
E value 1.0e-67
Match length 137
% identity 87

NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi\_1695692\_dbj\_BAA13096\_

(D86494) diminuto [Pisum sativum]

Seq. No. 211847

Seq. ID LIB3145-038-Q1-K1-D7

Method BLASTX
NCBI GI g3548802
BLAST score 267
E value 2.0e-23
Match length 98
% identity 52

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi\_4335769\_gb\_AAD17446\_ (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 211848

Seq. ID LIB3145-038-Q1-K1-D8

Method BLASTX
NCBI GI g114682
BLAST score 330
E value 8.0e-31
Match length 110
% identity 64

NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR

E value

Match length

NCBI Description

% identity

1.0e-57

thaliana]

116



(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi\_100471\_pir\_\_A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi\_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

```
211849
 Seg. No.
 Seq. ID
                   LIB3145-038-Q1-K1-E1
 Method
                   BLASTX
 NCBI GI
                   g3024385
 BLAST score
                   548
 E value
                   2.0e-56
 Match length
                   129
 % identity
                   75
 NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi 606652
                    (U09805) polygalacturonase [Gossypium barbadense]
 Seq. No.
                   211850
                   LIB3145-038-Q1-K1-E10
 Seq. ID
 Method
                   BLASTX
                   g3599491
 NCBI GI
BLAST score
                   564
                   3.0e-58
 E value
 Match length
                   134
 % identity
                   77
                   (AF085149) putative aminotransferase [Capsicum chinense]
 NCBI Description
 Seq. No.
                   211851
 Seq. ID
                   LIB3145-038-Q1-K1-E11
 Method
                   BLASTN
 NCBI GI
                   g668984
 BLAST score
                    40
 E value
                    4.0e-13
 Match length
                   126
 % identity
                   83
 NCBI Description S.tuberosum TYKY1 mRNA for NADH:ubiquinone oxidoreductase
 Seq. No.
                   211852
                   LIB3145-038-Q1-K1-E12
 Seg. ID
 Method
                   BLASTX
 NCBI GI
                   g2281330
 BLAST score
                   209
 E value
                   1.0e-16
 Match length
                   83
 % identity
                   51
 NCBI Description (U85646) putative pectate lyase Nt59 [Nicotiana tabacum]
 Seq. No.
                   211853
                   LIB3145-038-Q1-K1-E2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4510363
 BLAST score
                   559
```

29387

(AC007017) putative DNA-binding protein [Arabidopsis

NCBI Description



211854 Seq. No. LIB3145-038-Q1-K1-E5 Seq. ID BLASTX Method q1174613 NCBI GI 405 BLAST score 2.0e-39 E value 80 Match length 97 % identity 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 1) (TBP-1) >gi\_556560\_dbj\_BAA04614\_ (D17788) rice homologue of Tat binding protein [Oryza sativa] 211855 Seq. No. LIB3145-038-Q1-K1-F1 Seq. ID BLASTN Method g1777667 NCBI GI 62 BLAST score 2.0e-26 E value 66 Match length 98 % identity NCBI Description Eucryphia lucida 18S ribosomal RNA gene, partial sequence 211856 Seq. No. LIB3145-038-Q1-K1-F11 Seq. ID BLASTX Method g4508073 NCBI GI 411 BLAST score 3.0e-40 E value 106 Match length 70 % identity NCBI Description (AC005882) 43220 [Arabidopsis thaliana] 211857 Seq. No. LIB3145-038-Q1-K1-F12 Seq. ID BLASTN Method q404027 NCBI GI 49 BLAST score E value 2.0e-18 73 Match length 92 % identity Carthamus tinctorius (clone pCGN3264) oleoyl-acyl carrier NCBI Description protein thioesterase mRNA, complete cds 211858 Seq. No. LIB3145-038-Q1-K1-F4 Seq. ID BLASTX Method NCBI GI g2129842 174 BLAST score 2.0e-12 E value 53 Match length 58 % identity SE60 protein - soybean >gi 509769\_emb CAA79164\_ (Z18359)

29388

[Glycine max]

seed-specific low molecular weight sulfur-rich protein



```
211859
Seq. No.
                  LIB3145-038-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  q4107099
NCBI GI
                  390
BLAST score
                  6.0e-41
E value
                  111
Match length
% identity
                   (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                  >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                  thaliana]
                   211860
Seq. No.
                  LIB3145-038-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                   g2997684
NCBI GI
                   238
BLAST score
                   3.0e-20
E value
                   97
Match length
                   54
% identity
                   (AF053302) putative transcriptional co-activator
NCBI Description
                   [Arabidopsis thaliana]
                   211861
Seq. No.
                   LIB3145-038-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4098129
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   52
Match length
                   92
% identity
                   (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   211862
Seq. No.
                   LIB3145-038-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   q399940
NCBI GI
                   599
BLAST score
                   2.0e-62
E value
                   127
Match length
% identity
                   MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
NCBI Description
                   >gi_100004_pir__S25005 heat shock protein, 70K - kidney
                   bean >gi 22636_emb_CAA47345_ (X66874) 70 kDa heat shock
                   protein [Phaseolus vulgaris]
                   211863
Seq. No.
                   LIB3145-038-Q1-K1-G11
Seq. ID
Method
                   BLASTX
                   q2497702
NCBI GI
BLAST score
                   140
                   4.0e-11
E value
                   115
Match length
 % identity
                   39
                   OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
NCBI Description
```

>gi\_2121019\_pir\_\_I40710 outer membrane lipoprotein - Citrobacter freundii >gi\_717136 (U21727) lipocalin



95

87

Match length

% identity

## precursor [Citrobacter freundii]

```
211864
Seq. No.
                  LIB3145-038-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g2760326
NCBI GI
BLAST score
                  335
                  2.0e-31
E value
                  122
Match length
                  53
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                  211865
Seq. No.
                  LIB3145-038-Q1-K1-G7
Seq. ID
                  BLASTX
Method
                  g2961349
NCBI GI
                  374
BLAST score
                  6.0e-36
E value
                  132
Match length
% identity
                  52
                  (AL022140) LTR retrotransposon like protein [Arabidopsis
NCBI Description
                  thaliana]
                  211866
Seq. No.
                  LIB3145-038-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g2147966
NCBI GI
                  529
BLAST score
E value
                  4.0e-54
Match length
                   134
% identity
                  probable 1-acyl-sn-glycerol-3-phosphate acyltransferase -
NCBI Description
                   Limnanthes douglasii >gi 1067138 emb CAA88620 (Z48730)
                   1-acyl-sn-glycerol-3-phosphate acyltransferase (putative)
                   [Limnanthes douglasii]
Seq. No.
                   211867
                   LIB3145-038-Q1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914472
BLAST score
                   224
                   2.0e-18
E value
Match length
                   89
                   53
% identity
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                   >gi 322764 pir__S32021 photosystem II 10K protein - common
                   tobacco >gi 22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana
                   tabacum]
Seq. No.
                   211868
                   LIB3145-038-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   g2809385
NCBI GI
BLAST score
                   447
                   2.0e-44
E value
```

NCBI Description (AF024634) NADPH cytochrome P450 reductase [Petroselinum crispum]

Seq. No. 211869

Seq. ID LIB3145-038-Q1-K1-H4

Method BLASTX
NCBI GI g1346155
BLAST score 453
E value 6.0e-54
Match length 113
% identity 89

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi 481942 pir S40212 glycine

hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei

>gi\_437995\_emb\_CAA81078\_ (Z25859) glycine
hydroxymethyltransferase [Flaveria pringlei]

Seq. No. 211870

Seq. ID LIB3145-038-Q1-K1-H5

Method BLASTX
NCBI GI g4539292
BLAST score 452
E value 3.0e-45
Match length 96
% identity 86

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

Seq. No. 211871

Seq. ID LIB3145-038-Q1-K1-H7

Method BLASTX
NCBI GI 94432844
BLAST score 189
E value 3.0e-14
Match length 91
% identity 42

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 211872

Seq. ID LIB3145-038-Q1-K1-H8

Method BLASTX
NCBI GI g4097547
BLAST score 260
E value 1.0e-22
Match length 54
% identity 44

NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

Seq. No. 211873

Seq. ID LIB3145-038-Q1-K1-H9

Method BLASTX
NCBI GI g400650
BLAST score 200
E value 1.0e-15
Match length 96
% identity 43



NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX I-13KD-B) (CI-13KD-B) (B13) >qi 346535 pir S28244 NADH

I-13KD-B) (CI-13KD-B) (B13) >gi\_346535\_pir\_\_S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 -bovine >gi\_238\_emb\_CAA44903\_ (X63218) NADH dehydrogenase

was the same of the same

[Bos taurus]

Seq. No. 211874

Seq. ID LIB3145-039-Q1-K1-A10

Method BLASTN
NCBI GI g18058
BLAST score 312
E value 1.0e-175
Match length 362
% identity 97

% identity 97 NCBI Description Citrus limon cistron for 26S ribosomal RNA

Seq. No. 211875

Seq. ID LIB3145-039-Q1-K1-A11

Method BLASTX
NCBI GI g951427
BLAST score 475
E value 8.0e-48
Match length 134
% identity 67

NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus

communis]

Seq. No. 211876

Seq. ID LIB3145-039-Q1-K1-A12

Method BLASTX
NCBI GI g3024127
BLAST score 687
E value 1.0e-72
Match length 141
% identity 91

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi\_1655578\_emb\_CAA95857\_ (Z71272) S-adenosyl-L-methionine

 $synthetase \overline{2}$  [Catharanthus roseus]

Seq. No. 211877

Seq. ID LIB3145-039-Q1-K1-A2

Method BLASTX
NCBI GI g2842480
BLAST score 598
E value 3.0e-62
Match length 133
% identity 40

NCBI Description (AL021749) ADP, ATP carrier-like protein [Arabidopsis

thaliana]

Seq. No. 211878

Seq. ID LIB3145-039-Q1-K1-A6

MethodBLASTXNCBI GIg4469003BLAST score275E value2.0e-24

NCBI GI

BLAST score E value

Match length

% identity



```
Match length
                  52
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                  211879
Seq. No.
                  LIB3145-039-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g1168470
NCBI GI
                  166
BLAST score
                   1.0e-11
E value
                  79
Match length
                  52
% identity
                  PROTEIN KINASE APK1A >gi 282877 pir_S28615 protein kinase,
NCBI Description
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522)
                   protein tyrosine-serine-threonine kinase [Arabidopsis
                   thaliana]
                   211880
Seq. No.
                   LIB3145-039-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   g2662343
NCBI GI
                   278
BLAST score
                   7.0e-25
E value
                   60
Match length
                   92
% identity
                   (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   211881
Seq. No.
                   LIB3145-039-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g4544454
NCBI GI
                   375
BLAST score
                   4.0e-36
E value
                   98
Match length
                   72
% identity
                   (ACO06592) putative DNAJ protein [Arabidopsis thaliana]
NCBI Description
                   211882
Seq. No.
                   LIB3145-039-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   q3821280
NCBI GI
                   572
BLAST score
                   3.0e-59
E value
                   128
Match length
                   83
% identity
                   (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                   vulgaris]
                    211883
Seq. No.
                   LIB3145-039-Q1-K1-B5
 Seq. ID
                   BLASTN
Method
```

29393

q4469002

2.0e-18

49

102

7 è .



82

thaliana]

% identity

NCBI Description

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                  (ESSA project)
                  211884
Seq. No.
                  LIB3145-039-Q1-K1-B7
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3821780
BLAST score
                  36
                  7.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  211885
Seq. No.
                  LIB3145-039-Q1-K1-B8
Seq. ID
                  BLASTX
Method
                   g543187
NCBI GI
                   145
BLAST score
                   4.0e-09
E value
                   115
Match length
% identity
                   ankyrin, erythrocyte - mouse >gi_311817_emb_CAA48801_
NCBI Description
                   (X69063) erythroid ankyrin [Mus musculus]
Seq. No.
                   211886
                   LIB3145-039-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   q3821280
NCBI GI
BLAST score
                   181
                   2.0e-13
E value
                   79
Match length
                   44
% identity
                   (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                   vulgaris]
                   211887
Seq. No.
                   LIB3145-039-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g3021355
NCBI GI
BLAST score
                   529
                   4.0e-54
E value
                   117
Match length
                   83
 % identity
                   (AJ005081) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                   tetragonoloba]
                   211888
 Seq. No.
                   LIB3145-039-Q1-K1-C7
 Seq. ID
Method
                   BLASTX
                   g421826
 NCBI GI
                   166
 BLAST score
                   4.0e-12
 E value
                   34
Match length
```

29394

chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi 298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis

Seq. No.

Seq. ID

211894

LIB3145-039-Q1-K1-D9



```
211889
Seq. No.
                  LIB3145-039-Q1-K1-C8
Seq. ID
                  BLASTN
Method
                  g2829205
NCBI GI
                  130
BLAST score
                  7.0e-67
E value
                  382
Match length
                  17
% identity
NCBI Description Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
                  precursor (PRP) mRNA, complete cds
                  211890
Seq. No.
                  LIB3145-039-Q1-K1-C9
Seq. ID
Method
                  BLASTX
                  g289920
NCBI GI
                  596
BLAST score
                  1.0e-70
E value
                  136
Match length
                  97
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   211891
Seq. No.
                  LIB3145-039-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                   g1928981
NCBI GI
                   459
BLAST score
                   6.0e-46
E value
                   117
Match length
                   82
% identity
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   211892
Seq. No.
                   LIB3145-039-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3738325
BLAST score
                   398
                   9.0e-39
E value
Match length
                   112
                   72
% identity
                   (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                   thaliana]
                   211893
Seq. No.
                   LIB3145-039-Q1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512671
                   336
BLAST score
E value
                   2.0e-31
                   85
Match length
                   72
% identity
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
```

```
BLASTX
Method
                  q4103959
NCBI GI
BLAST score
                  178
                  6.0e-13
E value
                  126
Match length
% identity
                  22
NCBI Description (AF030033) calmodulin [Phaseolus vulgaris]
                  211895
Seq. No.
                  LIB3145-039-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1708422
                  172
BLAST score
                  4.0e-23
E value
                  100
Match length
% identity
                  63
                  ISOFLAVONE REDUCTASE HOMOLOG >gi 1030068 emb CAA63056_
NCBI Description
                   (X92075) NAD(P)H oxidoreductase, isoflavone reductase
                  homologue [Solanum tuberosum]
Seq. No.
                   211896
Seq. ID
                  LIB3145-039-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                   g3170548
BLAST score
                   167
E value
                   1.0e-11
Match length
                  86
                   37
% identity
NCBI Description (AF056116) unknown [Fugu rubripes]
                   211897
Seq. No.
Seq. ID
                   LIB3145-039-Q1-K1-E6
Method
                  BLASTN
                   q3821780
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   211898
Seq. No.
Seq. ID
                   LIB3145-039-Q1-K1-E7
Method
                   BLASTX
                   g4220521
NCBI GI
BLAST score
                   372
                   9.0e-36
E value
                   96
Match length
                   77
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                   211899
Seq. No.
Seq. ID
                   LIB3145-039-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   q3881978
BLAST score
                   174
```

29396

2.0e-12

42

E value Match length

Seq. No.

Seq. ID

211905

LIB3145-039-Q1-K1-G2



```
% identity
                  (Y11348) annexin-like protein [Medicago sativa]
NCBI Description
Seq. No.
                  211900
                  LIB3145-039-Q1-K1-F1
Seq. ID
                  BLASTX
Method
                  g3738339
NCBI GI
                  469
BLAST score
                  4.0e-47
E value
                  132
Match length
% identity
                  70
                  (AC005170) putative kinase [Arabidopsis thaliana]
NCBI Description
                  211901
Seq. No.
                  LIB3145-039-Q1-K1-F4
Seq. ID
Method
                  BLASTX
                  g1370192
NCBI GI
                  226
BLAST score
                  1.0e-18
E value
                  66
Match length
% identity
                  67
                  (Z73945) RAB8B [Lotus japonicus]
NCBI Description
                  211902
Seq. No.
                  LIB3145-039-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  q2529665
NCBI GI
BLAST score
                  585
E value
                  1.0e-60
                  129
Match length
% identity
                  88
                   (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                  thaliana]
                  211903
Seq. No.
                  LIB3145-039-Q1-K1-G1
Seq. ID
Method
                  BLASTX
                   g2459417
NCBI GI
BLAST score
                   510
                   6.0e-52
E value
Match length
                   133
% identity
                   74
                  (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   211904
                   LIB3145-039-Q1-K1-G10
Seq. ID
Method
                   BLASTX
                   g3860249
NCBI GI
                   246
BLAST score
E value
                   6.0e-21
                   90
Match length
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
```



```
BLASTX
Method
NCBI GI
                   g3775995
BLAST score
                   487
                   3.0e-49
E value
Match length
                   130
                   69
% identity
                  (AJ010461) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   211906
Seq. No.
                  LIB3145-039-Q1-K1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3687405
BLAST score
                   47
                   2.0e-17
E value
                   63
Match length
                   94
% identity
NCBI Description Lycopersicon esculentum mRNA for hypothetical protein
Seq. No.
                   211907
                   LIB3145-039-Q1-K1-G6
Seq. ID
Method
                   BLASTX
                                  3.
NCBI GI
                   q4544386
BLAST score
                   422
E value
                   1.0e-41
                   133
Match length
                   69
% identity
                   (AC007047) putative cell division control protein
NCBI Description
                   [Arabidopsis thaliana]
                   211908
Seq. No.
                   LIB3145-039-Q1-K1-G9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1335861
                   48
BLAST score
E value
                   3.0e-18
                   100
Match length
                   87
% identity
                  Glycine max clathrin heavy chain mRNA, complete cds
NCBI Description
                   211909
Seq. No.
                   LIB3145-039-Q1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4160300
BLAST score
                   152
                   6.0e-10
E value
                   59
Match length
                   47
% identity
                   (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]
NCBI Description
                   211910
Seq. No.
                   LIB3145-039-Q1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4566614
                   225
BLAST score
```

29398

1.0e-18

86

51

E value Match length

% identity



NCBI Description (AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No. 211911

Seq. ID LIB3145-039-Q1-K1-H2

Method BLASTX
NCBI GI g3355468
BLAST score 531
E value 2.0e-54
Match length 123
% identity 89

NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis

thaliana]

Seq. No. 211912

Seq. ID LIB3145-039-Q1-K1-H4

Method BLASTX
NCBI GI g1351359
BLAST score 291
E value 3.0e-26
Match length 69
% identity 71

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN

(MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi\_1071788\_pir\_\_S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein

- potato >gi\_488712\_emb\_CAA55860\_ (X79273)

ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No. 211913

Seq. ID LIB3145-039-Q1-K1-H8

Method BLASTX
NCBI GI g2961357
BLAST score 224
E value 2.0e-18
Match length 134
% identity 36

NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No. 211914

Seq. ID LIB3145-040-Q1-K1-A11

Method BLASTX
NCBI GI g549063
BLAST score 470
E value 3.0e-47
Match length 133
% identity 70

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 211915

Seq. ID LIB3145-040-Q1-K1-A12

Method BLASTX
NCBI GI g3763933
BLAST score 329
E value 1.0e-30

```
Match length
                  74
% identity
                  (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211916
Seq. No.
                  LIB3145-040-Q1-K1-A2
Seq. ID
                  BLASTX
Method
                  q1173218
NCBI GI
                                                         200
BLAST score
                  511
                  5.0e-52
E value
                  100
Match length
% identity
                  97
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  211917
                  LIB3145-040-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g2500354
NCBI GI
BLAST score
                  636
E value
                  1.0e-66
Match length
                  121
                  97
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
                   (AB001891) QM family protein [Solanum melongena]
                  211918
Seq. No.
                  LIB3145-040-Q1-K1-A6
Seq. ID
                  BLASTX
Method
                  g2289003
NCBI GI
BLAST score
                  259
                  2.0e-22
E value
Match length
                  133
% identity
                   61
                  (ACO02335) membrane transporter D1 isolog [Arabidopsis
NCBI Description
                  thaliana]
                  211919
Seq. No.
Seq. ID
                  LIB3145-040-Q1-K1-A7
                  BLASTX
Method
                   g2335098
NCBI GI
                   175
BLAST score
E value
                   1.0e-12
Match length
                   82
                   41
% identity
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
                   211920
Seq. No.
Seq. ID
                   LIB3145-040-Q1-K1-B1
```

Method BLASTX
NCBI GI g4325371
BLAST score 356
E value 6.0e-34
Match length 97
% identity 69

NCBI Description (AF128396) contains similarity to Medicago truncatula N7





## protein (GB:Y17613) [Arabidopsis thaliana]

```
Seq. No.
                  211921
                  LIB3145-040-Q1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  167
E value
                  1.0e-11
                  37
Match length
                  76
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  211922
Seq. No.
Seq. ID
                  LIB3145-040-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4115922
BLAST score
                  591
                  2.0e-61
E value
                  128
Match length
% identity
                  85
                   (AF118222) contains similarity to ubiquitin
NCBI Description
                  carboxyl-terminal hydrolase family 2 (Pfam: PF00443,
                  score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0
                  E=5.2e-08, N=1) [Arabidopsis thaliana]
Seq. No.
                  211923
                  LIB3145-040-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  393
E value
                  1.0e-38
Match length
                  77
% identity
                   94
NCBI Description
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                            . . .
                  211924
Seq. No.
Seq. ID
                  LIB3145-040-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                   g1399380
BLAST score
                   360
                   2.0e-34
E value
Match length
                  79
% identity
                   (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                  methyltransferase [Glycine max]
                  211925
Seq. No.
Seq. ID
                  LIB3145-040-Q1-K1-B6
Method
                  BLASTX
                   q132659
NCBI GI
BLAST score
                   364
E value
                   9.0e-35
Match length
                   85
                  79
% identity
```

NCBI Description 50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)





>gi\_81483\_pir\_\_A32033 ribosomal protein L13 precursor,
chloroplast - spinach >gi\_170133 (J04461) ribosomal protein
L13 [Spinacia oleracea]

Seq. No. 211926 Seq. ID LIB3145-040-Q1-K1-B7

Method BLASTX
NCBI GI g2160148
BLAST score 411
E value 2.0e-40
Match length 93
% identity 81

NCBI Description (AC000375) EST gb\_H37044 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 211927

Seq. ID LIB3145-040-Q1-K1-C11

Method BLASTN
NCBI GI g2275090
BLAST score 174
E value 4.0e-93
Match length 198
% identity 97

NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)

Seq. No. 211928

Seq. ID LIB3145-040-Q1-K1-C3

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 49
% identity 51

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 211929

Seq. ID LIB3145-040-Q1-K1-C5

Method BLASTX
NCBI GI g1168251
BLAST score 631
E value 4.0e-66
Match length 135
% identity 84

NCBI Description PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR

>gi\_1076384\_pir\_\_S46535 probable cysteine proteinase (EC
3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment)
>gi\_516865\_emb\_CAA52403\_ (X74359) putative thiol protease

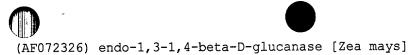
[Arabidopsis thaliana]

Seq. No. 211930

Seq. ID LIB3145-040-Q1-K1-C7

Method BLASTX
NCBI GI g3822036
BLAST score 222
E value 3.0e-18
Match length 113
% identity 46

Method NCBI GI



NCBI Description



```
211931
Seq. No.
                  LIB3145-040-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128218
BLAST score
                  175
                  1.0e-12
E value
Match length
                  44
                  70
% identity
                  (AC004077) putative end13 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211932
                  LIB3145-040-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129752
BLAST score
                  362
E value
                  1.0e-34
                  93
Match length
                  67
% identity
                  thioredoxin - Arabidopsis thaliana >gi 992964_emb_CAA84612_
NCBI Description
                   (Z35475) thioredoxin [Arabidopsis thaliana]
Seq. No.
                  211933
Seq. ID
                  LIB3145-040-Q1-K1-D12
                  BLASTX
Method
NCBI GI
                   q3786007
BLAST score
                   170
E value
                   2.0e-12
                   64
Match length
                   56
% identity
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   211934
Seq. ID
                   LIB3145-040-Q1-K1-D4
Method
                   BLASTX
                   g2245064
NCBI GI
BLAST score
                   219
E value
                   8.0e-18
Match length
                   116
% identity
                   46
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   211935
                   LIB3145-040-Q1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4508073
                   227
BLAST score
                   9.0e-19
E value
                   126
Match length
                   37
% identity
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
                   211936
Seq. No.
                   LIB3145-040-Q1-K1-E10
Seq. ID
                   BLASTX
```

g3540199



BLAST score 127 E value 3.0e-09 Match length 52 % identity 69

NCBI Description (AC004260) Putative monosaccharide transport protein

[Arabidopsis thaliana]

Seq. No. 211937

Seq. ID LIB3145-040-Q1-K1-E3

Method BLASTX
NCBI GI g224293
BLAST score 336
E value 1.0e-31
Match length 68
% identity 100

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 211938

Seq. ID LIB3145-040-Q1-K1-E4

Method BLASTN
NCBI GI g4038029
BLAST score 34
E value 1.0e-09
Match length 54
% identity 91

NCBI Description Arabidopsis thaliana chromosome II BAC F504 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 211939

Seq. ID LIB3145-040-Q1-K1-E7

Method BLASTX
NCBI GI g549063
BLAST score 456
E value 1.0e-45
Match length 105
% identity 82

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing

factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 211940

Seq. ID LIB3145-040-Q1-K1-E9

Method BLASTX
NCBI GI g1695719
BLAST score 637
E value 8.0e-67
Match length 130
% identity 96

NCBI Description (D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No. 211941

Seq. ID LIB3145-040-Q1-K1-F3

Method BLASTX
NCBI GI g2497219
BLAST score 181
E value 2.0e-13



Match length 110 % identity 36

NCBI Description HYPOTHETICAL 15.4 KD PROTEIN IN HAS1-JNM1 INTERGENIC REGION

>gi\_626266\_pir\_\_S47453 probable membrane protein YMR292w yeast (Saccharomyces cerevisiae) >gi\_530349\_emb\_CAA56801\_

(X80836) len:138, CAI:0.12, potential spliced gene, hydropho bic composition [Saccharomyces cerevisiae]

Seq. No. 211942

Seq. ID LIB3145-040-Q1-K1-F5

Method BLASTX
NCBI GI g131770
BLAST score 411
E value 3.0e-40
Match length 111
% identity 68

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)

(VEGETATIVE SPECIFIC PROTEIN V12) >gi\_70880\_pir\_\_R3D024

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi\_7353\_emb\_CAA29844\_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 211943

Seq. ID LIB3145-040-Q1-K1-F6

Method BLASTX
NCBI GI g2618688
BLAST score 463
E value 2.0e-46
Match length 104
% identity 82

NCBI Description (AC002510) putative esterase D [Arabidopsis thaliana]

Seq. No. 211944

Seq. ID LIB3145-040-Q1-K1-F7

Method BLASTX
NCBI GI g3128203
BLAST score 434
E value 5.0e-43
Match length 122
% identity 68

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 211945

Seq. ID LIB3145-040-Q1-K1-F8

Method BLASTX
NCBI GI g3063698
BLAST score 155
E value 2.0e-10
Match length 67
% identity 69

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 211946

Seq. ID LIB3145-040-Q1-K1-F9

Method BLASTX NCBI GI g123563 BLAST score 187



```
5.0e-14
E value
                   106
Match length
                   38
% identity
                   CHLOROPLAST SMALL HEAT SHOCK PROTEIN >gi_81786_pir__S00375
NCBI Description
                   heat shock 22K protein - soybean (fragment)
                   >gi 18659_emb_CAA30168_ (X07188) hsp22 (181 AA) [Glycine
                   max]
                   211947
Seq. No.
Seq. ID
                   LIB3145-040-Q1-K1-G1
                   BLASTX
Method
NCBI GI
                   q70762
BLAST score
                   354
                   9.0e-34
E value
                   90
Match length
% identity
                   83
                   histone H4 - bovine >gi_70763_pir__HSPG4 histone H4 - pig
NCBI Description
                   >gi_70765_pir__HSCH4 histone H4 - chicken
>gi_70766_pir__HSTR4 histone H4 - rainbow trout
                       3080463_emb_CAB11423_ (Z98744) histone H4 [Homo
                   sapiens]
Seq. No.
                   211948
                   LIB3145-040-Q1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2459421
BLAST score
                   449
E value
                   9.0e-45
Match length
                   129
% identity
                   61
                   (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                   [Arabidopsis thaliana]
                   211949
Seq. No.
                   LIB3145-040-Q1-K1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g418401
BLAST score
                   147
                   2.0e-09
E value
Match length
                   66
                   42
% identity
                   HYPOTHETICAL 18.5 KD PROTEIN IN GLY1-GDA1 INTERGENIC REGION
NCBI Description
                   >gi 320707 pir S30833 hypothetical protein YEL044w - yeast
                   (Saccharomyces cerevisiae) >gi 603635 (U18779) Yel044wp
                   [Saccharomyces cerevisiae]
                   211950
Seq. No.
Seq. ID
                   LIB3145-040-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g2244732
```

BLAST score 716 5.0e-76 E value Match length 138 87 % identity

(D88413) endo-xyloglucan transferase [Gossypium hirsutum] NCBI Description

Seq. No. 211951

Match length

% identity

82



```
LIB3145-040-Q1-K1-H1
Seq. ID
Method
                  BLASTN
                  g3047100
NCBI GI
BLAST score
                  36
                  9.0e-11
E value
Match length
                  106
% identity
                  89
NCBI Description Arabidopsis thaliana BAC F6N23
                  211952
Seq. No.
Seq. ID
                  LIB3145-040-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2765837
BLAST score
                  265
                  3.0e-23
E value
                  97
Match length
                  67
% identity
                  (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
                  211953
Seq. No.
Seq. ID
                  LIB3145-040-Q1-K1-H12
Method
                 BLASTX
NCBI GI
                  q4115936
BLAST score
                  193
E value
                  8.0e-15
                  81
Match length
% identity
                  44
NCBI Description
                  (AF118223) No definition line found [Arabidopsis thaliana]
                  211954
Seq. No.
Seq. ID
                  LIB3145-040-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2262100
BLAST score
                  207
E value
                  6.0e-20
Match length
                  84
% identity
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211955
                  LIB3145-040-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                  g1125691
NCBI GI
BLAST score
                  200
                  1.0e-22
E value
                  73
Match length
% identity
                  88
NCBI Description
                  (X94301) DnaJ protein [Solanum tuberosum]
Seq. No.
                  211956
Seq. ID
                  LIB3145-041-Q1-K1-A1
Method
                  BLASTX
                  g4056488
NCBI GI
BLAST score
                  465
                  7.0e-47
E value
                  97
```

Seq. ID

Method





```
(AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211957
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-A12
                  BLASTX
Method
                  g2809237
NCBI GI
BLAST score
                  171
                  2.0e-12
E value
Match length
                  44
                  64
% identity
                  (AC002560) F21B7.6 [Arabidopsis thaliana]
NCBI Description
                  211958
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-A4
                  BLASTX
Method
NCBI GI
                  g3643594
BLAST score
                  368
                  2.0e-35
E value
                  95
Match length
                  75
% identity
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211959
Seq. No.
                  LIB3145-041-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q2191171
NCBI GI
BLAST score
                  162
                  1.0e-11
E value
                  55
Match length
                   53
% identity
                   (AF007270) similar to A. thaliana DI19 mRNA (NID:g469110)
NCBI Description
                   [Arabidopsis thaliana]
                   211960
Seq. No.
                  LIB3145-041-Q1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2760537
                   348
BLAST score
E value
                   4.0e-33
                   90
Match length
                   76
% identity
                  (Y16088) cytosolic form of cyclophilin [Lupinus luteus]
NCBI Description
Seq. No.
                   211961
Seq. ID
                   LIB3145-041-Q1-K1-B3
Method
                   BLASTX
                   g2664210
NCBI GI
BLAST score
                   268
E value
                   8.0e-24
                   89
Match length
                   60
% identity
                  (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   211962
```

29408

LIB3145-041-Q1-K1-B7

BLASTX



```
NCBI GI
                  q3063396
BLAST score
                  358
                  2.0e-34
E value
Match length
                  74
% identity
                  86
NCBI Description (AB012947) vcCyP [Vicia faba]
                  211963
Seq. No.
                  LIB3145-041-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3170548
BLAST score
                  167
                  5.0e-12
E value
Match length
                  94
                  37
% identity
NCBI Description (AF056116) unknown [Fugu rubripes]
Seq. No.
                  211964
                  LIB3145-041-Q1-K1-C12
Seq. ID
Method
                  BLASTX
                  q4235644
NCBI GI
                  159
BLAST score
E value
                  5.0e-11
Match length
                  85
% identity
                  36
NCBI Description (AF119040) polyprotein [Lycopersicon esculentum]
                  211965
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3170480
                  203
BLAST score
E value
                  3.0e-16
Match length
                  87
% identity
NCBI Description (AF052863) PISTILLATA homolog MfPI-1 [Michelia figo]
                  211966
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q461753
BLAST score
                  359
E value
                  2.0e-34
Match length
                  90
% identity
                  83
                 ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                  PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB
                  proteinase regulatory chain homolog precursor, chloroplast
```

- garden pea >gi 169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

211967 Seq. No.

LIB3145-041-Q1-K1-C6 Seq. ID

BLASTX Method g3395938 NCBI GI 140 BLAST score 8.0e-09 E value



```
Match length
                  62
% identity
                  (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  211968
Seq. ID
                  LIB3145-041-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q1169384
BLAST score
                  306
                  3.0e-28
E value
Match length
                  85
% identity
                  66
                  DNAJ PROTEIN HOMOLOG ANJ1 >gi 543510 pir JQ2142 chaperone
NCBI Description
                  ANJ1 protein - Atriplex nummularia
Seq. No.
                  211969
                  LIB3145-041-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493144
BLAST score
                  283
E value
                  1.0e-25
Match length
                  72
% identity
                  82
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
NCBI Description
                  16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir S60132
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                  (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana]
                  211970
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g3461845
BLAST score
                  159
                  5.0e-11
E value
Match length
                  53
% identity
                  49
                  (AC005315) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  211971
Seq. No.
                  LIB3145-041-Q1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334113
                  412
BLAST score
E value
                  1.0e-40
Match length
                  79
                  97
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >qi 1006831 (U35015)
NCBI Description
```

acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No. 211972

Seq. ID LIB3145-041-Q1-K1-D11

Method BLASTN NCBI GI g440170 BLAST score 222

BLAST score

Match length % identity

E value

250 1.0e-21

63

81



```
E value
                  1.0e-122
Match length
                  258
% identity
                  97
NCBI Description Z.mays (C6000237) trpA gene
Seq. No.
                  211973
                  LIB3145-041-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642648
BLAST score
                  322
E value
                  4.0e-30
Match length
                  76
% identity
                  88
                  (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                  [Spinacia oleracea] >gi 2660768 (AF034616) cytosolic heat
                  shock 70 protein [Spinacia oleracea] >gi 2660770 (AF034617)
                  cytosolic heat shock 70 protein [Spinacia oleracea]
                  211974
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4539335
BLAST score
                  418
E value
                  2.0e-41
Match length
                  94
                  85
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211975
Seq. ID
                  LIB3145-041-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3068713
BLAST score
                  177
                  4.0e-13
E value
Match length
                  86
% identity
                  44
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  211976
                  LIB3145-041-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  g541816
NCBI GI
BLAST score
                  204
E value
                  1.0e-16
                  49
Match length
                  78
% identity
                  protein kinase - common ice plant >gi_457689_emb_CAA82990_
NCBI Description
                   (Z30329) protein kinase [Mesembryanthemum crystallinum]
                  211977
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-E10
                  BLASTX
Method
NCBI GI
                  g2342735
```

NCBI Description





```
(AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                  211978
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3023858
BLAST score
                  387
E value
                  9.0e-38
Match length
                  92
                  79
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 1256608 (U44850) G protein beta subunit
                  [Glycine max]
                  211979
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1888485
BLAST score
                  408
                  3.0e-40
E value
Match length
                  96
% identity
                  77
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
Seq. No.
                  211980
                  LIB3145-041-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914703
BLAST score
                  200
                  6.0e-16
E value
Match length
                  86
% identity
                  51
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                  211981
Seq. ID
                  LIB3145-041-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q115840
BLAST score
                  240
                  1.0e-20
E value
                  68
Match length
                  76
% identity
                  CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y
NCBI Description
                  PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN
                  SUBUNIT B)
                  211982
Seq. No.
Seq. ID
                  LIB3145-041-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q729274
BLAST score
                  154
                  2.0e-10
E value
Match length
                  89
                  39
% identity
```

40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)

(ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED PROTEIN) >gi\_422797\_pir\_\_A45981 peptidylprolyl isomerase



```
(EC 5.2.1.8) CyP-40 - human >gi_348910 (L11667) cyclophilin-40 [Homo sapiens] >gi_1769812_dbj_BAA09923_ (D63861) cyclophilin 40 [Homo sapiens]
```

Seq. No. 211983

Seq. ID LIB3145-041-Q1-K1-F8

Method BLASTX
NCBI GI g2244792
BLAST score 427
E value 2.0e-42
Match length 92
% identity 82

NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 211984

Seq. ID LIB3145-041-Q1-K1-G1

Method BLASTX
NCBI GI g131770
BLAST score 216
E value 1.0e-17
Match length 61
% identity 67

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi\_70880\_pir\_\_R3D024

ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi\_7353\_emb\_CAA29844\_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 211985

Seq. ID LIB3145-041-Q1-K1-G2

Method BLASTX
NCBI GI g4539543
BLAST score 408
E value 3.0e-40
Match length 81
% identity 96

NCBI Description (AJ133422) glyceraldehyde-3-phosphate dehydrogenase

[Nicotiana tabacum]

Seq. No. 211986

Seq. ID LIB3145-041-Q1-K1-G3

Method BLASTX
NCBI GI g2924777
BLAST score 296
E value 4.0e-27
Match length 90
% identity 70

NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 211987

Seq. ID LIB3145-041-Q1-K1-G6

Method BLASTX
NCBI GI g728744
BLAST score 259
E value 9.0e-23
Match length 84



% identity AUXIN-INDUCED PROTEIN PCNT115 >gi 100305 pir S16390 NCBI Description auxin-induced protein - common tobacco >gi 19799\_emb\_CAA39708\_ (X56267) auxin-induced protein [Nicotiana tabacum] 211988 Seq. No. LIB3145-041-Q1-K1-G7 Seq. ID Method BLASTX NCBI GI q134792 279 BLAST score E value 4.0e-25 Match length 92 61 % identity MICROSOMAL SIGNAL PEPTIDASE 21 KD SUBUNIT (SPC21) NCBI Description >gi\_89064\_pir\_\_A34229 signal peptidase (EC 3.4.99.-) 21K chain - dog >gi 164084 (J05069) signal peptidase 21 kDa subunit [Canis familiaris] Seq. No. 211989 LIB3145-041-Q1-K1-H1 Seq. ID Method BLASTX NCBI GI q425194 BLAST score 485 3.0e-49E value Match length 95 98 % identity (L26243) heat shock protein [Spinacia oleracea] >gi\_2660772 NCBI Description (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea] 211990 Seq. No. LIB3145-041-Q1-K1-H2 Seq. ID BLASTX Method g4455199 NCBI GI 373 BLAST score 3.0e-36 E value 95 Match length % identity 80 (AL035440) putative protein [Arabidopsis thaliana] NCBI Description 211991 Seq. No. LIB3145-041-Q1-K1-H3 Seq. ID BLASTX Method g3641837 NCBI GI 360 BLAST score 1.0e-34 E value 95 Match length 73 % identity (AL023094) Nonclathrin coat protein gamma - like protein NCBI Description [Arabidopsis thaliana] 211992

Seq. No.

Seq. ID LIB3145-041-Q1-K1-H7

Method BLASTX NCBI GI g2213425 BLAST score 167

```
6.00-1
```

E value 6.0e-12 Match length 37 % identity 78

NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

Seq. No. 211993

Seq. ID LIB3145-042-Q1-K1-A11

Method BLASTX
NCBI GI g129916
BLAST score 666
E value 3.0e-70
Match length 140
% identity 93

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi\_66911\_pir\_\_TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi\_21835\_emb\_CAA33302\_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 211994

Seq. ID LIB3145-042-Q1-K1-A12

Method BLASTX
NCBI GI g3402683
BLAST score 238
E value 5.0e-20
Match length 104
% identity 53

NCBI Description (AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No. 211995

Seq. ID LIB3145-042-Q1-K1-A3

Method BLASTX
NCBI GI g3334261
BLAST score 174
E value 2.0e-12
Match length 35
% identity 80

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi\_1655851 (U61973)

metallothionein-like protein [Malus domestica]

Seq. No. 211996

Seq. ID LIB3145-042-Q1-K1-A4

Method BLASTX
NCBI GI g3687251
BLAST score 430
E value 2.0e-42
Match length 109
% identity 73

NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 211997

Seq. ID LIB3145-042-Q1-K1-A6

Method BLASTX
NCBI GI g3859607
BLAST score 375
E value 5.0e-36
Match length 102
% identity 71



(AF104919) contains similarity to cysteine proteases (Pfam: NCBI Description PF00112, E=.21, N=1) [Arabidopsis thaliana]

211998 Seq. No.

LIB3145-042-Q1-K1-A9 Seq. ID

Method BLASTX NCBI GI g972921 BLAST score 294 E value 7.0e-27 Match length 100 % identity 57

NCBI Description (U18411) IAA9 [Arabidopsis thaliana]

>gi 2832666 emb CAA16692 (AL021684) auxin-induced protein

IAA9 [Arabidopsis thaliana]

Seq. No. 211999

Seq. ID LIB3145-042-Q1-K1-B12

Method BLASTX NCBI GI q548774 BLAST score 402 E value 3.0e-39 Match length 99 % identity 78

60S RIBOSOMAL PROTEIN L7A >gi\_542158\_pir\_\_S38360 ribosomal protein L7a - rice >gi\_303855\_dbj\_BAA02156\_ (D12631) NCBI Description

ribosomal protein L7A [Oryza sativa]

Seq. No. 212000

Seq. ID LIB3145-042-Q1-K1-B2

Method BLASTX NCBI GI g4325371 BLAST score 245 E value 7.0e-21 Match length 64 % identity 73

(AF128396) contains similarity to Medicago truncatula N7 NCBI Description

protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No. 212001

Seq. ID LIB3145-042-Q1-K1-B3

Method BLASTX NCBI GI g170753 BLAST score 522 E value 2.0e-53 Match length 112 79 % identity

(M95819) initiation factor (iso) 4F p28 subunit [Triticum NCBI Description

aestivum]

212002 Seq. No.

Seq. ID LIB3145-042-Q1-K1-B4

Method BLASTX g1063415 NCBI GI BLAST score 202 E value 7.0e-23 Match length 104 % identity 58

29416



```
(L40948) K+ channel protein [Arabidopsis thaliana]
212003
LIB3145-042-Q1-K1-B6
```

Seq. ID Method BLASTX NCBI GI g2493052 BLAST score 333 4.0e-31 E value Match length 69 % identity 86

ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL NCBI Description

>gi\_1655486\_dbj\_BAA13602\_ (D88377) epsilon subunit of

mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No. 212004

NCBI Description

Seq. No.

Seq. ID LIB3145-042-Q1-K1-B7

Method BLASTX NCBI GI g1223579 BLAST score 323 E value 5.0e-30 Match length 133 52 % identity

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

212005 Seq. No.

Seq. ID LIB3145-042-Q1-K1-B9

Method BLASTX NCBI GI q3063396 BLAST score 512 E value 4.0e-52 Match length 115 % identity 83

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 212006

Seq. ID LIB3145-042-Q1-K1-C6

Method BLASTX NCBI GI g4510363 BLAST score 201 9.0e-16 E value Match length 42 % identity 86

(AC007017) putative DNA-binding protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 212007

Seq. ID LIB3145-042-Q1-K1-C7

Method BLASTX NCBI GI q2924512 BLAST score 175 1.0e-12 E value 72 Match length 49 % identity

(AL022023) beta-galactosidase - like protein [Arabidopsis NCBI Description

thaliana]

212008 Seq. No.

29417



```
LIB3145-042-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g2245107
NCBI GI
                  429
BLAST score
                  2.0e-42
E value
Match length
                  124
% identity
                  44
                  (Z97343) thioesterase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212009
                  LIB3145-042-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g139780
BLAST score
                  278
                  1.0e-24
E value
Match length
                  102
% identity
                  55
                  WOUND-INDUCED PROTEIN 1 >gi 82293 pir JQ0398 wun1 protein
NCBI Description
                  - potato
                  212010
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q515377
BLAST score
                  163
                  3.0e-11
E value
Match length
                  59
                  63
% identity
NCBI Description (X79715) histone H4 [Lolium temulentum]
Seq. No.
                  212011
                  LIB3145-042-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1905785
BLAST score
                  287
                  7.0e-26
E value
                  93
Match length
                  63
% identity
NCBI Description (Y10685) G/HBF-1 [Glycine max]
                  212012
Seq. No.
                  LIB3145-042-Q1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4336436
BLAST score
                  418
                  4.0e-41
E value
                  114
Match length
                  68
% identity
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
NCBI Description
                  212013
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3757522
BLAST score
                  371
```

29418

9.0e-36

115

E value Match length



```
% identity
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.
                  212014
                  LIB3145-042-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4102861
BLAST score
                  542
E value
                  1.0e-55
Match length
                  116
% identity
                  87
                  (AF016893) copper/zinc-superoxide dismutase [Populus
NCBI Description
                  tremuloides]
                  212015
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q2507281
BLAST score
                  698
                  5.0e-74
E value
                  125
Match length
% identity
                  99
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                  (X97380) atran2 [Arabidopsis thaliana]
                  212016
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q2102691
BLAST score
                  404
E value
                  2.0e-39
                  126
Match length
% identity
                   65
NCBI Description (U64817) fructokinase [Lycopersicon esculentum]
Seq. No.
                   212017
                  LIB3145-042-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                                                                      2
NCBI GI
                  g2244792
BLAST score
                  599
                   2.0e-62
E value
Match length
                  133
% identity
                  79
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]
                   212018
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-E1
Method
                  BLASTX
NCBI GI
                   g3876465
BLAST score
                   321
                  1.0e-29
E value
                   79
Match length
                   77
% identity
```

NCBI Description

(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene;

% identity

NCBI Description

87



```
212019
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-E10
                  BLASTX
Method
NCBI GI
                  g81661
                  375
BLAST score
                  4.0e-36
E value
                  137
Match length
                  58
% identity
                  tryptophan synthase (EC 4.2.1.20) beta-2 chain -
NCBI Description
                  Arabidopsis thaliana
                  212020
Seq. No.
                  LIB3145-042-Q1-K1-E11
Seq. ID
                  BLASTX
Method
                  g2281330
NCBI GI
BLAST score
                  205
                   4.0e-16
E value
                  99
Match length
% identity
                   43
                  (U85646) putative pectate lyase Nt59 [Nicotiana tabacum]
NCBI Description
Seq. No.
                  212021
                  LIB3145-042-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                   q4512657
NCBI GI
BLAST score
                   193
                   2.0e-16
E value
                   109
Match length
                   45
% identity
                   (AC006931) putative APG protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4544463_gb_AAD22370.1_AC006580 2 (AC006580) putative
                   APG isolog protein [Arabidopsis thaliana]
Seq. No.
                   212022
                   LIB3145-042-Q1-K1-E5
Seq. ID
                   BLASTX
Method
                   g2982453
NCBI GI
BLAST score
                   203
                   5.0e-16
E value
                   57
Match length
                   68
% identity
                   (AL022223) fructose-bisphosphate aldolase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   212023
Seq. No.
Seq. ID
                   LIB3145-042-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   q2499498
                   210
BLAST score
E value
                   9.0e-17
Match length
                   47
```

>gi 1161602\_emb\_CAA88840\_ (Z48976) phosphoglycerate kinase

PHOSPHOGLYCERATE KINASE, CYTOSOLIC

(PGK) [Nicotiana tabacum]

```
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2129656
BLAST score
                  168
E value
                  4.0e-12
Match length
                  67
                  60
% identity
                  OBP33pep protein - Arabidopsis thaliana (fragment)
NCBI Description
                  >gi 1022801 (U37699) OBP33pep [Arabidopsis thaliana]
Seq. No.
                  212025
Seq. ID
                  LIB3145-042-Q1-K1-F1
Method
                  BLASTX
                  q1168410
NCBI GI
                  595
BLAST score
                  7.0e-62
E value
Match length
                  139
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2
NCBI Description
                  >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
Seq. No.
                  212026
                  LIB3145-042-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2246454
BLAST score
                  478
                  3.0e-48
E value
                  108
Match length
% identity
                  81
                  (U71108) S-adenosyl-methionine-sterol-C- methyltransferase
NCBI Description
                  [Nicotiana tabacum]
Seq. No.
                  212027
Seq. ID
                  LIB3145-042-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  599
                  3.0e-62
E value
Match length
                  145
% identity
                  79
NCBI Description
                  (AC005967) unknown protein [Arabidopsis thaliana]
                  212028
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-F2
Method
                  BLASTX
                  q3193286
NCBI GI
BLAST score
                  213
                  3.0e-17
E value
```

74 Match length 59 % identity

(AF069298) T14P8.22 gene product [Arabidopsis thaliana] NCBI Description

212029 Seq. No.

LIB3145-042-Q1-K1-F5 Seq. ID



```
BLASTX
Method
NCBI GI
                  q4538967
BLAST score
                  256
                  4.0e-22
E value
Match length
                  63
% identity
                  78
                  (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
NCBI Description
                  thaliana]
                  212030
Seq. No.
                  LIB3145-042-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1419088
BLAST score
                  572
                  4.0e-59
E value
Match length
                  137
% identity
                  75
NCBI Description (Z71395) calreticulin [Nicotiana plumbaginifolia]
                  212031
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3901014
BLAST score
                  235
E value
                  1.0e-19
Match length
                  55
% identity
                  76
NCBI Description
                  (AJ130886) metallothionein-like protein class II [Fagus
                  sylvatica]
Seq. No.
                  212032
Seq. ID
                  LIB3145-042-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3341693
BLAST score
                  149
                  1.0e-09
E value
Match length
                  137
                  33
% identity
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]
                  212033
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g401322
BLAST score
                  554
E value
                  4.0e-57
Match length
                  122
                  89
% identity
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                  SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
                  subunit [Gossypium hirsutum]
```

Seq. ID LIB3145-042-Q1-K1-G7

Method BLASTX NCBI GI q4531444 BLAST score 605



```
5.0e-63
E value
                  142
Match length
% identity
                  78
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212035
                  LIB3145-042-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3153902
BLAST score
                  420
                  2.0e-41
E value
Match length
                  107
% identity
                  78
                  (AF066076) 14-3-3-like protein [Helianthus annuus]
NCBI Description
Seq. No.
                  212036
Seq. ID
                  LIB3145-042-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g100099
BLAST score
                  544
                  7.0e-56
E value
Match length
                  135
% identity
                  78
NCBI Description
                  DNA-binding protein VBP1 - fava bean >gi 1372966 (M81827)
                  CREB-like protein [Vicia faba]
Seq. No.
                  212037
Seq. ID
                  LIB3145-042-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4335763
BLAST score
                  287
                  1.0e-25
E value
Match length
                  104
% identity
                  50
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                  212038
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g322750
BLAST score
                  464
                  1.0e-46
E value
Match length
                  89
                  99
% identity
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                  >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
                  212039
Seq. No.
Seq. ID
                  LIB3145-042-Q1-K1-H2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g421867
BLAST score 266
E value 2.0e-23
Match length 88
% identity 65

NCBI Description ubiquitin / ribosomal protein CEP52 - turnip >gi\_347064

(L21898) ubiquitin/ribosomal protein [Brassica rapa] >gi\_395079\_emb\_CAA80863\_ (Z24738) ubiquitin/ribosomal protein [Brassica rapa]

Seq. No. 212040

Seq. ID LIB3145-042-Q1-K1-H6

Method BLASTX
NCBI GI g2529721
BLAST score 221
E value 4.0e-18
Match length 111
% identity 42

NCBI Description (AF001891) unknown [Homo sapiens]

Seq. No. 212041

Seq. ID LIB3145-043-Q1-K1-A10

Method BLASTX
NCBI GI g3892722
BLAST score 169
E value 4.0e-12
Match length 44
% identity 70

NCBI Description (AL033545) putative protein [Arabidopsis thaliana]

Seq. No. 212042

Seq. ID LIB3145-043-Q1-K1-A11

Method BLASTX
NCBI GI g3334157
BLAST score 339
E value 8.0e-32
Match length 70
% identity 94

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi\_1220142\_emb\_CAA59468\_ (X85185) cyclophilin

[Catharanthus roseus]

Seq. No. 212043

Seq. ID LIB3145-043-Q1-K1-A5

Method BLASTN
NCBI GI g3873174
BLAST score 55
E value 4.0e-22
Match length 160
% identity 90

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No. 212044

Seq. ID LIB3145-043-Q1-K1-A7

Method BLASTX
NCBI GI g1129145
BLAST score 566
E value 2.0e-58
Match length 124
% identity 91

NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

E value

Match length

% identity

3.0e-17

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

66 73



```
212045
Seq. No.
                  LIB3145-043-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130004
BLAST score
                  237
                  5.0e-20
E value
Match length
                  63
% identity
                  65
                  squamosa-promoter binding protein 2 - garden snapdragon
NCBI Description
                  >qi 1183864 emb CAA63061 (X92079) squamosa-promoter
                  binding protein 2 [Antirrhinum majus]
                  212046
Seq. No.
Seq. ID
                  LIB3145-043-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q479406
BLAST score
                  546
E value
                  4.0e-56
                  122
Match length
% identity
                  chlorophyll a/b-binding protein - garden pea
NCBI Description
                  >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
                  212047
Seq. No.
                  LIB3145-043-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024017
BLAST score
                  502
                  6.0e-51
E value
Match length
                  99
% identity
                  95
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
NCBI Description
                   (EIF-4C) >gi 2565421 (AF026804) eukaryotic translation
                  initiation factor eIF-1A [Onobrychis viciifolia]
                  212048
Seq. No.
                  LIB3145-043-Q1-K1-C11
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  8.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  212049
Seq. No.
Seq. ID
                  LIB3145-043-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  209
```



```
212050
Seq. No.
                  LIB3145-043-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g3892051
NCBI GI
                  279
BLAST score
                  6.0e-25
E value
                  93
Match length
                  60
% identity
                   (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   212051
                  LIB3145-043-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                   q3142295
NCBI GI
BLAST score
                   382
                   5.0e-37
E value
Match length
                   105
                   41
% identity
                   (AC002411) Strong similarity to phosphoribosylanthranilate
NCBI Description
                   transferase gb_D86180 from Pisum sativum. [Arabidopsis
                   thaliana]
                   212052
Seq. No.
Seq. ID
                   LIB3145-043-Q1-K1-C9
Method
                   BLASTX
                   q1345965
NCBI GI
BLAST score
                   305
                   7.0e-28
E value
Match length
                   61
                   100
% identity
                   FLORAL HOMEOTIC PROTEIN FBP2 (FLORAL BINDING PROTEIN 2)
NCBI Description
                   >gi_1181186 (M91666) transcription factor [Petunia hybrida]
Seq. No.
                   212053
                   LIB3145-043-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   g2662343
NCBI GI
BLAST score
                   648
                   4.0e-68
E value
                   128
Match length
                   98
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   212054
Seq. No.
                   LIB3145-043-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g4406764
NCBI GI
BLAST score
                   368
                   2.0e-35
E value
                   107
Match length
                   27
% identity
                   (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
```

Seq. ID

thaliana]

LIB3145-043-Q1-K1-D4

```
Method
NCBI GI
                  q3033381
BLAST score
                  390
                  8.0e-38
E value
                  86
Match length
                  83
% identity
                  (ACO04238) putative UDP-galactose-4-epimerase [Arabidopsis
NCBI Description
                  212056
Seq. No.
Seq. ID
                  LIB3145-043-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q169363
                  215
BLAST score
                  2.0e-17
E value
Match length
                  55
                  62
% identity
NCBI Description
                 (M75856) PVPR3 [Phaseolus vulgaris]
                  212057
Seq. No.
                  LIB3145-043-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3493172
BLAST score
                  435
                  2.0e-43
E value
Match length
                  94
% identity
                  61
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  212058
                  LIB3145-043-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3493172
BLAST score
                  312
E value
                  6.0e-29
Match length
                  74
% identity
NCBI Description
                 (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  212059
Seq. ID
                  LIB3145-043-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3126969
BLAST score
                  184
E value
                  1.0e-13
Match length
                  95
                  46
% identity
NCBI Description
                  (AF061808) chalcone isomerase [Elaeagnus umbellata]
Seq. No.
                  212060
                  LIB3145-043-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  g1346225
NCBI GI
BLAST score
                  289
E value
                  5.0e-26
                  131
Match length
```

40

% identity



ENDOGLUCANASE PRECURSOR (ENDO-1,4-BETA-GLUCANASE)

(ABSCISSION CELLULASE) >gi\_349601 (M57400) cellulase

[Phaseolus vulgaris]

Seq. No. 212061

NCBI Description

Seq. ID LIB3145-043-Q1-K1-E6

Method BLASTX
NCBI GI g548441
BLAST score 570
E value 5.0e-59
Match length 105
% identity 96

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT

>gi\_486805\_pir\_\_S35502 phosphoprotein phosphatase (EC
3.1.3.16) 2A - alfalfa >gi\_287811\_emb\_CAA49849\_ (X70399)
phosphoprotein phosphatase type 2A [Medicago sativa]

Seq. No. 212062

Seq. ID LIB3145-043-Q1-K1-E7

Method BLASTX
NCBI GI g4510423
BLAST score 321
E value 9.0e-30
Match length 88
% identity 66

NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No. 212063

Seq. ID LIB3145-043-Q1-K1-E8

Method BLASTX
NCBI GI g1657617
BLAST score 315
E value 4.0e-29
Match length 72
% identity 83

NCBI Description (U72503) G2p [Arabidopsis thaliana] >gi\_3068707 (AF049236)

putative nuclear DNA-binding protein G2p [Arabidopsis

thalianal

Seq. No. 212064

Seq. ID LIB3145-043-Q1-K1-E9

Method BLASTX
NCBI GI g1710587
BLAST score 212
E value 2.0e-17
Match length 48
% identity 92

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic

ribosomal protein PO [Glycine max]

Seq. No. 212065

Seq. ID LIB3145-043-Q1-K1-F11

Method BLASTX
NCBI GI g2982247
BLAST score 222
E value 7.0e-20
Match length 98



53

% identity

NCBI Description

```
% identity
                  (AF051206) probable thioredoxin H [Picea mariana]
NCBI Description
                  212066
Seq. No.
                  LIB3145-043-Q1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432825
BLAST score
                  567
E value
                  1.0e-58
Match length
                  118
% identity
                  (AC006593) putative SOP2p protein [Arabidopsis thaliana]
NCBI Description
                  212067
Seq. No.
Seq. ID
                  LIB3145-043-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3047106
BLAST score
                  199
E value
                  1.0e-15
Match length
                  46
                  89
% identity
                   (AF058919) Arabidopsis thaliana homeodomain protein AHDP
NCBI Description
                   (SP:P93041) [Arabidopsis thaliana]
                  212068
Seq. No.
Seq. ID
                  LIB3145-043-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q1843527
BLAST score
                   388
E value
                  1.0e-37
Match length
                  105
% identity
                   75
NCBI Description
                  (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   212069
                  LIB3145-043-Q1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q643469
BLAST score
                   427
                   3.0e-42
E value
                  111
Match length
% identity
                   71
                  (U19886) unknown [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  212070
Seq. ID
                  LIB3145-043-Q1-K1-G1
Method
                  BLASTX
                  g2129803
NCBI GI
BLAST score
                   217
                  7.0e-18
E value
Match length
                  91
```

29429

protein kinase [Brassica napus]

probable serine/threonine-specific protein kinase (EC

2.7.1.-) BSK2 - rape >gi\_289374 (L12394) serine/threonine protein kinase [Brassica napus] >gi 1097354 prf\_\_2113401B



```
Seq. No.
                   212071
Seq. ID
                  LIB3145-043-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g2673912
BLAST score
                   333
                   5.0e-34
E value
Match length
                   98
                   72
% identity
                  (AC002561) unknown protein [Arabidopsis thaliana]
NCBI Description
                   212072
Seq. No.
Seq. ID
                   LIB3145-043-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   g3128195
BLAST score
                   508
                   9.0e-52
E value
Match length
                   109
% identity
                   93
NCBI Description
                   (AC004521) putative phosphoribosyl pyrophosphate synthetase
                   [Arabidopsis thaliana] >gi 3341673 (AC003672) putative
                   phosphoribosyl pyrophosphate synthetase [Arabidopsis
                   thaliana]
                   212073
Seq. No.
Seq. ID
                   LIB3145-043-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g2673912
BLAST score
                   343
                   2.0e-32
E value
Match length
                   85
                   74
% identity
NCBI Description
                  (AC002561) unknown protein [Arabidopsis thaliana]
Seq. No.
                   212074
                   LIB3145-043-Q1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4559358
BLAST score
                   147
                   2.0e-09
E value
Match length
                   50
% identity
                   50
                   (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   212075
Seq. ID
                  LIB3145-043-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q122083
BLAST score
                   212
E value
                   5.0e-17
Match length
                   60
                  72
% identity
NCBI Description
                  HISTONE H3 >gi_70751_pir__HSEAH3 histone H3 - Altenstein's
                  bread tree >gi_224865_prf__1202289A histone H3
```

But.

Seq. No. 212076

[Encephalartos sp.]



```
LIB3145-043-Q1-K1-H5
Seq. ID
                  BLASTN
Method
                  g2138087
NCBI GI
                  59
BLAST score
                  1.0e-24
E value
Match length
                  59
                  100
% identity
NCBI Description Castilleja miniata 18S ribosomal RNA gene, partial sequence
                  212077
Seq. No.
                  LIB3145-043-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1658197
BLAST score
                  590
E value
                  2.0e-61
Match length
                  117
% identity
                  91
                  (U74630) calreticulin [Ricinus communis] >gi_1763297
NCBI Description
                  (U74631) calreticulin [Ricinus communis]
                  212078
Seq. No.
Seq. ID
                  LIB3145-043-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  q3421087
BLAST score
                  462
E value
                  2.0e-46
Match length
                  96
                  96
% identity
                  (AF043524) 20S proteasome subunit PAE1 [Arabidopsis
NCBI Description
                  thaliana]
                  212079
Seq. No.
Seq. ID
                  LIB3145-044-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g441457
BLAST score
                  285
                  7.0e-26
E value
                  55
Match length
% identity
                  96
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  212080
Seq. ID
                  LIB3145-044-Q1-K1-A2
                  BLASTX
Method
                  g629602
NCBI GI
BLAST score
                  320
E value
                  9.0e-30
                  109
Match length
                  52
% identity
NCBI Description probable imbibition protein - wild cabbage
                  >gi_488787_emb_CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
```

Seq. ID LIB3145-044-Q1-K1-A5

Method BLASTX

```
NCBI GI
                   q4126401
BLAST score
                   555
E value
                   2.0e-57
Match length
                   110
% identity
                   91
NCBI Description
                  (AB011795) flavanone 3-hydroxylase [Citrus sinensis]
                   212082
Seq. No.
                   LIB3145-044-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2098705
BLAST score
                   247
                   5.0e-21
E value
Match length
                   125
% identity
                   46
NCBI Description
                  (U82973) pectinesterase [Citrus sinensis]
Seq. No.
                   212083
Seq. ID
                   LIB3145-044-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q3183347
BLAST score
                   170
E value
                   4.0e-12
Match length
                   64
% identity
                   52
NCBI Description
                   HYPOTHETICAL 48.5 KD PROTEIN C23C11.04C IN CHROMOSOME I
                   >gi_2330768_emb_CAB11157_ (Z98559) SPAC23C11.04c;
len:421aa, similar eg. to C. elegans Q19683, F21D5.5,
                   (250aa), fasta scores, opt:395, E():1.1e-32, (41.7%
                   identity in 223 aa overlap) also similar eg. to YMR156C,
                   YM31_YEAST, Q03796, hypothetical 27.4 kd
Seq. No.
                   212084
Seq. ID
                   LIB3145-044-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g3063701
BLAST score
                   381
E value
                   7.0e-37
                   107
Match length
                   67
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   212085
Seq. ID
                   LIB3145-044-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   g4337197
BLAST score
                   392
E value
                   4.0e-38
                   121
Match length
                   63
% identity
NCBI Description (AC006403) putative AIG2 protein [Arabidopsis thaliana]
```

Seq. ID LIB3145-044-Q1-K1-B11

Method BLASTX NCBI GI g4510395 BLAST score 431



E value 9.0e-43 Match length 100 % identity 83

NCBI Description (AC006587) putative beta-galactosidase precursor

[Arabidopsis thaliana]

Seq. No. 212087

Seq. ID LIB3145-044-Q1-K1-B3

Method BLASTX
NCBI GI g4115377
BLAST score 241
E value 1.0e-20
Match length 96
% identity 49

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 212088

Seq. ID LIB3145-044-Q1-K1-B4

Method BLASTX
NCBI GI g3096922
BLAST score 205
E value 3.0e-16
Match length 45
% identity 89

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 212089

Seq. ID LIB3145-044-Q1-K1-B8

Method BLASTX
NCBI GI g124224
BLAST score 591
E value 2.0e-61
Match length 115
% identity 96

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi\_100345\_pir\_\_S21060 translation initiation factor eIF-5A

- common tobacco >gi 19887 emb\_CAA45105\_ (X63543)

eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 212090

Seq. ID LIB3145-044-Q1-K1-B9

Method BLASTX
NCBI GI g2554835
BLAST score 615
E value 3.0e-64
Match length 124
% identity 93

NCBI Description Chain I, Acetohydroxy Acid Isomeroreductase Complexed With

Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate) >gi\_2554836\_pdb\_1YVE\_J Chain J,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi\_2554837\_pdb\_1YVE\_K Chain K,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,

Magnesium And Inhibitor Ipoha (N-Hydroxy-N-

Isopropyloxamate) >gi 2554838\_pdb\_1YVE\_L Chain L,

Acetohydroxy Acid Isomeroreductase Complexed With Nadph,



Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropyloxamate)

```
Seq. No.
                  212091
                  LIB3145-044-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1332579
BLAST score
                  497
                  2.0e-50
E value
Match length
                  101
% identity
                  10
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  212092
Seq. No.
                  LIB3145-044-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3461849
BLAST score
                   497
E value
                  2.0e-50
Match length
                  115
                   75
% identity
                  (AC005315) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212093
Seq. ID
                  LIB3145-044-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  q3688177
BLAST score
                   310
E value
                   1.0e-28
Match length
                   90
% identity
                   64
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   212094
Seq. No.
                  LIB3145-044-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                   q3024689
NCBI GI
BLAST score
                   165
                   1.0e-11
E value
                   106
Match length
                   36
% identity
                   TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT
NCBI Description
                   (TAFII-100) (TAFII100) >gi 1491718 emb CAA64777_ (X95525)
                   hTAFII100 [Homo sapiens]
Seq. No.
                   212095
                   LIB3145-044-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g2688824
NCBI GI
BLAST score
                   341
                   3.0e-32
E value
                   90
Match length
                   76
% identity
                   (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniada]
```

Seq. No. 212096



LIB3145-044-Q1-K1-C8 Seq. ID Method BLASTX NCBI GI q122106 BLAST score 410 3.0e-40 E value 82 Match length 100 % identity HISTONE H4 >gi\_70771\_pir\_\_HSZM4 histone H4 - maize NCBI Description >gi\_81642\_pir\_\_S06904 histone H4 - Arabidopsis thaliana >gi\_2119028\_pir\_\_S60475 histone H4 - garden pea >gi\_21795\_emb\_CAA24924\_ (X00043) histone H4 [Triticum aestivum] >gi\_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi\_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi\_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi\_168501 (M13370) histone H4 [Zea mays] >gi\_168503 (M13377) histone H4 [Zea mays] >gi\_498898 (U10042) histone H4 homolog [Pisum sativum] >gi\_1806285\_emb\_CAB01914\_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi\_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi\_4580385\_gb\_AAD24364.1\_AC007184\_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi\_225838\_prf\_ 1314298A histone H4 [Arabidopsis thaliana] 212097 Seq. No. Seq. ID LIB3145-044-Q1-K1-D11 Method BLASTX g584825 NCBI GI 270 BLAST score 4.0e-24 E value Match length 56 % identity 88 B2 PROTEIN >gi\_322726\_pir\_\_S32124 B2 protein - carrot NCBI Description >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus carota] 212098 Seq. No. LIB3145-044-Q1-K1-D12 Seq. ID Method BLASTX q464981 NCBI GI BLAST score 274 2.0e-24 E value 55 Match length 93 % identity UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum] 212099 Seq. No. LIB3145-044-Q1-K1-D2 Seq. ID Method BLASTX NCBI GI q2626753 189 BLAST score

2.0e-14 E value 82 Match length % identity 46

NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]



```
212100
Seq. No.
Seq. ID
                  LIB3145-044-Q1-K1-D3
Method
                  BLASTX
                  q1653488
NCBI GI
BLAST score
                  145
                  4.0e-09
E value
                  51
Match length
% identity
                  47
NCBI Description (D90914) hypothetical protein [Synechocystis sp.]
                  212101
Seq. No.
                  LIB3145-044-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                  q729252
NCBI GI
BLAST score
                  367
                  4.0e-35
E value
                  108
Match length
                   63
% identity
                  CYTOCHROME B5 >gi 167140 (M87514) cytochrome b-5 [Brassica
NCBI Description
                  oleracea] >gi_384338_prf__1905426A cytochrome b5 [Brassica
                  oleracea]
                  212102
Seq. No.
                  LIB3145-044-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                   g2245095
NCBI GI
                   195
BLAST score
                   4.0e-15
E value
                   48
Match length
                   77
% identity
                  (Z97343) formyltransferase purU homolog [Arabidopsis
NCBI Description
                   thaliana]
                   212103
Seq. No.
                   LIB3145-044-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2511689
                   410
BLAST score
                   3.0e-40
E value
Match length
                   120
% identity
                   62
                  (Z99952) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
                   212104
Seq. No.
                   LIB3145-044-Q1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2367392
BLAST score
                   273
                   3.0e-24
E value
Match length
                   111
% identity
                   45
                  (U82513) random slug cDNA25 protein [Dictyostelium
NCBI Description
                   discoideum]
```

Seq. ID LIB3145-044-Q1-K1-E2

Method BLASTX

```
NCBI GI
                  q4530585
BLAST score
                  357
                  5.0e-34
E value
Match length
                  85
                  74
% identity
                  (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
Seq. No.
                  212106
                  LIB3145-044-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q125887
BLAST score
                  263
E value
                  5.0e-23
                  118
Match length
                   45
% identity
NCBI Description
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                  >gi_82092 pir__S04765 LAT52 protein precursor - tomato
                  >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                   esculentum]
                   212107
Seq. No.
                  LIB3145-044-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2129472
                   530
BLAST score
                   3.0e-54
E value
                   119
Match length
                   84
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                   precursor - Scotch pine >gi_1100225 (L32561)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                   212108
Seq. No.
                   LIB3145-044-Q1-K1-E7
Seq. ID
Method
                   BLASTX
                   g2459417
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
Match length
                   124
                   57
% identity
                   (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                   [Arabidopsis thaliana]
                   212109
Seq. No.
                   LIB3145-044-Q1-K1-E9
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
                   37
Match length
                   61
 % identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   212110
Seq. No.
                   LIB3145-044-Q1-K1-F11
Seq. ID
```

29437

BLASTX

g2129726

Method NCBI GI



BLAST score 4.0e-10 E value Match length 32 91 % identity RNA polymerase II third largest chain RPB35.5A -NCBI Description Arabidopsis thaliana >gi\_514318 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi\_4544370\_gb\_AAD22281.1\_AC006920\_5 (AC006920) RNA polymerase II, third largest subunit [Arabidopsis thaliana] 212111 Seq. No. LIB3145-044-Q1-K1-F12 Seq. ID Method BLASTX g3176709 NCBI GI 182 BLAST score 1.0e-13 E value 104 Match length 35 % identity (AC002392) putative anthranilate NCBI Description N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana] 212112 Seq. No. LIB3145-044-Q1-K1-F2 Seq. ID Method BLASTX NCBI GI q3738283 BLAST score 402 3.0e-39 E value 82 Match length 85 % identity (AC005309) unknown protein [Arabidopsis thaliana] NCBI Description 212113 Seq. No. LIB3145-044-Q1-K1-F3 Seq. ID BLASTX Method NCBI GI q1931647 BLAST score 595 6.0e-62 E value 117 Match length % identity 92 (U95973) endomembrane protein EMP70 precusor isolog NCBI Description [Arabidopsis thaliana] 212114 Seq. No. Seq. ID LIB3145-044-Q1-K1-F4 Method BLASTX NCBI GI q4455158 BLAST score 369 E value 1.0e-35

Match length 90 % identity 78

(AL021687) kinase-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 212115

LIB3145-044-Q1-K1-F6 Seq. ID

Method BLASTX g4490331 NCBI GI

```
BLAST score
E value
                  2.0e-45
                  109
Match length
                  82
% identity
                  (AL035656) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212116
Seq. ID
                  LIB3145-044-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2735841
BLAST score
                  219
E value
                  7.0e-18
Match length
                  116
                  41
% identity
NCBI Description
                  (AF010283) No definition line found [Sorghum bicolor]
                  212117
Seq. No.
Seq. ID
                  LIB3145-044-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  q1370186
BLAST score
                  584
E value
                  1.0e-60
Match length
                  120
% identity
                  90
NCBI Description
                  (Z73942) RAB7C [Lotus japonicus]
                  212118
Seq. No.
Seq. ID
                  LIB3145-044-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3540199
BLAST score
                  167
E value
                  9.0e-12
Match length
                  66
% identity
                  58
NCBI Description
                  (AC004260) Putative monosaccharide transport protein
                   [Arabidopsis thaliana]
```

Seq. ID LIB3145-044-Q1-K1-G2

Method BLASTX
NCBI GI g2335097
BLAST score 535
E value 6.0e-55
Match length 111
% identity 92

NCBI Description (AC002339) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 212120

Seq. ID LIB3145-044-Q1-K1-G3

Method BLASTX
NCBI GI 94559334
BLAST score 379
E value 1.0e-36
Match length 131
% identity 48

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  212121
                  LIB3145-044-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  q3337361
NCBI GI
                  451
BLAST score
E value
                  4.0e-45
Match length
                  107
% identity
                  71
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                  212122
Seq. No.
Seq. ID
                  LIB3145-044-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3426038
BLAST score
                  449
                  8.0e-45
E value
                  121
Match length
                  63
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  212123
Seq. No.
                  LIB3145-044-Q1-K1-H1
Seq. ID
Method
                  BLASTN
                  g1848213
NCBI GI
BLAST score
                  45
                  3.0e-16
E value
Match length
                  101
                  86
% identity
NCBI Description N.tabacum mRNA for uracil phosphoribosyltransferase
                  212124
Seq. No.
                  LIB3145-044-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g2511594
NCBI GI
BLAST score
                  392
                  4.0e-38
E value
Match length
                  80
                  94
% identity
                  (Y13694) multicatalytic endopeptidase complex, proteasome
NCBI Description
                  precursor, beta subunit [Arabidopsis thaliana]
                  >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic
                   endopeptidase complex, proteasome precursor, beta subunit
                   [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                  proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                  212125
                  LIB3145-044-Q1-K1-H4
Seq. ID
Method
                  BLASTX
                   g2244827
NCBI GI
BLAST score
                   331
                   5.0e - 31
E value
                  84
Match length
                   40
% identity
```

NCBI Description

(Z97336) hypothetical protein [Arabidopsis thaliana]

Method

NCBI GI BLAST score



```
Seq. ID
                  LIB3145-044-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2996096
BLAST score
                  288
                  5.0e-26
E value
Match length
                  56
% identity
                  98
                  (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                  alpha [Oryza sativa]
Seq. No.
                  212127
Seq. ID
                  LIB3145-044-Q1-K1-H8
Method
                  BLASTX
                  q3805845
NCBI GI
BLAST score
                  371
                  1.0e-35
E value
Match length
                  130
                  61
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                  212128
Seq. No.
                  LIB3145-045-Q1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3643607
BLAST score
                  410
                  4.0e-40
E value
                  100
Match length
                  40
% identity
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                  212129
Seq. No.
                  LIB3145-045-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415908
BLAST score
                   163
E value
                   3.0e-11
Match length
                   48
                   54
% identity
                  (AC006282) unknown protein [Arabidopsis thaliana]
NCBI Description
                   212130
Seq. No.
Seq. ID
                   LIB3145-045-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g3367593
BLAST score
                   185
E value
                   6.0e-14
Match length
                   57
                   56
% identity
                   (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3805841 emb CAA21461 (AL031986) putative protein
                   [Arabidopsis thaliana]
٠٠,
Seq. No.
                   212131
                   LIB3145-045-Q1-K1-A3
Seq. ID
```

34

BLASTN g972930

29441



```
2.0e-09
E value
                  90
Match length
                  84
% identity
NCBI Description Arabidopsis thaliana IAA14 (IAA14) gene, partial cds
Seq. No.
                  212132
Seq. ID
                  LIB3145-045-Q1-K1-A5
Method
                  BLASTN
NCBI GI
                  g4193387
BLAST score
                  34
E value
                  1.0e-09
Match length
                  50
% identity
                  92
NCBI Description
                  Hevea brasiliensis translationally controlled tumor protein
                  (TCTP) mRNA, complete cds
Seq. No.
                  212133
Seq. ID
                  LIB3145-045-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  q136739
BLAST score
                  533
E value
                  1.0e-54
Match length
                  110
% identity
                  87
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  212134
Seq. ID
                  LIB3145-045-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2842478
BLAST score
                  172
                  3.0e-12
E value
Match length
                  118
% identity
                  36
NCBI Description
                  (AL021749) receptor protein kinase like protein
                  [Arabidopsis thaliana]
Seq. No.
                  212135
Seq. ID
                  LIB3145-045-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  g4097585
BLAST score
                  565
E value
                  2.0e-58
Match length
                  141
                  77
% identity
NCBI Description
                  (U64925) NTGP4 [Nicotiana tabacum]
Seq. No.
                  212136
```

Seq. ID LIB3145-045-Q1-K1-B11

Method BLASTX
NCBI GI g1008904
BLAST score 468
E value 4.0e-47



```
Match length
% identity
                  78
NCBI Description
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
                  212137
Seq. No.
Seq. ID
                  LIB3145-045-Q1-K1-B12
Method
                  BLASTX
                  q3746069
NCBI GI
BLAST score
                  159
                  1.0e-10
E value
Match length
                  99
% identity
                  34
NCBI Description
                  (AC005311) putative reverse transcriptase [Arabidopsis
                  thalianal
                  212138
Seq. No.
                  LIB3145-045-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4160300
BLAST score
                  346
E value
                  1.0e-32
Match length
                  130
                  55
% identity
NCBI Description
                  (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]
Seq. No.
                  212139
                  LIB3145-045-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3201969
                  646
BLAST score
                  7.0e-68
E value
                  133
Match length
% identity
                  85
NCBI Description
                  (AF068332) submergence induced protein 2A [Oryza sativa]
Seq. No.
                  212140
Seq. ID
                  LIB3145-045-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q1431629
BLAST score
                  181
E value
                  2.0e-13
Match length
                  52
% identity
                  63
NCBI Description
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
Seq. No.
                  212141
Seq. ID
                  LIB3145-045-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2317906
BLAST score
                  461
E value
                  4.0e-46
```

Match length 91 % identity 98

NCBI Description (U89959) ARA-5 [Arabidopsis thaliana]

212142 Seq. No.

LIB3145-045-Q1-K1-C2 Seq. ID

29443

Method

NCBI GI BLAST score BLASTX

350

g2500116



```
Method
                  BLASTN
NCBI GI
                  q2687438
BLAST score
                  62
E value
                  3.0e-26
                  66
Match length
                  98
% identity
                  Saxifraga mertensiana large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
                  212143
Seq. No.
Seq. ID
                  LIB3145-045-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4263713
                  179
BLAST score
                  4.0e-13
E value
                  83
Match length
                  52
% identity
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  212144
Seq. No.
                  LIB3145-045-Q1-K1-D1
Seq. ID
Method
                  BLASTX -
NCBI GI
                  g1724102
BLAST score
                  475
                  7.0e-48
E value
Match length
                  95
                   96
% identity
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
NCBI Description
                   [Mesembryanthemum crystallinum]
                   212145
Seq. No.
                  LIB3145-045-Q1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2827559
BLAST score
                   326
E value
                   3.0e-30
Match length
                   138
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3292808_emb_CAA19798_ (AL031018) putative protein
                   [Arabidopsis thaliana]
                   212146
Seq. No.
Seq. ID
                   LIB3145-045-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   q20634
BLAST score
                   47
E value
                   1.0e-17
Match length
                   67
                   93
% identity
NCBI Description P.sativum mRNA for actin
Seq. No.
                   212147
Seq. ID
                   LIB3145-045-Q1-K1-D5
```

29444

~ y.=



```
4.0e-33
E value
Match length
                  80
                  85
% identity
                  GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (GOR2)
NCBI Description
                  >gi 1370285 emb CAA66924_ (X98274) glutathione reductase
                  [Pisum sativum]
                  212148
Seq. No.
                  LIB3145-045-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g3821280
NCBI GI
BLAST score
                  620
                  9.0e-65
E value
Match length
                  125
% identity
                  94
                  (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                  vulgaris]
Seq. No.
                  212149
                  LIB3145-045-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703446
BLAST score
                  271
E value
                  5.0e-24
                  91
Match length
                  63
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                  >qi 1076292 pir S53127 asparaginase - Arabidopsis thaliana
                      735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis
                   thaliana]
                   212150
Seq. No.
Seq. ID
                  LIB3145-045-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                   g4106696
BLAST score
                  266
                  2.0e-23
E value
                   66
Match length
                  79
% identity
                  (AB021872) ribosome-sedimenting protein [Pisum sativum]
NCBI Description
Seq. No.
                   212151
                   LIB3145-045-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                   g1703108
NCBI GI
BLAST score
                   519
E value
                   6.0e-53
Match length
                   95
                   100
% identity
```

ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis thaliana >gi\_1049307 (U37281) actin-2 [Arabidopsis NCBI Description

thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis

thaliana]

212152 Seq. No.

Seq. ID LIB3145-045-Q1-K1-E1



```
BLASTX
Method
                   g1172873
NCBI GI
                   434
BLAST score
                   6.0e-43
E value
                   135
Match length
                   61
% identity
                   CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
NCBI Description
                   drought-inducible cysteine proteinase (\overline{EC}\ 3.4.\overline{22.-)}\ RD21A
                   precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                   (D13043) thiol protease [Arabidopsis thaliana]
                   212153
Seq. No.
                   LIB3145-045-Q1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q441457
BLAST score
                   699
                   5.0e-74
E value
                   131
Match length
                   98
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                   esculentum]
                   212154
Seq. No.
                   LIB3145-045-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   q4512699
NCBI GI
                   572
BLAST score
                   4.0e-59
E value
Match length
                   142
                   79
% identity
                   (AC006569) putative NADH-ubiquinone oxireductase
NCBI Description
                    [Arabidopsis thaliana]
                   212155
Seq. No.
                   LIB3145-045-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   q1256509
NCBI GI
                    496
BLAST score
                    3.0e-50
E value
                   110
Match length
                    77
 % identity
                   (X92943) pectate lyase [Musa acuminata]
NCBI Description
                    212156
 Seq. No.
                    LIB3145-045-Q1-K1-E3
 Seq. ID
 Method
                    BLASTX
                    q2244979
 NCBI GI
                    547
 BLAST score
                    3.0e-56
 E value
 Match length
                    134
 % identity
                    78
                   (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
 NCBI Description
                    thaliana]
```

Seq. ID LIB3145-045-Q1-K1-E6

Method BLASTX



```
q2829881
NCBI GI
BLAST score
                  212
E value
                  5.0e-17
Match length
                  60
                   63
% identity
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  212158
Seq. No.
                  LIB3145-045-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  q2244898
NCBI GI
                   398
BLAST score
E value
                  1.0e-38
Match length
                  116
                   67
% identity
                   (Z97338) strong similarity to protein phosphatase 2A
NCBI Description
                  regulatory chain, 74K [Arabidopsis thaliana]
                   212159
Seq. No.
                  LIB3145-045-Q1-K1-E8
Seq. ID
                   BLASTX
Method
                   g549060
NCBI GI
                   288
BLAST score
                   4.0e-26
E value
Match length
                   90
                   64
% identity
                   T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
NCBI Description
                   >gi 631656_pir__S43058 CCTeta protein eta chain - mouse
                   >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of
                   the chaperonin containing TCP-1 (CCT) [Mus musculus]
                   212160
Seq. No.
                   LIB3145-045-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                   q2459421
NCBI GI
BLAST score
                   525
E value
                   1.0e-53
                   140
Match length
% identity
                   66
                   (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                   [Arabidopsis thaliana]
                   212161
Seq. No.
                   LIB3145-045-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2191175
BLAST score
                   194
                   7.0e-15
E value
Match length
                   48
                   75
% identity
                   (AF007270) A IG002P16.24 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   212162
Seq. No.
                   LIB3145-045-Q1-K1-F5
Seq. ID
```

BLASTX

g2662343

Method

NCBI GI



```
BLAST score
                  3.0e-54
E value
                  104
Match length
                  97
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  212163
Seq. No.
                  LIB3145-045-Q1-K1-F6
Seq. ID
                  BLASTX
Method
                  g4249382
NCBI GI
                  474
BLAST score
                  1.0e-47
E value
                  106
Match length
                  84
% identity
                  (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   212164
Seq. No.
                   LIB3145-045-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g1914683
NCBI GI
                   488
BLAST score
                   3.0e-49
E value
                   124
Match length
% identity
                   78
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                   212165
Seq. No.
                   LIB3145-045-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   g4490737
NCBI GI
                   292
BLAST score
                   2.0e-26
E value
                   87
Match length
                   64
% identity
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   212166
Seq. No.
                   LIB3145-045-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                   q4454307
NCBI GI
                   704
BLAST score
                   1.0e-74
E value
                   142
Match length
                   87
% identity
                  (AJ132763) cyclophilin [Pseudotsuga menziesii]
NCBI Description
                   212167
Seq. No.
                   LIB3145-045-Q1-K1-G5
Seq. ID
Method
                   BLASTX
                   q4574320
NCBI GI
                   176
 BLAST score
 E value
                   1.0e-12
Match length
                   59
```

NCBI Description (AF117224) wound-induced protein WI12 [Mesembryanthemum

63

% identity



## crystallinum]

```
212168
Seq. No.
                  LIB3145-045-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g2738949
NCBI GI
BLAST score
                  626
                  2.0e-65
E value
Match length
                  130
% identity
                  88
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                  ananassa]
                  212169
Seq. No.
                  LIB3145-045-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3660469
BLAST score
                  354
                  1.0e-33
E value
Match length
                  80
                  93
% identity
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                  thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                  succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
Seq. No.
                  212170
Seq. ID
                  LIB3145-045-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1173055
BLAST score
                  671
                  9.0e-71
E value
Match length
                  134
% identity
                  99
                  60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir_S42497
NCBI Description
                  ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819
                  RL5 ribosomal protein - alfalfa >gi 463252 emb CAA55090
                   (X78284) RL5 ribosomal protein [Medicago sativa]
Seq. No.
                  212171
Seq. ID
                  LIB3145-045-Q1-K1-H2
                  BLASTX
Method
NCBI GI
                  g3080427
BLAST score
                  542
                  1.0e-55
E value
                  118
Match length
                  86
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  212172
Seq. ID
                  LIB3145-045-Q1-K1-H6
                  BLASTX
Method
NCBI GI
                  g2213624
BLAST score
                  230
                   4.0e-19
E value
Match length
                  128
                   41
% identity
```

NCBI Description (AC000103) F21J9.16 [Arabidopsis thaliana]



```
Seq. No.
                  212173
Seq. ID
                  LIB3145-046-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3608479
BLAST score
                  497
E value
                  8.0e-52
Match length
                  142
% identity
                  (AF088912) ribosomal protein L15 [Petunia x hybrida]
NCBI Description
Seq. No.
                  212174
Seq. ID
                  LIB3145-046-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4455158
                  484
BLAST score
                  5.0e-49
E value
Match length
                  114
% identity
                  79
                  (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212175
Seq. ID
                  LIB3145-046-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2924777
                  185
BLAST score
                  9.0e-14
E value
                  137
Match length
% identity
                   35
                  (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  212176
Seq. No.
Seq. ID
                  LIB3145-046-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                   q2369714
BLAST score
                   604
E value
                   5.0e-63
Match length
                  118
% identity
                   96
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  212177
Seq. ID
                   LIB3145-046-Q1-K1-A8
Method
                  BLASTX
                   g4220443
NCBI GI
BLAST score
                   191
E value
                   2.0e-14
                   120
Match length
% identity
                   38
                   (AC006216) Similar to gb X74772 SF16 protein from
NCBI Description
                  Helianthus annuus and contains calmodulin-binding motif
                  PF 00612. [Arabidopsis thaliana]
```

od BLASTX

212178

LIB3145-046-Q1-K1-A9

Seq. No. Seq. ID

Method

29450



```
q4220443
NCBI GI
BLAST score
                  140
                  1.0e-08
E value
Match length
                  106
                  32
% identity
                  (AC006216) Similar to gb_X74772 SF16 protein from
NCBI Description
                  Helianthus annuus and contains calmodulin-binding motif
                  PF 00612. [Arabidopsis thaliana]
                  212179
Seq. No.
                  LIB3145-046-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g462195
NCBI GI
BLAST score
                  155
                  1.0e-12
E value
                  59
Match length
                  75
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
                  212180
Seq. No.
                  LIB3145-046-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  q3024386
NCBI GI
                  332
BLAST score
```

2.0e-31 E value 74 Match length % identity 81

POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) NCBI Description

>gi 2129500\_pir\_\_S52006 polygalacturonase - upland cotton >gi\_606650 (U09717) polygalacturonase [Gossypium hirsutum]

Seq. No. LIB3145-046-Q1-K1-B3 Seq. ID Method BLASTX a2648032 NCBI GI BLAST score 682 5.0e-72 E value Match length 140

(AJ001374) alpha-glucosidase [Solanum tuberosum] NCBI Description

212182 Seq. No.

% identity

LIB3145-046-Q1-K1-B5 Seq. ID

212181

BLASTX Method NCBI GI g3334245 165 BLAST score E value 2.0e-11 36 Match length 86 % identity

LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) NCBI Description

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi 2909424 emb\_CAA12028\_ (AJ224520) Glyoxalase I [Cicer

Method

NCBI GI



## arietinum]

```
212183
Seq. No.
                  LIB3145-046-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g2244744
NCBI GI
                  356
BLAST score
                  8.0e-34
E value
                  123
Match length
                  59
% identity
NCBI Description (Y13676) bZIP DNA-binding protein [Antirrhinum majus]
                  212184
Seq. No.
                  LIB3145-046-Q1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2760326
                  356
BLAST score
                  7.0e-34
E value
                  129
Match length
% identity
                  53
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                   212185
Seq. No.
                  LIB3145-046-Q1-K1-B9
Seq. ID
Method
                   BLASTN
                   g2687434
NCBI GI
BLAST score
                   317
                   1.0e-178
E value
                   372
Match length
                   97
% identity
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                   partial sequence
                   212186
Seq. No.
                   LIB3145-046-Q1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q507166
                   408
BLAST score
                   6.0e-40
E value
Match length
                   143
% identity
                   57
                  (U04819) PITSLRE beta 1 [Homo sapiens]
NCBI Description
                   212187
Seq. No.
                   LIB3145-046-Q1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2739010
BLAST score
                   456
                   1.0e-45
E value
Match length
                   135
% identity
                   70
                  (AF022464) CYP77A3p [Glycine max]
NCBI Description
                   212188
Seq. No.
                   LIB3145-046-Q1-K1-C2
Seq. ID
                   BLASTX
```

29452

g507429



```
BLAST score
                  7.0e-38
E value
                  133
Match length
                  58
% identity
                  (U07705) PITSLRE isoform PBETA22 [Homo sapiens]
NCBI Description
                  212189
Seq. No.
                  LIB3145-046-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g4099914
NCBI GI
BLAST score
                  308
                  4.0e-28
E value
Match length
                  109
                  59
% identity
                  (U91857) ethylene-responsive element binding protein
NCBI Description
                  homolog [Stylosanthes hamata]
Seq. No.
                  212190
                  LIB3145-046-Q1-K1-C5
Seq. ID
Method
                  BLASTX
                  q4469023
NCBI GI
                  488
BLAST score
E value
                  2.0e-49
Match length
                  110
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                  212191
Seq. No.
Seq. ID
                  LIB3145-046-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                  g4220631
BLAST score
                   66
E value
                  1.0e-28
                   171
Match length
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5J14, complete sequence [Arabidopsis thaliana]
Seq. No.
                   212192
                   LIB3145-046-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g1778051
NCBI GI
                   355
BLAST score
                   1.0e-33
E value
                   139
Match length
                   47
% identity
                   (U62583) Prt1 homolog [Homo sapiens]
NCBI Description
                   >gi_4503527_ref_NP_003742.1_pEIF3S9_ UNKNOWN
                   212193
Seq. No.
```

Seq. ID LIB3145-046-Q1-K1-D1

Method BLASTX
NCBI GI g2707336
BLAST score 486
E value 4.0e-49
Match length 126
% identity 71



```
(AF037442) histone acetyltransferase [Arabidopsis thaliana]
NCBI Description
                  212194
Seq. No.
                  LIB3145-046-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g3914435
NCBI GI
                   515
BLAST score
                   2.0e-52
E value
                   120
Match length
                   80
% identity
                  PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin
NCBI Description
                   [Glycine max]
                   212195
Seq. No.
                   LIB3145-046-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   g3834325
NCBI GI
                   491
BLAST score
                   1.0e-49
E value
                   131
Match length
                   67
% identity
                   (AC005679) Strong similarity to gb_AF067141 gamma-glutamyl
NCBI Description
                   hydrolase from Arabidopsis thaliana. ESTs gb_R83955,
                   gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and
                   gb AI00672 come from this gene. [Arabidopsis thaliana]
                   212196
Seq. No.
                   LIB3145-046-Q1-K1-D6
Seq. ID
                   BLASTX
Method
                   g2244772
NCBI GI
                   603
BLAST score
                   9.0e-63
E value
                   140
Match length
                   80
 % identity
                   (Z97335) transport protein [Arabidopsis thaliana]
NCBI Description
                   212197
 Seq. No.
                   LIB3145-046-Q1-K1-D8
 Seq. ID
                   BLASTX
Method
                   q2829927
 NCBI GI
                   303
 BLAST score
                   1.0e-27
 E value
                   115
 Match length
                    58
 % identity
 NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
                    212198
 Seq. No.
                    LIB3145-046-Q1-K1-E1
 Seq. ID
                    BLASTX
 Method
                    g2780194
 NCBI GI
 BLAST score
                    241
                    2.0e-20
 E value
                    52
 Match length
                    92
 % identity
 NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]
```

212199

Seq. No.



```
LIB3145-046-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  q4126403
NCBI GI
                  336
BLAST score
                  1.0e-31
E value
                  104
Match length
% identity
                  (AB011796) flavonol synthase [Citrus unshiu]
NCBI Description
                  212200
Seq. No.
                  LIB3145-046-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g2826882
NCBI GI
BLAST score
                  413
                  1.0e-40
E value
                   90
Match length
                   89
% identity
                   (AJ223634) transcription factor IIA small subunit
NCBI Description
                   [Arabidopsis thaliana]
                   212201
Seq. No.
                   LIB3145-046-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g4262233
NCBI GI
                   229
BLAST score
                   5.0e-19
E value
                   84
Match length
                   56
% identity
                  (AC006200) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   212202
Seq. No.
                   LIB3145-046-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g1653444
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   102
Match length
% identity
                   51
                   (D90913) hypothetical protein [Synechocystis sp.]
NCBI Description
                   212203
Seq. No.
                   LIB3145-046-Q1-K1-F1
Seq. ID
                   BLASTX
Method
                   g2827139
NCBI GI
BLAST score
                   608
E value
                   2.0e-63
                   119
Match length
                   92
 % identity
                   (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_4049343_emb_CAA22568
                                                                       (AL034567)
                   cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                   thaliana]
                   212204
 Seq. No.
                   LIB3145-046-Q1-K1-F10
 Seq. ID
```

BLASTX

g3738306

Method

NCBI GI



```
BLAST score
                  1.0e-20
E value
                  88
Match length
                   51
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  212205
Seq. No.
                  LIB3145-046-Q1-K1-F11
Seq. ID
```

BLASTX Method g2244956 NCBI GI 334 BLAST score 2.0e-31 E value 118 Match length 52 % identity

(Z97340) strong similarity to pectinesterase [Arabidopsis NCBI Description

thaliana]

212206 Seq. No. LIB3145-046-Q1-K1-F2 Seq. ID BLASTX Method g3953471 NCBI GI 240 BLAST score

2.0e-20 E value 95 Match length 46 % identity

(AC002328) F2202.16 [Arabidopsis thaliana] NCBI Description

212207 Seq. No.

LIB3145-046-Q1-K1-F3 Seq. ID

BLASTX Method q417103 NCBI GI 605 BLAST score 4.0e-63 E value 121 Match length 100 % identity

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa]  $>gi_488567$  ( $\overline{U}09460$ ) histone H3.2 [Medicago sativa]  $>gi_488569$  ( $\overline{U}09461$ ) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >gi 488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] (AB015760) histone H3 [Nicotiana >qi 3273350 dbj BAA31218\_ tabacum]  $>gi_3885890$  (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

212208 Seq. No.

LIB3145-046-Q1-K1-F5 Seq. ID

Method

NCBI GI

BLAST score



```
Method
NCBI GI
                  q3023839
                  346
BLAST score
                  7.0e - 33
E value
                  98
Match length
                  80
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 2
NCBI Description
                  >gi 1835163_emb_CAB06619_ (Z84821) G protein beta subunit
                   [Nicotiana tabacum]
                  212209
Seq. No.
                  LIB3145-046-Q1-K1-F7
Seq. ID
                   BLASTX
Method
                   g1402891
NCBI GI
                   159
BLAST score
                   1.0e-10
E value
                   97
Match length
                   40
% identity
NCBI Description (X98130) unknown [Arabidopsis thaliana]
                   212210
Seq. No.
                   LIB3145-046-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g115492
NCBI GI
BLAST score
                   544
                   7.0e-56
E value
                   109
Match length
% identity
                   51
                   CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
NCBI Description
                   calmodulin-related protein [Petunia hybrida]
                   212211
Seq. No.
                   LIB3145-046-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   q2129622
NCBI GI
BLAST score
                   444
E value
                   3.0e-44
                   95
Match length
                   86
 % identity
                   immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406
NCBI Description
                   (U52046) immunophilin [Arabidopsis thaliana]
                   212212
 Seq. No.
                   LIB3145-046-Q1-K1-G1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q623588
 BLAST score
                   147
                   4.0e-12
 E value
 Match length
                   58
                   67
 % identity
                  (L29274) putative [Nicotiana tabacum]
 NCBI Description
                   212213
 Seq. No.
                   LIB3145-046-Q1-K1-G4
 Seq. ID
                   BLASTN
```

29457

g2687434



```
E value
                  212
Match length
% identity
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
                  212214
Seq. No.
                  LIB3145-046-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  g3643608
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
                   43
Match length
                   91
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                   212215
Seq. No.
                  LIB3145-046-Q1-K1-G8
Seq. ID
                   BLASTX
Method
                   g2911071
NCBI GI
                   247
BLAST score
                   4.0e-21
E value
                   113
Match length
                   50
% identity
NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]
                   212216
Seq. No.
                   LIB3145-046-Q1-K1-H12
Seq. ID
                   BLASTX
Method
                   g2760326
NCBI GI
                   343
BLAST score
                   2.0e-32
E value
                   119
Match length
                   53
% identity
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]
                   212217
Seq. No.
                   LIB3145-046-Q1-K1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4454018
BLAST score
                   208
                   2.0e-16
E value
                   97
Match length
                   44
% identity
NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]
                   212218
 Seq. No.
                   LIB3145-046-Q1-K1-H4
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q3821780
```

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 212219



```
LIB3145-046-Q1-K1-H5
Seq. ID
                  BLASTX
Method
                  q2267567
NCBI GI
                  426
BLAST score
                  3.0e-42
E value
                  93
Match length
                  86
% identity
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
                  212220
Seq. No.
                  LIB3145-046-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g2649345
NCBI GI
                  324
BLAST score
                  3.0e-30
E value
                  111
Match length
                  53
% identity
                  (AE001019) tryptophan synthase, subunit beta (trpB-1)
NCBI Description
                   [Archaeoglobus fulgidus]
                  212221
Seq. No.
                  LIB3145-046-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                  q4262149
NCBI GI
                   606
BLAST score
                   4.0e-63
E value
                   141
Match length
                   74
% identity
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
                   212222
Seq. No.
                   LIB3145-047-Q1-K1-A12
Seq. ID
                   BLASTX
Method
                   g1888485
NCBI GI
                   419
BLAST score
                   3.0e-41
E value
                   103
Match length
                   76
% identity
                  (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
NCBI Description
                   212223
Seq. No.
                   LIB3145-047-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   q420110
NCBI GI
                   211
BLAST score
                   6.0e-17
E value
Match length
                   59
 % identity
                   61
                  transcription factor R-kappa-B - human >gi_476274 (U08191)
NCBI Description
                   R kappa B [Homo sapiens]
```

Seq. No. 212224

Seq. ID LIB3145-047-Q1-K1-A4

Method BLASTX

```
q2832664
NCBI GI
                   250
BLAST score
                   1.0e-21
E value
Match length
                    90
                    53
% identity
                   (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                   thaliana]
                    212225
Seq. No.
                   LIB3145-047-Q1-K1-A5
Seq. ID
                    BLASTX
Method
                    g585450
NCBI GI
                    393
BLAST score
                    3.0e - 38
E value
                    113
Match length
% identity
                    67
                   MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 65 KD ISOFORM
NCBI Description
                    PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
                    (NAD-ME) >gi_1076271_pir__A49983 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) precursor, mitochondrial -
                    prince's feather >gi_437104 (U01162) C4 photosynthetic
                    NAD-dependent malic enzyme subunit alpha precursor
                    [Amaranthus hypochondriacus]
                    212226
Seq. No.
                    LIB3145-047-Q1-K1-A9
Seq. ID
                    BLASTX
Method
                    g4510381
NCBI GI
                    148
BLAST score
                    2.0e-09
E value
                    73
Match length
                    40
% identity
                    (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                    212227
 Seq. No.
                    LIB3145-047-Q1-K1-B11
 Seq. ID
                    BLASTX
Method
NCBI GI
                    g2443329
BLAST score
                    482
                    1.0e-48
 E value
 Match length
                    120
                    76
 % identity
                    (D86122) Mei2-like protein [Arabidopsis thaliana]
 NCBI Description
                    212228
 Seq. No.
                    LIB3145-047-Q1-K1-B7
 Seq. ID
                    BLASTX
 Method
                     g122007
 NCBI GI
```

Method BLASTX
NCBI GI g122007
BLAST score 301
E value 2.0e-27
Match length 82
% identity 74

NCBI Description HISTONE H2A >gi\_100161\_pir\_\_S11498 histone H2A - parsley >gi\_20448 emb\_CAA37828 (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 212229

NCBI Description



```
LIB3145-047-Q1-K1-B8
Seq. ID
Method
                   BLASTX
                   q2632254
NCBI GI
BLAST score
                   515
                   1.0e-52
E value
Match length
                   112
                   84
% identity
                   (Y12465) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   212230
Seq. No.
                   LIB3145-047-Q1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2583135
BLAST score
                   268
                   1.0e-23
E value
                   93
Match length
                   58
% identity
                   (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
                   >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs
                   protein [Arabidopsis thaliana]
                    212231
Seq. No.
                   LIB3145-047-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                    g400923
NCBI GI
BLAST score
                    366
                    4.0e-35
E value
                    72
Match length
                    100
% identity
                   RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600_ (X65650)
NCBI Description
                    RAS-related GTP-binding protein [Pisum sativum]
Seq. No.
                    212232
                    LIB3145-047-Q1-K1-C3
Seq. ID
Method
                    BLASTX
                    q4098129
NCBI GI
BLAST score
                    516
                    9.0e-53
E value
                    110
Match length
% identity
                   (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                    212233
Seq. No.
                    LIB3145-047-Q1-K1-C4
Seq. ID
                    BLASTX
Method
                    q549060
NCBI GI
BLAST score
                    409
                    3.0e-40
E value
Match length
                    113
                    71
% identity
```

T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)

>gi 631656 pir S43058 CCTeta protein eta chain - mouse >gi 468504 emb CAA83274 (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

% identity

58



```
212234
Seq. No.
                  LIB3145-047-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                  g128592
NCBI GI
                   245
BLAST score
                   5.0e-21
E value
                   100
Match length
                   56
% identity
                  POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                   >gi_82190_pir__S22495 pollen-specific protein precursor -
                   common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
                   specific protein [Nicotiana tabacum]
Seq. No.
                   212235
                   LIB3145-047-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g441457
NCBI GI
                   583
BLAST score
                   2.0e-60
E value
                   110
Match length
                   99
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                   esculentum]
                   212236
Seq. No.
                   LIB3145-047-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   q1707021
NCBI GI
BLAST score
                   376
                   3.0e-36
E value
                   102
Match length
% identity
                   65
                   (U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog
NCBI Description
                   [Arabidopsis thaliana]
                   212237
Seq. No.
                   LIB3145-047-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   q3334157
NCBI GI
                   316
BLAST score
                   3.0e-29
E value
                   65
Match length
                   94
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi 1220142_emb_CAA59468_ (X85185) cyclophilin
                   [Catharanthus roseus]
                   212238
Seq. No.
                   LIB3145-047-Q1-K1-D4
Seq. ID
Method
                   BLASTX
                   q2914706
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   124
Match length
```

NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]

BLAST score

Match length

E value

3.0e-14



```
212239
Seq. No.
                  LIB3145-047-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g584825
NCBI GI
                  418
BLAST score
                  3.0e-41
E value
                  83
Match length
                  92
% identity
                  B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                  >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                  carota]
                  212240
Seq. No.
                  LIB3145-047-Q1-K1-E10
Seq. ID
                  BLASTX
Method
                  g3121731
NCBI GI
                  144
BLAST score
                  2.0e-09
E value
                  79
Match length
                  46
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi_2145473_emb_CAA65735_ (X97012) aconitate
                  hydratase [Solanum tuberosum]
                  212241
Seq. No.
                  LIB3145-047-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g3962377
NCBI GI
                   615
BLAST score
                   2.0e-64
E value
                   128
Match length
                   93
% identity
NCBI Description (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
                   212242
Seq. No.
                   LIB3145-047-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   q134892
NCBI GI
BLAST score
                   375
                   3.0e-36
E value
                   110
Match length
 % identity
                   SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
NCBI Description
                   (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                   >gi_88607_pir__A29440 signal recognition particle receptor
                   - human >gi_30866 emb_CAA29608_ (X06272) docking protein
                   [Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal
                   recognition particle receptor ('docking protein')
                   212243
 Seq. No.
                   LIB3145-047-Q1-K1-E9
 Seq. ID
                   BLASTX
 Method
                   g1262595
 NCBI GI
                   188
```

Method

BLASTX



```
% identity
                  (D17510) PSII I protein [Pinus thunbergii]
NCBI Description
Seq. No.
                  212244
                  LIB3145-047-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  q1843527
NCBI GI
                  339
BLAST score
                  5.0e-32
E value
Match length
                  102
                  39
% identity
                  (U73747) annexin [Gossypium hirsutum]
NCBI Description
                  212245
Seq. No.
                  LIB3145-047-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  q2160163
NCBI GI
                  221
BLAST score
                  5.0e-18
E value
Match length
                  88
                   46
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   212246
Seq. No.
                  LIB3145-047-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   q2245021
NCBI GI
BLAST score
                   394
                   2.0e-38
E value
                   111
Match length
                   70
% identity
                  (Z97341) heat shock protein 110 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   212247
Seq. No.
                   LIB3145-047-Q1-K1-F4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2369766
                   431
BLAST score
                   1.0e-42
E value
Match length
                   114
                   69
% identity
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
                   212248
Seq. No.
                   LIB3145-047-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q3687251
NCBI GI
BLAST score
                   357
E value
                   5.0e-34
Match length
                   91
                   73
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
                   212249
Seq. No.
                   LIB3145-047-Q1-K1-F7
Seq. ID
```



```
g4140326
NCBI GI
BLAST score
                  237
                  5.0e-20
E value
Match length
                  75
                  61
% identity
                  (AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to
NCBI Description
                  many (archae)bacterial, worm and yeast hypothetical
                  proteins) [Homo sapiens]
                  212250
Seq. No.
                  LIB3145-047-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1706319
                  192
BLAST score
                  1.0e-14
E value
                   90
Match length
% identity
                  HISTIDINE DECARBOXYLASE (HDC) (TOM92)
NCBI Description
                  >gi_481829_pir__S39554 histidine decarboxylase (EC
                   4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900)
                   histidine decarboxylase [Lycopersicon esculentum]
                   212251
Seq. No.
                   LIB3145-047-Q1-K1-G2
Seq. ID
Method
                   BLASTX
                   g2708743
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
                   93
Match length
                   32
% identity
                   (AC003952) putative Tal-1-like reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
                   212252
Seq. No.
                   LIB3145-047-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3953471
                   625
BLAST score
                   2.0e-65
E value
Match length
                   139
                   81
 % identity
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   212253
 Seq. No.
                   LIB3145-047-Q1-K1-G9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4056432
 BLAST score
                   606
                   4.0e-63
 E value
                   135
 Match length
                   79
 % identity
                   (AC005990) Similar to gi_2245014 glucosyltransferase
 NCBI Description
                   homolog from Arabidopsis thaliana chromosome 4 contig
                   gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this
```

Seq. No. 212254

gene. [Arabidopsis thaliana]

Seq. No.

Seq. ID Method



```
LIB3145-047-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   g2500047
NCBI GI
                   505
BLAST score
                   2.0e-51
E value
                   98
Match length
                   92
 % identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
 NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi_534916_emb_CAA85362
                   (Z36894) soluble inorganic pyrophosphatase [Solanum
                   tuberosum]
                   212255
 Seq. No.
                   LIB3145-047-Q1-K1-H11
 Seq. ID
 Method
                   BLASTN
                   g2924257
 NCBI GI
 BLAST score
                   33
                   5.0e-09
 E value
                   72
Match length
 % identity
                   93
 NCBI Description Tobacco chloroplast genome DNA
                   212256
 Seq. No.
                   LIB3145-047-Q1-K1-H4
 Seq. ID
                   BLASTX
 Method
                   g4455223
 NCBI GI
                    392
 BLAST score
                    6.0e-43
 E value
                    131
 Match length
                    27
 % identity
                   (AL035440) putative DNA binding protein [Arabidopsis
 NCBI Description
                    thaliana]
                    212257
 Seq. No.
                    LIB3145-047-Q1-K1-H5
 Seq. ID
                    BLASTN
 Method
                    q2924257
 NCBI GI
                    37
 BLAST score
                    2.0e-11
 E value
                    129
 Match length
                    98
 % identity
 NCBI Description Tobacco chloroplast genome DNA
                    212258
  Seq. No.
                    LIB3145-047-Q1-K1-H7
  Seq. ID
                    BLASTX
 Method
                    q3643249
 NCBI GI
                    316
 BLAST score
                    3.0e-29
  E value
                    115
 Match length
  % identity
                    57
                    (AF090143) thaumatin-like protein precursor Mdtl1 [Malus
  NCBI Description
                    domestica]
                    212259
```

29466

LIB3145-048-Q1-K1-A12

BLASTX



```
NCBI GI
                  g2864610
BLAST score
                  245
                  7.0e-21
E value
Match length
                  68
% identity
NCBI Description
                  (AL021811) putative protein [Arabidopsis thaliana]
                  >gi 4049336 emb_CAA22561_ (AL034567) putative protein
                   [Arabidopsis thaliana]
                  212260
Seq. No.
Seq. ID
                  LIB3145-048-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3242077
                  551
BLAST score
                  1.0e-56
E value
Match length
                  122
% identity
                  (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212261
                  LIB3145-048-Q1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3549666
BLAST score
                   357
                   5.0e-34
E value
                   87
Match length
% identity
                  (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
                   212262
Seq. No.
                  LIB3145-048-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4249382
BLAST score
                   291
E value
                   3.0e-26
Match length
                   64
% identity
                   84
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   212263
Seq. No.
                   LIB3145-048-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   g3559816
NCBI GI
BLAST score
                   614
E value
                   4.0e-64
Match length
                   127
% identity
                  (Y15782) transketolase 2 [Capsicum annuum]
NCBI Description
                   212264
Seq. No.
Seq. ID
                   LIB3145-048-Q1-K1-A9
                   BLASTX
Method
                   g2414570
NCBI GI
```

29467

150

9.0e-10

BLAST score E value



```
Match length
% identity
                  43
NCBI Description
                  (Z99173) cysteine proteinase precursor [Nicotiana tabacum]
                  212265
Seq. No.
Seq. ID
                  LIB3145-048-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q2342526
BLAST score
                  168
E value
                  7.0e-12
Match length
                  60
% identity
                  57
NCBI Description (Y14314) IgE autoantigen [Homo sapiens]
Seq. No.
                  212266
Seq. ID
                  LIB3145-048-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                  g2687434
BLAST score
                  209
                  1.0e-114
E value
Match length
                  269
% identity
                  94
NCBI Description Eucryphia lucida large subunit 26S ribosomal RNA gene,
                  partial sequence
Seq. No.
                  212267
Seq. ID
                  LIB3145-048-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2598599
BLAST score
                  315
                  4.0e-29
E value
Match length
                  88
% identity
                  67
NCBI Description (Y15372) MtN4 [Medicago truncatula]
                  212268
Seq. No.
Seq. ID
                  LIB3145-048-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g533692
BLAST score
                  210
                  9.0e-17
E value
Match length
                  72
% identity
NCBI Description
                  (U12150) protease inhibitor [Glycine max]
                  212269
Seq. No.
Seq. ID
                  LIB3145-048-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2231702
BLAST score
                  643
E value
                  2.0e-67
Match length
                  127
% identity
                  93
NCBI Description
                  (U92086) clathrin assembly protein AP19 homolog
                  [Arabidopsis thaliana] >gi 3080409 emb CAA18728 (AL022604)
                  clathrin assembly protein AP19 homolog [Arabidopsis
```

29468

thaliana]



```
212270
Seq. No.
                    LIB3145-048-Q1-K1-B8
Seq. ID
                    BLASTX
Method
NCBI GI
                    q1916292
BLAST score
                    160
                    6.0e-11
E value
                    70
Match length
% identity
                    (U89793) allergen Amb a VI [Ambrosia artemisiifolia]
NCBI Description
                    212271
Seq. No.
                    LIB3145-048-Q1-K1-C11
Seq. ID
                    BLASTX
Method
                    q3421384
NCBI GI
BLAST score
                    431
                    1.0e-42
E value
                    125
Match length
% identity
                    (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
NCBI Description
                     [Arabidopsis thaliana]
                     212272
Seq. No.
                    LIB3145-048-Q1-K1-C2
Seq. ID
                     BLASTX
Method
                     g132770
NCBI GI
BLAST score
                     300
                     2.0e-27
E value
                     76
Match length
% identity
                    CHLOROPLAST 50S RIBOSOMAL PROTEIN L20 >gi_71275_pir__R5NT20
NCBI Description
                     ribosomal protein L20 - common tobacco chloroplast >gi_11852 emb_CAA77372_ (Z00044) ribosomal protein L20 [Nicotiana tabacum] >gi_225221_prf__1211235BC ribosomal
                     protein L20 [Nicotiana tabacum]
                     212273
 Seq. No.
                     LIB3145-048-Q1-K1-C3
 Seq. ID
                     BLASTN
 Method
                     g2696018
 NCBI GI
 BLAST score
                     40
                     4.0e-13
 E value
 Match length
                     80
                     94
 % identity
                     Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                     MXC9, complete sequence [Arabidopsis thaliana]
                     212274
 Seq. No.
                     LIB3145-048-Q1-K1-C4
 Seq. ID
                     BLASTX
 Method
                     g1351856
 NCBI GI
                      317
 BLAST score
                      3.0e-29
 E value
                      69
 Match length
                      87
 % identity
                     ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
 NCBI Description
```

(ACONITASE) >gi\_868003\_dbj\_BAA06108\_ (D29629) aconitase



## [Cucurbita sp.]

```
212275
Seq. No.
Seq. ID
                  LIB3145-048-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q2746719
                  284
BLAST score
                  2.0e-25
E value
                  68
Match length
% identity
NCBI Description (AF038386) histone H2B [Capsicum annuum]
                  212276
Seq. No.
                  LIB3145-048-Q1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3757529
BLAST score
                  261
                  9.0e-23
E value
                  111
Match length
% identity
NCBI Description (AC005167) tetracycline transporter-like protein
                   [Arabidopsis thaliana]
                   212277
Seq. No.
                  LIB3145-048-Q1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2244734
                   644
BLAST score
                   1.0e-67
E value
                   127
Match length
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
                   212278
Seq. No.
                   LIB3145-048-Q1-K1-D2
Seq. ID
                   BLASTX
Method
                   g2245086
NCBI GI
BLAST score
                   489
                   2.0e-49
E value
                   122
Match length
% identity
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                   212279
Seq. No.
                   LIB3145-048-Q1-K1-D3
 Seq. ID
                   BLASTX
Method
                   g2829910
NCBI GI
BLAST score
                   456
E value
                   1.0e-45
Match length
                   128
                   13
 % identity
                   (AC002291) Unknown protein, contains regulator of
 NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                  212280
 Seq. No.
                   LIB3145-048-Q1-K1-D4
 Seq. ID
```

BLASTX

Method



```
g2459421
NCBI GI
BLAST score
                  316
                  3.0e-29
E value
Match length
                  79
% identity
                  68
                  (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  212281
                  LIB3145-048-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1223922
BLAST score
                  235
E value
                  1.0e-19
Match length
                  55
% identity
                  75
                  (U49445) Vigna radiata vicilin peptidohydrolase [Vigna
NCBI Description
                  radiata]
Seq. No.
                  212282
                  LIB3145-048-Q1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827715
BLAST score
                  650
E value
                  2.0e-68
Match length
                  127
                  94
% identity
NCBI Description
                  (AL021684) receptor protein kinase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  212283
                  LIB3145-048-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1279563
BLAST score
                  419
                  3.0e-41
E value
Match length
                  127
% identity
                  36
NCBI Description (X88845) nuM1 [Medicago sativa]
Seq. No.
                  212284
                  LIB3145-048-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g2129927
NCBI GI
BLAST score
                  527
                  6.0e-54
E value
Match length
                  124
% identity
                  zeta-carotene desaturase precursor - pepper
NCBI Description
                  >gi_1176437_bbs_171885 zeta-carotene desaturase,
                  CapZDS=phytoene desaturase homolog [Capsicum annuum, early
```

ripening fruit, Peptide, 588 aa]

212285 Seq. No.

LIB3145-048-Q1-K1-E12 Seq. ID

Method BLASTX NCBI GI g2760830



```
BLAST score
E value
                  3.0e-52
                  99
Match length
                  93
% identity
                  (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  212286
Seq. No.
                  LIB3145-048-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  g2829205
NCBI GI
                  140
BLAST score
                   8.0e-73
E value
Match length
                   377
                  19
% identity
                  Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein
NCBI Description
                  precursor (PRP) mRNA, complete cds
                   212287
Seq. No.
                   LIB3145-048-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g2618698
NCBI GI
BLAST score
                   247
                   4.0e-21
E value
Match length
                   111
% identity
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                   212288
Seq. No.
                   LIB3145-048-Q1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3204106
BLAST score
                   426
                   4.0e-42
E value
Match length
                   125
% identity
                   66
                  (AJ006763) putative beta-amilase [Cicer arietinum]
NCBI Description
                   212289
Seq. No.
Seq. ID
                   LIB3145-048-Q1-K1-E8
Method
                   BLASTX
                   g4376203
NCBI GI
                   138
BLAST score
                   8.0e-17
E value
Match length
                   119
                   42
% identity
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
                   212290
Seq. No.
                   LIB3145-048-Q1-K1-E9
Seq. ID
Method
                   BLASTX
                   g2398521
NCBI GI
                   226
BLAST score
E value
                   1.0e-18
```

29472

88

56

Match length

% identity



```
Seq. No.
                   212291
                   LIB3145-048-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   g3123161
NCBI GI
BLAST score
                   130
                   9.0e-09
E value
                   91
Match length
                   42
% identity
                   HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN
NCBI Description
                   F35G12.4 IN CHROMOSOME III >gi 3876723_emb CAA86335
                   (Z46242) similar to beta-transducin; \overline{\text{cDNA}} EST EMBL:\overline{\text{Z}}14703
                   comes from this gene; cDNA EST EMBL: D67532 comes from this
                   gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST
                   EMBL: D64515 comes from this gene; cDNA EST EMBL: D655
Seq. No.
                   212292
Seq. ID
                   LIB3145-048-Q1-K1-F12
                   BLASTX
Method
                   g2500354
NCBI GI
                   145
BLAST score
E value
                   2.0e-13
Match length
                   94
                   49
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   212293
Seq. No.
                   LIB3145-048-Q1-K1-F4
Seq. ID
                   BLASTX
Method
                   g1703380
NCBI GI
BLAST score
                   410
                   3.0e-40
E value
Match length
                   78
                   100
% identity
                   ADP-RIBOSYLATION FACTOR >gi 1132483_dbj_BAA04607_ (D17760)
NCBI Description
                   ADP-ribosylation factor [Oryza sativa]
Seq. No.
                   212294
                   LIB3145-048-Q1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729671
BLAST score
                   235
                   9.0e-20
E value
                   69
Match length
% identity
                   70
NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
Seq. No.
                   212295
                   LIB3145-048-Q1-K1-F9
Seq. ID
                   BLASTX
Method
                   g1841464
NCBI GI
                   248
BLAST score
                   3.0e-21
E value
```

NCBI Description (Y13720) transcription factor [Arabidopsis thaliana]

29473

53

43

Match length

% identity



NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 212296

Seq. ID LIB3145-048-Q1-K1-G1

Method BLASTX
NCBI GI g481821
BLAST score 428
E value 2.0e-42
Match length 129
% identity 66

NCBI Description probable glutathione transferase (EC 2.5.1.18) (clone ERD11) - Arabidopsis thaliana >gi\_497788\_dbj\_BAA04553\_

(D17672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 212297

Seq. ID LIB3145-048-Q1-K1-G10

Method BLASTX
NCBI GI g4105772
BLAST score 423
E value 7.0e-42
Match length 90
% identity 43

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 212298

Seq. ID LIB3145-048-Q1-K1-G3

Method BLASTX
NCBI GI g1707021
BLAST score 266
E value 2.0e-23
Match length 64
% identity 70

NCBI Description (U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog

[Arabidopsis thaliana]

Seq. No. 212299

Seq. ID LIB3145-048-Q1-K1-G6

Method BLASTX
NCBI GI g3193303
BLAST score 211
E value 5.0e-17
Match length 94
% identity 44

NCBI Description (AF069298) similar to several proteins containing a tandem

repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 212300

Seq. ID LIB3145-048-Q1-K1-G8

Method BLASTX
NCBI GI g4336436
BLAST score 266
E value 2.0e-23
Match length 77
% identity 70

NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]



```
212301
Seq. No.
                  LIB3145-048-Q1-K1-G9
Seq. ID
                  BLASTX
Method
                  g4417293
NCBI GI
                  212
BLAST score
                  2.0e-17
E value
                  49
Match length
                  80
% identity
                  (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                  212302
Seq. No.
                  LIB3145-048-Q1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2506139
                  558
BLAST score
                   1.0e-57
E value
Match length
                   126
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                   (ARCHAIN) >gi 1314049_emb_CAA91901_ (Z67962)
                   archain/delta-COP [Oryza sativa]
Seq. No.
                   212303
                   LIB3145-048-Q1-K1-H2
Seq. ID
                   BLASTX
Method
                   q2244865
NCBI GI
                   408
BLAST score
E value
                   6.0e-40
                   129
Match length
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212304
                   LIB3145-048-Q1-K1-H6
Seq. ID
Method
                   BLASTX
                   q114268
NCBI GI
                   255
BLAST score
                   2.0e-22
E value
                   75
Match length
                   67
 % identity
                   L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE)
NCBI Description
                   >gi_541907_pir__$23763 gene Bp10 protein - rape
                   >gi 17789 emb CAA45554 (X64257) protein homologous to
                   ascorbate oxidase [Brassica napus]
                   212305
 Seq. No.
                   LIB3145-048-Q1-K1-H7
 Seq. ID
                   BLASTX
 Method
                   q3650030
 NCBI GI
                   264
 BLAST score
                   4.0e-23
 E value
                   108
 Match length
                   56
 % identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
 NCBI Description
```

29475

212306

Seq. No.

NCBI Description



```
Seq. ID
                  LIB3145-048-Q1-K1-H8
Method
                  BLASTX
                  q731676
NCBI GI
                  205
BLAST score
                  3.0e-16
E value
Match length
                  80
% identity
                  HYPOTHETICAL 44.9 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION
NCBI Description
                  >gi_626632_pir__S46814 hypothetical protein YHR075c - yeast
                   (Saccharomyces cerevisiae) >gi_500835 (U10556) Yhr075cp
                   [Saccharomyces cerevisiae]
                  212307
Seq. No.
                  LIB3145-048-Q1-K1-H9
Seq. ID
                  BLASTX
Method
                  q1053047
NCBI GI
                  573
BLAST score
                  2.0e-59
E value
Match length
                  116
                   99
% identity
                  (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
Seq. No.
                   212308
                  LIB3145-049-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   g1905930
NCBI GI
                   183
BLAST score
                   5.0e-14
E value
                   38
Match length
                   97
% identity
NCBI Description (U31994) MADS box protein [Oryza sativa]
                   212309
Seq. No.
                   LIB3145-049-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g629602
NCBI GI
                   432
BLAST score
E value
                   9.0e-43
                   108
Match length
% identity
                   probable imbibition protein - wild cabbage
NCBI Description
                   >gi_488787_emb_CAA55893_ (X79330) putative imbibition
                   protein [Brassica oleracea]
                   212310
Seq. No.
Seq. ID
                   LIB3145-049-Q1-K1-A6
Method
                   BLASTX
                   g465898
NCBI GI
                   276
BLAST score
                   2.0e-24
E value
                   120
Match length
                   30
 % identity
                   HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III
```

29476

>gi 630692 pir S44849 K12H4.8 protein - Caenorhabditis elegans >gi\_289703 (L14331) homology with eukaryotic



initiation factor-4A (eIF-4A) and E. coli Ribonuclease III; coded for by C. elegans cDNA GenBank: T02268; putative [Caenorhabditis elegans]

```
212311
Seq. No.
                  LIB3145-049-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g3024385
NCBI GI
                  588
BLAST score
                  4.0e-61
E value
Match length
                  129
                  88
% identity
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_606652
NCBI Description
                   (U09805) polygalacturonase [Gossypium barbadense]
                  212312
Seq. No.
                  LIB3145-049-Q1-K1-B3
Seq. ID
Method
                  BLASTN
                  g2160689
NCBI GI
                   33
BLAST score
                   6.0e-09
E value
                  109
Match length
% identity
                  Arabidopsis thaliana B' regulatory subunit of PP2A
NCBI Description
                   (AtB'alpha) mRNA, complete cds
                   212313
Seq. No.
                   LIB3145-049-Q1-K1-B6
Seq. ID
Method
                   BLASTX
                   g4558556
NCBI GI
                   341
BLAST score
                   4.0e-32
E value
Match length
                   129
% identity
                   53
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   212314
Seq. ID
                   LIB3145-049-Q1-K1-B8
Method
                   BLASTX
                   g2832661
NCBI GI
BLAST score
                   477
                   4.0e-48
E value
Match length
                   126
% identity
                   82
                   (AL021710) pherophorin - like protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 212315

Seq. ID LIB3145-049-Q1-K1-C1

Method BLASTX
NCBI GI g2662343
BLAST score 571
E value 4.0e-59
Match length 109
% identity 100

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. ID



```
Seq. No.
                  212316
                  LIB3145-049-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1234900
                  161
BLAST score
E value
                  5.0e-11
                  53
Match length
% identity
                  66
NCBI Description (X92489) homeobox-leucine zipper protein [Glycine max]
                  212317
Seq. No.
Seq. ID
                  LIB3145-049-Q1-K1-C3
Method
                  BLASTX
                  q1174592
NCBI GI
                  553
BLAST score
                  5.0e-57
E value
Match length
                  129
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
Seq. No.
                   212318
                  LIB3145-049-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   q3702121
NCBI GI
                   456
BLAST score
E value
                   1.0e-45
                   130
Match length
% identity
                   (AJ011681) retinoblastoma-related protein [Chenopodium
NCBI Description
                   rubrum]
Seq. No.
                   212319
                   LIB3145-049-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   q4454033
NCBI GI
BLAST score
                   378
                   2.0e-36
E value
Match length
                   93
                   74
% identity
                   (AL035394) putative potassium transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   212320
Seq. No.
                   LIB3145-049-Q1-K1-D12
Seq. ID
Method
                   BLASTX
                   g1841464
NCBI GI
BLAST score
                   362
                   6.0e-35
E value
                   86
Match length
% identity
                   48
                  (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
NCBI Description
                   212321
Seq. No.
```

LIB3145-049-Q1-K1-D2



Method BLASTX
NCBI GI g1730107
BLAST score 538
E value 3.0e-55
Match length 127
% identity 80

NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN

HYDROXYLASE) >gi\_421870\_pir\_\_S33144 anthocyanidin

hydroxylase - apple tree >gi\_296844\_emb\_CAA50498\_ (X71360)

anthocyanidin hydroxylase [Malus sp.]

Seq. No. 212322

Seq. ID LIB3145-049-Q1-K1-D3

Method BLASTX
NCBI GI g3063392
BLAST score 479
E value 3.0e-48
Match length 130
% identity 75

NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No. 212323

Seq. ID LIB3145-049-Q1-K1-D4

Method BLASTX
NCBI GI g2558962
BLAST score 281
E value 4.0e-25
Match length 56
% identity 100

NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 212324

Seq. ID LIB3145-049-Q1-K1-D6

Method BLASTX
NCBI GI g2494299
BLAST score 296
E value 7.0e-27
Match length 59
% identity 93

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT

(EIF-2-BETA) >gi\_1732361 (U80269) translation initiation

factor 2 beta [Malus domestica]

Seq. No. 212325

Seq. ID LIB3145-049-Q1-K1-E12

Method BLASTX
NCBI GI g3421096
BLAST score 322
E value 3.0e-30
Match length 70
% identity 93

NCBI Description (AF043528) 20S proteasome subunit PAG1 [Arabidopsis

thaliana] >gi\_3885332 (AC005623) proteasome component

[Arabidopsis Thaliana]

Seq. No. 212326

Seq. ID LIB3145-049-Q1-K1-E4



```
Method
                  BLASTX
                  a2651313
NCBI GI
                  290
BLAST score
                  4.0e-26
E value
                  91
Match length
% identity
                  60
                  (AC002336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  212327
Seq. No.
                  LIB3145-049-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2632105
BLAST score
                  461
                  3.0e-46
E value
                   125
Match length
                   74
% identity
                   (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  >gi 4539426 emb CAB38959.1 (AL049171) arginyl-tRNA
                   synthetase [Arabidopsis thaliana]
                   212328
Seq. No.
                   LIB3145-049-Q1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2460200
                   341
BLAST score
                   4.0e-32
E value
                   108
Match length
% identity
                   (AF020833) eukaryotic translation initiation factor 3
NCBI Description
                   subunit [Homo sapiens]
                   212329
Seq. No.
                   LIB3145-049-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   q4567286
NCBI GI
BLAST score
                   581
E value
                   3.0e-60
                   129
Match length
% identity
                   (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
                   212330
Seq. No.
                   LIB3145-049-Q1-K1-F11
Seq. ID
Method
                   BLASTX
                   g3023816
NCBI GI
BLAST score
                   276
                   2.0e-24
E value
                   57
Match length
                   89
 % identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >qi 968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
```

LIB3145-049-Q1-K1-F12 Seq. ID

212331

BLASTX Method

Seq. No.

% identity



```
g2244732
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
Match length
                  123
                  91
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                  212332
Seq. No.
                  LIB3145-049-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  q3126969
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
Match length
                  87
                  48
% identity
NCBI Description (AF061808) chalcone isomerase [Elaeagnus umbellata]
                  212333
Seq. No.
                  LIB3145-049-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g3914435
NCBI GI
                  497
BLAST score
                  2.0e-50
E value
                  117
Match length
% identity
                   79
NCBI Description PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin
                   [Glycine max]
                   212334
Seq. No.
                   LIB3145-049-Q1-K1-G4
Seq. ID
                   BLASTN
Method
                   g532574
NCBI GI
BLAST score
                   53
                   3.0e-21
E value
Match length
                   93
                   89
% identity
NCBI Description Gossypium hirsutum L. 18S ribosomal RNA (18S rRNA) gene, 5'
Seq. No.
                   212335
                   LIB3145-049-Q1-K1-H1
Seq. ID
                   BLASTX
Method
                   g2842490
NCBI GI
                   304
BLAST score
E value
                   9.0e-28
                   91
Match length
 % identity
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
 Seq. No.
                   212336
                   LIB3145-049-Q1-K1-H2
 Seq. ID
                   BLASTX
 Method
                   g166951
 NCBI GI
                   183
 BLAST score
                   1.0e-13
 E value
                   93
 Match length
                   43
```

Seq. No.

Seq. ID

212342

LIB3145-050-Q1-K1-A8



```
NCBI Description (L06094) polygalacturonase [Persea americana]
                  212337
Seq. No.
                  LIB3145-049-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  g4457221
NCBI GI
                   211
BLAST score
                   7.0e-17
E value
                   71
Match length
                   58
% identity
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
NCBI Description
                   chinense]
Seq. No.
                   212338
                   LIB3145-049-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   q4539401
NCBI GI
                   287
BLAST score
                   8.0e-26
E value
                   123
Match length
                   50
% identity
                   (AL035526) putative protein [Arabidopsis thaliana]
NCBI Description
                   212339
Seq. No.
                   LIB3145-050-Q1-K1-A10
Seq. ID
                   BLASTX
Method
                   g4006827
NCBI GI
                   474
BLAST score
                   9.0e-48
E value
                   123
Match length
% identity
                   74
                   (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   212340
Seq. No.
                   LIB3145-050-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   q4063739
NCBI GI
                                                              ٠<u>۴</u>,
                   155
BLAST score
                   3.0e-10
E value
Match length
                   39
                   72
% identity
                   (AC005851) putative copper/zinc superoxide dismutase
NCBI Description
                   [Arabidopsis thaliana]
                   212341
Seq. No.
                   LIB3145-050-Q1-K1-A7
Seq. ID
                   BLASTN
Method
                   g3241917
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
Match length
                   80
                   86
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19B1, complete sequence [Arabidopsis thaliana]
```



```
BLASTX
Method
NCBI GI
                  q2225877
                  444
BLAST score
                  3.0e-44
E value
                  111
Match length
                  78
% identity
                  (AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694)
NCBI Description
                  Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_
                  (AB001581) DNA helicase p50 [Rattus norvegicus]
                  212343
Seq. No.
                  LIB3145-050-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  g3063643
NCBI GI
                  184
BLAST score
                  5.0e-14
E value
                  64
Match length
                  67
% identity
                  (AF056622) putative Cu/Zn superoxide dismutase precursor
NCBI Description
                   [Vitis vinifera]
                  212344
Seq. No.
                  LIB3145-050-Q1-K1-B10
Seq. ID
Method
                  BLASTX
                  g1174592
NCBI GI
BLAST score
                   451
                   6.0e-46
E value
                   118
Match length
% identity
                   TUBULIN ALPHA-1 CHAIN >gi_2119270 pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
Seq. No.
                   212345
                   LIB3145-050-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2627181
                   172
BLAST score
                   2.0e-12
E value
Match length
                   35
% identity
                   (D89619) cycloartenol synthase [Pisum sativum]
NCBI Description
                   212346
Seq. No.
                   LIB3145-050-Q1-K1-B2
Seq. ID
Method
                   BLASTX
                   g1916292
NCBI GI
BLAST score
                   198
                   2.0e-15
E value
                   93
Match length
                   39
% identity
                   (U89793) allergen Amb a VI [Ambrosia artemisiifolia]
NCBI Description
                   212347
Seq. No.
                   LIB3145-050-Q1-K1-B5
Seq. ID
```

29483

BLASTX

g1335862

Method

NCBI GI

NCBI Description



```
BLAST score
                  9.0e-66
E value
                  132
Match length
                  89
% identity
NCBI Description (U42608) clathrin heavy chain [Glycine max]
                  212348
Seq. No.
                  LIB3145-050-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                   q2065531
NCBI GI
BLAST score
                   297
                   4.0e-27
E value
                   104
Match length
% identity
                   58
NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
                   212349
Seq. No.
                   LIB3145-050-Q1-K1-C1
Seq. ID
Method
                   BLASTX
                   g533692
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
                   59
Match length
                   58
% identity
NCBI Description (U12150) protease inhibitor [Glycine max]
                   212350
Seq. No.
                   LIB3145-050-Q1-K1-C11
Seq. ID
                   BLASTX
Method
                   g1103712
NCBI GI
BLAST score
                   556
E value
                   3.0e-57
                   131
Match length
% identity
                   89
                   (X83729) inorganic pyrophosphatase [Nicotiana tabacum]
NCBI Description
Seq. No.
                   212351
                   LIB3145-050-Q1-K1-C2
Seq. ID
Method
                   BLASTX
                   g2244847
NCBI GI
BLAST score
                   276
                   5.0e-25
E value
Match length
                   60
                   88
 % identity
                   (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                    [Arabidopsis thaliana]
                   212352
 Seq. No.
 Seq. ID
                   LIB3145-050-Q1-K1-C5
Method
                   BLASTN
                   g598848
 NCBI GI
                   32
 BLAST score
                   6.0e-09
 E value
                   64
 Match length
 % identity
                   88
```

Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Match length

% identity

118 69



```
212353
Seq. No.
                  LIB3145-050-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                  q1346735
NCBI GI
                  405
BLAST score
                  1.0e-39
E value
                  117
Match length
                  68
% identity
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                  (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_1076562_pir__S49647 phosphoglycerate mutase (EC
                  5.4.2.1) - castor bean >gi_474170_emb_CAA49995_ (X70652)
                  phosphoglycerate mutase [Ricinus communis]
                  212354
Seq. No.
                  LIB3145-050-Q1-K1-C8
Seq. ID
                  BLASTX
Method
                  g4098129
NCBI GI
                  561
BLAST score
                  5.0e-58
E value
                  109
Match length
                  98
% identity
                  (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                  212355
Seq. No.
                  LIB3145-050-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  g1408471
NCBI GI
                   440
BLAST score
                   1.0e-43
E value
                   119
Match length
                   71
% identity
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   212356
Seq. No.
                   LIB3145-050-Q1-K1-D10
Seq. ID
                   BLASTX
Method
                   q3776559
NCBI GI
BLAST score
                   251
                   1.0e-21
E value
                   122
Match length
% identity
                   (AC005388) Strong similarity to gene F14J9.26 gi_3482933
NCBI Description
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb AC003970. ESTs gb_Z35332 and gb_F19907 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   212357
Seq. ID
                   LIB3145-050-Q1-K1-D11
                   BLASTX
Method
NCBI GI
                   q2244898
BLAST score
                   277
                   5.0e-45
E value
```



NCBI Description (Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 212358

Seq. ID LIB3145-050-Q1-K1-D2

Method BLASTX
NCBI GI g3080400
BLAST score 258
E value 2.0e-22
Match length 52
% identity 94

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi\_4455264\_emb\_CAB36800.1\_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No. 212359

Seq. ID LIB3145-050-Q1-K1-D7

Method BLASTX
NCBI GI g1703375
BLAST score 466
E value 9.0e-47
Match length 90

% identity 100

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi\_965483\_dbj\_BAA08259\_ (D45420)

DcARF1 [Daucus carota]

Seq. No. 212360

Seq. ID LIB3145-050-Q1-K1-D8

Method BLASTX
NCBI GI g1778093
BLAST score 561
E value 6.0e-58
Match length 129
% identity 84

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 212361

Seq. ID LIB3145-050-Q1-K1-D9

Method BLASTX
NCBI GI g3901014
BLAST score 235
E value 1.0e-19
Match length 55
% identity 76

NCBI Description (AJ130886) metallothionein-like protein class II [Fagus

sylvatica]

Seq. No. 212362

Seq. ID LIB3145-050-Q1-K1-E6

Method BLASTX
NCBI GI g3269285
BLAST score 451
E value 5.0e-45
Match length 125
% identity 71



```
NCBI Description (AL030978) hypothetical protein [Arabidopsis thaliana]
                  212363
Seq. No.
                  LIB3145-050-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  q3269285
NCBI GI
                  196
BLAST score
                  3.0e-15
E value
                  59
Match length
                  66
% identity
NCBI Description (AL030978) hypothetical protein [Arabidopsis thaliana]
                  212364
Seq. No.
                  LIB3145-050-Q1-K1-E8
Seq. ID
                  BLASTX
Method
                  a2388561
NCBI GI
                  490
BLAST score
                  1.0e-49
E value
                  120
Match length
                  78
% identity
                  (AC000098) Similar to Arabidopsis hypothetical protein
NCBI Description
                  PID:e326839 (gb Z97337). [Arabidopsis thaliana]
                  212365
Seq. No.
                  LIB3145-050-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g3269285
NCBI GI
                  252
BLAST score
                  8.0e-22
E value
                  72
Match length
                   69
% identity
NCBI Description (AL030978) hypothetical protein [Arabidopsis thaliana]
                   212366
Seq. No.
                  LIB3145-050-Q1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1350783
                   220
BLAST score
                   6.0e-18
E value
Match length
                   130
% identity
                   RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
NCBI Description
                   >gi 282883 pir S27756 receptor-like protein kinase
                   precursor - Arabidopsis thaliana >gi_166850 (M84660)
                   receptor-like protein kinase [Arabidopsis thaliana]
                   >gi 2842492 emb CAA16889 (AL021749) receptor-like protein
                   kinase 5 precursor (RLK5) [Arabidopsis thaliana]
 Seq. No.
                   212367
                   LIB3145-050-Q1-K1-F3
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g2642215
 BLAST score
                   181
                   2.0e-13
E value
Match length
                   70
                   51
 % identity
 NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]
```



```
212368
Seq. No.
                  LIB3145-050-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  g2961300
NCBI GI
                  304
BLAST score
                  5.0e-28
E value
                  63
Match length
                  97
% identity
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
                  212369
Seq. No.
                  LIB3145-050-Q1-K1-G1
Seq. ID
Method
                  BLASTX
                  g3122032
NCBI GI
                  226
BLAST score
                  1.0e-18
E value
                   94
Match length
                   46
% identity
                  HYPOTHETICAL 56.3 KD PROTEIN C47E12.8 IN CHROMOSOME IV
NCBI Description
                   >gi_3875109_emb_CAA93104_ (Z68882) predicted using
                   Genefinder; Similarity to Mouse Ulip protein (PIR Acc. No.
                   S55525) [Caenorhabditis elegans]
                   212370
Seq. No.
                   LIB3145-050-Q1-K1-G3
Seq. ID
                   BLASTX
Method
                   g2078350
NCBI GI
                   596
BLAST score
                   5.0e-62
E value
                   132
Match length
                   89
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   212371
                   LIB3145-050-Q1-K1-G5
Seq. ID
Method
                   BLASTX
                   a2505940
NCBI GI
                   380
BLAST score
                   1.0e-36
E value
Match length
                   101
% identity
                   (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
NCBI Description
                   212372
Seq. No.
                   LIB3145-050-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   q4510342
NCBI GI
BLAST score
                   489
                   2.0e-49
E value
Match length
                   132
                   73
% identity
                   (AC006921) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
```

29488

212373

LIB3145-050-Q1-K1-G9

Seq. No.

Seq. ID



BLASTX Method q464628 NCBI GI 141 BLAST score 6.0e-09 E value 46 Match length 65 % identity 60S RIBOSOMAL PROTEIN L22 (EPSTEIN-BARR VIRUS SMALL RNA NCBI Description

ASSOCIATED PROTEIN) (EBER ASSOCIATED PROTEIN) (EAP) (HEPARIN BINDING PROTEIN HBP15) >gi\_542841\_pir\_\_JC2120 heparin-binding protein 15 - human >gi\_31062\_emb CAA42007 (X59357) Epstein-Barr virus small RNA associated protein [Homo sapiens] >gi\_409070\_dbj\_BAA04545 (D17652) HBp15/L22

[Homo sapiens] >gi 4506613 ref NP 000974.1 pRPL22\_

ribosomal protein L22

Seq. No. 212374

LIB3145-050-Q1-K1-H7 Seq. ID

Method BLASTX NCBI GI g2218150 BLAST score 712 1.0e-75E value Match length 134 % identity

(AF005278) type IIIa membrane protein cp-wap11 [Vigna NCBI Description

unguiculata]

Seq. No. 212375

LIB3145-051-Q1-K1-A1 Seq. ID

Method BLASTX NCBI GI g416922 BLAST score 514 2.0e-52 E value Match length 119 81 % identity

DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) NCBI Description

(DUTP PYROPHOSPHATASE) (P18) >gi 282947\_pir\_\_JQ1599 dUTP

pyrophosphatase (EC 3.6.1.23) - tomato

>gi\_251897\_bbs\_109276 (S40549) deoxyuridine triphosphatase,

dUTPase,  $P\overline{1}8$  { $\overline{E}C$  3.6.1.23} [tomatoes, Tint Tim cultivar

LA154, Peptide, 169 aa] [Lycopersicon esculentum]

212376 Seq. No.

LIB3145-051-Q1-K1-A2 Seq. ID

BLASTX Method g1843527 NCBI GI 362 BLAST score 1.0e-34 E value Match length 98 % identity

(U73747) annexin [Gossypium hirsutum] NCBI Description

212377 Seq. No.

LIB3145-051-Q1-K1-A7 Seq. ID

Method BLASTX NCBI GI g1351408 BLAST score 487 2.0e-49 E value



```
Match length
                  83
% identity
                  VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                  >gi_1076563_pir__S51117 cystein proteinase - sweet orange
                  >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by
                  similarity) [Citrus sinensis] >gi_1588548_prf_2208463A
                  vascular processing protease [Citrus sinensis]
                  212378
Seq. No.
                  LIB3145-051-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g1903034
NCBI GI
                  341
BLAST score
                  3.0e-32
E value
                  99
Match length
                  68
% identity
NCBI Description (X94625) amp-binding protein [Brassica napus]
                  212379
Seq. No.
                  LIB3145-051-Q1-K1-B9
Seq. ID
                  BLASTX
Method
                  g2501449
NCBI GI
                   335
BLAST score
                   2.0e-31
E value
                   66
Match length
                   97
% identity
                  UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773_emb_CAA67922_
NCBI Description
                   (X99608) ubiquitin-like protein [Oryza sativa]
                   212380
Seq. No.
                   LIB3145-051-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g3915826
NCBI GI
                   449
BLAST score
                   7.0e-45
E value
                   112
Match length
                   72
% identity
                   60S RIBOSOMAL PROTEIN L5
NCBI Description
                   212381
Seq. No.
                   LIB3145-051-Q1-K1-C8
Seq. ID
Method
                   BLASTX
                   g730526
NCBI GI
                   408
BLAST score
E value
                   4.0e-40
                   101
Match length
                   79
 % identity
                   60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
 NCBI Description
                   >gi 480787_pir_ S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi_404166 emb_CAA53005_ (X75162) BBC1 protein
                   [Arabidopsis thaliana]
```

212382 Seq. No.

LIB3145-051-Q1-K1-C9 Seq. ID

Method BLASTX g1706958 NCBI GI BLAST score 394

NCBI Description



```
2.0e-38
E value
                  103
Match length
                  71
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  212383
Seq. No.
                  LIB3145-051-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  g1082766
NCBI GI
                  180
BLAST score
                  2.0e-13
E value
Match length
                  49
                  67
% identity
                  ribosomal protein L29 - human >gi_793843_emb_CAA89008_
NCBI Description
                   (Z49148) ribosomal protein L29 [Homo sapiens]
                   212384
Seq. No.
                   LIB3145-051-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3522938
BLAST score
                   259
E value
                   1.0e-22
Match length
                   92
% identity
                   54
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                   212385
Seq. No.
                   LIB3145-051-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1850546
                   228
BLAST score
                   5.0e-19
E value
Match length
                   105
% identity
                   53
                   (U88045) syntaxin related protein AtVam3p [Arabidopsis
NCBI Description
                   thaliana]
                   212386
Seq. No.
                   LIB3145-051-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3738322
NCBI GI
                   382
BLAST score
                   6.0e-37
E value
                   78
Match length
% identity
                   (AC005170) putative small nuclear ribonucleoprotein
NCBI Description
                   [Arabidopsis thaliana]
                   212387
Seq. No.
Seq. ID
                   LIB3145-051-Q1-K1-E1
                   BLASTX
Method
                   g1619300
NCBI GI
BLAST score
                   506
                   2.0e-51
E value
                   105
Match length
                   90
% identity
```

(X95269) LRR protein [Lycopersicon esculentum]

NCBI Description

. . . -



```
Seq. No.
                   212388
                   LIB3145-051-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   g3023637
NCBI GI
                   299
BLAST score
                   2.0e-27
E value
                   87
Match length
                   66
% identity
                   PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN
NCBI Description
                   8) >gi_1362899_pir__A56236 probable RNA helicase 1 - human
                   >gi 807817_dbj_BAA09078_ (D50487) RNA helicase (HRH1) [Homo
                   sapīens]
                   212389
Seq. No.
                   LIB3145-051-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g170354
NCBI GI
BLAST score
                   499
                   7.0e-51
E value
                   100
Match length
                   20
% identity
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                   212390
                   LIB3145-051-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g549063
NCBI GI
                    400
BLAST score
                    4.0e-39
E value
                    91
Match length
                    82
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
                    212391
Seq. No.
Seq. ID
                    LIB3145-051-Q1-K1-F1
Method
                    BLASTX
                    q3176669
NCBI GI
                    287
BLAST score
                    9.0e-26
E value
                    89
Match length
% identity
                    60
                    (AC004393) End is cut off. [Arabidopsis thaliana]
NCBI Description
                    212392
Seq. No.
                    LIB3145-051-Q1-K1-F11
Seq. ID
                    BLASTX
Method
NCBI GI
                    q131770
BLAST score
                    170
                    2.0e-12
E value
Match length
                    63
% identity
                    56
                    40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
```

29492

(VEGETATIVE SPECIFIC PROTEIN V12) >gi\_70880\_pir\_\_R3D024



ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi 7353 emb CAA29844 (X06636) rp1024 protein [Dictyostelium discoideum]

212393 Seq. No. Seq. ID LIB3145-051-Q1-K1-F3 Method BLASTX NCBI GI g3176707 BLAST score 192 E value 8.0e-15 Match length 90 44

% identity (AC002392) putative proline-rich protein APG [Arabidopsis NCBI Description

Seq. No. 212394

Seq. ID LIB3145-051-Q1-K1-F5

Method BLASTX NCBI GI g3913006 BLAST score 455 1.0e-45 E value 107 Match length % identity

AGAMOUS PROTEIN >gi\_478387\_pir\_\_JQ2212 pMADS3 protein - garden petunia >gi\_313113\_emb\_CAA51417\_ (X72912) pMADS3 NCBI Description

[Petunia x hybrida]

Seq. No. 212395

LIB3145-051-Q1-K1-F6 Seq. ID

Method BLASTN NCBI GI g3738256 BLAST score 35 E value 3.0e-10 47 Match length % identity 94

Populus nigra PnCytPGK1 mRNA for cytosolic phosphoglycerate NCBI Description

kinase 1, complete cds

212396 Seq. No.

LIB3145-051-Q1-K1-F7 Seq. ID

BLASTX Method g2947063 NCBI GI 187 BLAST score 5.0e-14 E value 109 Match length 26 % identity

(AC002521) putative Ser/Thr protein kinase [Arabidopsis NCBI Description

thaliana]

212397 Seq. No.

Seq. ID LIB3145-051-Q1-K1-G10

BLASTX Method NCBI GI g543813 164 BLAST score 6.0e-12 E value 38 Match length % identity 89



```
FLORAL HOMEOTIC PROTEIN APETALA1 (AGL7 PROTEIN)
  NCBI Description
                    >qi 16162 emb CAA78909 (Z16421) AP1 [Arabidopsis thaliana]
                    212398
  Seq. No.
                    LIB3145-051-Q1-K1-G3
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g4204257
                    308
BLAST score
                    2.0e-28
  E value
                    87
  Match length
  % identity
                    (AC005223) 5493 [Arabidopsis thaliana]
  NCBI Description
                     212399
  Seq. No.
                    LIB3145-051-Q1-K1-G6
  Seq. ID
  Method
                    BLASTN
                    g2281081
  NCBI GI
  BLAST score
                     40
                     3.0e-13
  E value
                     52
  Match length
  % identity
                    Arabidopsis thaliana chromosome II BAC F18019 genomic
  NCBI Description
                     sequence, complete sequence [Arabidopsis thaliana]
  Seq. No.
                     212400
                     LIB3145-051-Q1-K1-G9
  Seq. ID
                     BLASTX
  Method
                     q2065531
  NCBI GI
  BLAST score
                     395
                     2.0e-38
  E value
                     95
  Match length
                     74
  % identity
  NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
  Seq. No.
                     212401
                     LIB3145-051-Q1-K1-H10
  Seq. ID
  Method
                     BLASTN
                     g3821780
  NCBI GI
  BLAST score
                     33
                     4.0e-09
  E value
  Match length
                     36
                     97
  % identity
  NCBI Description Xenopus laevis cDNA clone 27A6-1
                     212402
  Seq. No.
                     LIB3145-051-Q1-K1-H2
  Seq. ID
  Method
                     BLASTX
                     g2914706
  NCBI GI
                     347
  BLAST score
                     6.0e-33
  E value
                     86
  Match length
```

74 % identity

(AC003974) putative homeobox protein [Arabidopsis thaliana] NCBI Description

212403 Seq. No.

LIB3145-051-Q1-K1-H9 Seq. ID

Method BLASTX



```
NCBI GI
                   q2459442
                  289
BLAST score
                   4.0e-26
E value
                  89
Match length
% identity
                   (AC002332) putative DNA-binding protein PD1 [Arabidopsis
NCBI Description
                   thaliana]
                   212404
Seq. No.
                   LIB3145-052-Q1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g127041
BLAST score
                   357
E value
                   5.0e-34
                   125
Match length
                   68
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_81647_pir__JN0131 methionine adenosyltransferase (EC
                   2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
                   S-adenosylmethionine synthetase [Arabidopsis thaliana]
                   212405
Seq. No.
                   LIB3145-052-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   q2281330
NCBI GI
                   442
BLAST score
                   6.0e-44
E value
Match length
                   127
                   65
% identity
                   (U85646) putative pectate lyase Nt59 [Nicotiana tabacum]
NCBI Description
                   212406
Seq. No.
                   LIB3145-052-Q1-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1665777
BLAST score
                   151
                   2.0e-10
E value
                  ` 50
Match length
% identity
                   60
                   (D87444) Similar to S.cerevisiae EMP70 protein precursor
NCBI Description
                    (S25110) [Homo sapiens]
                   212407
Seq. No.
                   LIB3145-052-Q1-K1-A6
 Seq. ID
                   BLASTX
Method
                   g2498490
NCBI GI
                   265
BLAST score
                   2.0e-23
 E value
                   99
Match length
                   51
 % identity
                   VIRAL INTEGRATION SITE PROTEIN INT-6 >gi 1854579 (L35556)
 NCBI Description
                   Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse
                   Int-6 [Homo sapiens] >gi 2351382 (U54562) eIF3-p48 [Homo
                    sapiens] >gi 2688818 (U8\overline{5}947) Int-6 [Homo sapiens]
```

>gi\_2695701 (U94175) mammary tumor-associated protein INT6
[Homo sapiens] >gi\_4503521\_ref\_NP\_001559.1\_pEIF3S6\_ murine



mammary tumor integration site 6 (oncogene homolog)

```
Seq. No.
                  LIB3145-052-Q1-K1-A7
Seq. ID
                  BLASTX
Method
                  q1703115
NCBI GI
BLAST score
                  631
                  4.0e-66
E value
                  117
Match length
                  99
% identity
                  ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
NCBI Description
                  thaliana >gi 1145695 (U39480) actin [Arabidopsis thaliana]
                  >gi 3236244 (AC004684) actin 3 protein [Arabidopsis
                  thalianal
                  212409
Seq. No.
                  LIB3145-052-Q1-K1-A9
Seq. ID
                  BLASTX
Method
                  g3024127
NCBI GI
                  613
BLAST score
                  5.0e-64
E value
                  118
Match length
                   96
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine
                   synthetase 2 [Catharanthus roseus]
                   212410
Seq. No.
                   LIB3145-052-Q1-K1-B1
Seq. ID
                   BLASTX
Method
                   g418777
NCBI GI
BLAST score
                   262
                   8.0e-23
E value
                   49
Match length
                   98
% identity
                   phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic
NCBI Description
                   chain (clone EP7) - Arabidopsis thaliana (fragment)
Seq. No.
                   212411
                   LIB3145-052-Q1-K1-B11
Seq. ID
                   BLASTX
Method
                   q3688600
NCBI GI
                   492
BLAST score
E value
                   9.0e-50
                   125
Match length
 % identity
                   (AB009030) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
                   212412
 Seq. No.
                   LIB3145-052-Q1-K1-B12
 Seq. ID
 Method
                   BLASTX
                   g346685
 NCBI GI
                   389
 BLAST score
 E value
                   1.0e-37
                   97
 Match length
```

29496

70

% identity



66

% identity

NCBI Description

```
NCBI Description developmentally-regulated GTP-binding protein - mouse
                  212413
Seq. No.
                  LIB3145-052-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  g2129955
NCBI GI
BLAST score
                   418
                   4.0e-41
E value
                   127
Match length
                   57
% identity
                  photoassimilate-responsive protein PAR-1b precursor -
NCBI Description
                   common tobacco >gi 871487 emb CAA58731 (X83851) mRNA
                   inducible by sucrose and salicylic acid expressed in
                   sugar-accumulating tobacco plants [Nicotiana tabacum]
Seq. No.
                   212414
Seq. ID
                   LIB3145-052-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g2827715
BLAST score
                   720
                   2.0e-76
E value
Match length
                   135
% identity
                   98
                   (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   212415
Seq. ID
                   LIB3145-052-Q1-K1-C10
Method
                   BLASTX
                   g3859570
NCBI GI
                   177
BLAST score
                   5.0e-13
E value
Match length
                   43
                   77
% identity
                  (AF098753) unknown [Oryza sativa]
NCBI Description
                   212416
Seq. No.
                   LIB3145-052-Q1-K1-C11
Seq. ID
                   BLASTN
Method
                   g3869074
NCBI GI
                   33
BLAST score
                   6.0e-09
E value
Match length
                   33
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMI9, complete sequence [Arabidopsis thaliana]
                   212417
Seq. No.
                   LIB3145-052-Q1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2281330
BLAST score
                   499
                   1.0e-50
E value
Match length
                   142
```

(U85646) putative pectate lyase Nt59 [Nicotiana tabacum]



Seq. No. 212418

Seq. ID LIB3145-052-Q1-K1-C3

Method BLASTX
NCBI GI g122085
BLAST score 506
E value 2.0e-51
Match length 119
% identity 86

NCBI Description HISTONE H3 >gi\_81641\_pir\_\_S06250 histone H3 - Arabidopsis

>gi 225459 prf 1303352A histone H3 [Helicoverpa zea]
>gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 212419

Seq. ID LIB3145-052-Q1-K1-C4

Method BLASTX
NCBI GI g2979552
BLAST score 450
E value 7.0e-45
Match length 137
% identity 66

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 212420

Seq. ID LIB3145-052-Q1-K1-C6

Method BLASTX
NCBI GI g1928960
BLAST score 462
E value 3.0e-46
Match length 131
% identity 69

NCBI Description (U92286) pyrroline-5-carboxylate synthetase [Actinidia

deliciosa]

Seq. No. 212421

Seq. ID LIB3145-052-Q1-K1-C8

Method BLASTX

29498

ł

Match length

134



```
NCBI GI
                  q3650030
BLAST score
                  247
                  4.0e-21
E value
Match length
                  79
% identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                  212422
Seq. No.
                  LIB3145-052-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350548
BLAST score
                  301
E value
                  2.0e-27
                   95
Match length
                  57
% identity
NCBI Description (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                  212423
                  LIB3145-052-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  q1518540
NCBI GI
                   548
BLAST score
E value
                   2.0e-56
Match length
                   121
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                   212424
Seq. ID
                  LIB3145-052-01-K1-D12
Method
                   BLASTX
NCBI GI
                   q1346485
BLAST score
                   645
E value
                   9.0e-68
Match length
                   135
                   90
% identity
                   MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
NCBI Description
                   MALIC ENZYME) (NADP-ME) >gi 20469 emb CAA39690_ (X56233)
                   malic enzyme [Populus balsamifera subsp. trichocarpa]
                   212425
Seq. No.
                   LIB3145-052-Q1-K1-D5
Seq. ID
                   BLASTX
Method
                   g1213450
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
                   86
Match length
% identity
                   58
                   (U48963) isopentenyl pyrophosphate isomerase [Clarkia
NCBI Description
                   breweri]
                   212426
Seq. No.
Seq. ID
                   LIB3145-052-Q1-K1-D6
                   BLASTX
Method
                   g3309243
NCBI GI
BLAST score
                   657
                   4.0e-69
E value
```



```
% identity
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                  limon]
                  212427
Seq. No.
                  LIB3145-052-Q1-K1-D8
Seq. ID
                  BLASTX
Method
                  g1888557
NCBI GI
                  580
BLAST score
                  4.0e-60
E value
                  127
Match length
                  79
% identity
NCBI Description (U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase
                  [Lupinus angustifolius]
                  212428
Seq. No.
                  LIB3145-052-Q1-K1-D9
Seq. ID
                  BLASTX
Method
                  q3451068
NCBI GI
                  220
BLAST score
                  4.0e-18
E value
                  89
Match length
                  53
% identity
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                  212429
Seq. No.
                  LIB3145-052-Q1-K1-E3
Seq. ID
                  BLASTX
Method
                  g2829909
NCBI GI
                  190
BLAST score
                  2.0e-14
E value
                  135
Match length
                  44
% identity
NCBI Description (AC002291) Hypothetical protein [Arabidopsis thaliana]
                  212430
Seq. No.
                  LIB3145-052-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  q2662415
NCBI GI
                   141
BLAST score
                  1.0e-08
E value
                   48
Match length
                   56
% identity
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]
Seq. No.
                   212431
                   LIB3145-052-Q1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1706918
                   266
BLAST score
E value
                   2.0e-23
                   95
Match length
                   47
% identity
                  FLAVONOL SULFOTRANSFERASE-LIKE >gi 498647 (U10277)
NCBI Description
                   sulfotransferase-like flavonol [Flaveria bidentis]
```

Seq. No. 212432

```
LIB3145-052-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g2764941
NCBI GI
                  410
BLAST score
                  3.0e-40
E value
Match length
                  101
% identity
                  70
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
Seq. No.
                  212433
                  LIB3145-052-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  q2764941
NCBI GI
                  285
BLAST score
                   1.0e-25
E value
Match length
                   90
% identity
                   58
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                   thaliana]
Seq. No.
                   212434
                  LIB3145-052-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   q4539363
NCBI GI
                   154
BLAST score
E value
                   4.0e-10
                   88
Match length
% identity
                   41
                  (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
                   212435
Seq. No.
                   LIB3145-052-Q1-K1-F7
Seq. ID
Method
                   BLASTX
                   q4006911
NCBI GI
                   205
BLAST score
                   4.0e-16
E value
Match length
                   75
% identity
                   87
                   (Z99708) trichohyalin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212436
                   LIB3145-052-Q1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q461812
                   230
BLAST score
                   5.0e-19
E value
Match length
                   142
                   39
% identity
                  CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
NCBI Description
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                   Cytochrome P-450 protein [Catharanthus roseus]
                   >gi 445604 prf__1909351A cytochrome P450 [Catharanthus
                   roseus]
```

```
Seq. No.
Seq. ID
                  LIB3145-052-Q1-K1-G2
                  BLASTX
Method
                  g1351359
NCBI GI
                  291
BLAST score
                  3.0e-26
E value
Match length
                  69
                  71
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN
NCBI Description
                   (MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi 1071788_pir__S48690
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein
                  - potato >gi_488712_emb_CAA55860 (X79273)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
Seq. No.
                  212438
                  LIB3145-052-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539355
                  166
BLAST score
                  1.0e-11
E value
                  47
Match length
                   68
% identity
                  (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212439
                  LIB3145-052-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                   a3024386
NCBI GI
BLAST score
                   504
E value
                   3.0e-51
                   139
Match length
                   62
% identity
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                   >gi 2129500 pir_ S52006 polygalacturonase - upland cotton
                   >gi_606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                   212440
                   LIB3145-052-Q1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4325367
BLAST score
                   185
                   8.0e-14
E value
                   97
Match length
                   48
% identity
                   (AF128396) contains similarity to Nicotiana tabacum B-type
NCBI Description
                   cyclin (GB:D50737) [Arabidopsis thaliana]
Seq. No.
                   212441
                   LIB3145-052-Q1-K1-G8
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1706403
BLAST score 317
E value 2.0e-29
Match length 65
% identity 94

NCBI Description GLUTAMATE DEHYDROGENASE (GDH) >gi\_1085815\_pir\_\_S54797 glutamate dehydrogenase (EC 1.4.1.2) - Vitis vinifera

```
>gi 806595 emb CAA60507 (X86924) glutamate dehydrogenase
                  [Vitis vinifera]
                  212442
Seq. No.
                  LIB3145-052-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g505482
NCBI GI
                  279
BLAST score
                  4.0e-25
E value
                  83
Match length
                  73
% identity
                  (X64349) 33 kDa polypeptide of water-oxidizing complex of
NCBI Description
                  photosystem II [Nicotiana tabacum]
                  212443
Seq. No.
Seq. ID
                  LIB3145-052-Q1-K1-H5
Method
                  BLASTX
                  g629858
NCBI GI
                  476
BLAST score
                  6.0e-48
E value
Match length
                  115
% identity
                  80
NCBI Description protein kinase C inhibitor - maize
                  212444
Seq. No.
                  LIB3145-052-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g3123745
NCBI GI
BLAST score
                   182
                  2.0e-13
E value
                  118
Match length
                   35
% identity
NCBI Description (AB013447) aluminum-induced [Brassica napus]
                  212445
Seq. No.
                  LIB3145-052-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                   g872116
NCBI GI
                   646
BLAST score
                   7.0e-68
E value
                   131
Match length
                   33
% identity
NCBI Description (X79770) sti (stress inducible protein) [Glycine max]
                   212446
Seq. No.
                   LIB3145-052-Q1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q872116
                   582
BLAST score
                   2.0e-60
E value
                   135
Match length
% identity
                   31
                  (X79770) sti (stress inducible protein) [Glycine max]
NCBI Description
Seq. No.
                   212447
Seq. ID
                   LIB3145-053-Q1-K1-A3
                   BLASTX
Method
```

```
q2351374
NCBI GI
                  354
BLAST score
                  1.0e-33
E value
Match length
                  115
% identity
                  69
                  (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                  [Arabidopsis thaliana]
                  212448
Seq. No.
                  LIB3145-053-Q1-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q296442
BLAST score
                  33
                  6.0e-09
E value
Match length
                  65
% identity
                  88
NCBI Description G.max ADR11 mRNA
Seq. No.
                  212449
                  LIB3145-053-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084349
BLAST score
                  585
                  9.0e-61
E value
Match length
                  120
                  90
% identity
                  aldehyde dehydrogenase homolog btg-26 - rape
NCBI Description
                  >gi_913941_bbs_164188 (S77096) aldehyde dehydrogenase
                  homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494
                  aa] [Brassica napus]
                  212450
Seq. No.
Seq. ID
                  LIB3145-053-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4325371
                  245
BLAST score
                  8.0e-21
E value
                  103
Match length
% identity
                   53
                  (AF128396) contains similarity to Medicago truncatula N7
NCBI Description
                  protein (GB:Y17613) [Arabidopsis thaliana]
Seq. No.
                  212451
Seq. ID
                  LIB3145-053-Q1-K1-A7
                  BLASTN
Method
NCBI GI
                  g3789728
                   48
BLAST score
                  7.0e-18
E value
                   48
Match length
                  100
% identity
NCBI Description Tortula ruralis 18S ribosomal RNA gene, partial sequence
Seq. No.
                  212452
Seq. ID
                  LIB3145-053-Q1-K1-B1
```

29504

BLASTX

204

g3522938

Method NCBI GI

BLAST score

```
3.0e-16
E value
Match length
                  98
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                  212453
Seq. No.
                  LIB3145-053-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  q4490292
NCBI GI
                  180
BLAST score
E value
                  3.0e-13
Match length
                  52
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
```

212454 Seq. No.

LIB3145-053-Q1-K1-B2 Seq. ID

Method BLASTX g4567210 NCBI GI 456 BLAST score 6.0e-50 E value Match length 108 86 % identity

(AC007168) unknown protein [Arabidopsis thaliana] NCBI Description

212455 Seq. No.

LIB3145-053-Q1-K1-B3 Seq. ID

BLASTX Method NCBI GI g2809326 424 BLAST score 8.0e-42 E value 113 Match length 73 % identity

NCBI Description (U72663) uricase II [Phaseolus vulgaris]

212456 Seq. No.

LIB3145-053-Q1-K1-B4 Seq. ID

BLASTX Method NCBI GI q1362051 674 BLAST score 4.0e-71 E value 135 Match length 93 % identity

protein kinase 3 - soybean >gi\_310582 (L19361) protein NCBI Description

kinase 3 [Glycine max]

212457 Seq. No.

LIB3145-053-Q1-K1-B8 Seq. ID

BLASTX Method q4033349 NCBI GI 476 BLAST score 6.0e-48 E value 123 Match length 75 % identity

(AJ223496) phosphoenolpyrovate carboxylase [Brassica NCBI Description

juncea]

```
Seq. No.
                   212458
                   LIB3145-053-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   q3287881
NCBI GI
BLAST score
                   227
                   9.0e-19
E value
                   131
Match length
% identity
                   NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ)
                   >qi 2655053 (AF020351) NADH:ubiquinone oxidoreductase 18
                   kDa IP subunit [Homo sapiens]
                   >gi_4505369_ref_NP_002486.1_pNDUFS4_ NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q
                   reductase)
                   212459
Seq. No.
                   LIB3145-053-Q1-K1-C12
Seq. ID
                   BLASTX
Method
                   g3128228
NCBI GI
                   570
BLAST score
                   5.0e-59
E value
                   116
Match length
                   91
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   212460
Seq. No.
                   LIB3145-053-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g3287695
NCBI GI
BLAST score
                   413
                   2.0e-40
E value
Match length
                   132
                   58
% identity
                   (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                   thaliana]
Seq. No.
                   212461
Seq. ID
                   LIB3145-053-Q1-K1-C6
                   BLASTX
Method
                   q1084419
NCBI GI
BLAST score
                   161
                   6.0e-11
E value
                   127
Match length
                   36
% identity
NCBI Description histone H1 - common tobacco >gi_790929 (L29456) histone H1
                    [Nicotiana tabacum]
```

Seq. No. 212462

Seq. ID LIB3145-053-Q1-K1-C9

MethodBLASTXNCBI GIg100069BLAST score172E value3.0e-12

```
Match length
                   45
% identity
                  cysteine proteinase tpp (EC 3.4.22.-) - garden pea
NCBI Description
                  >qi 3980198 emb CAA46863_ (X66061) thiolprotease [Pisum
                   satīvum]
                   212463
Seq. No.
                  LIB3145-053-Q1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1531672
                   687
BLAST score
                   1.0e-72
E value
                   130
Match length
                   100
% identity
                   (U68461) actin [Striga asiatica]
NCBI Description
                   212464
Seq. No.
                   LIB3145-053-Q1-K1-D3
Seq. ID
Method
                   BLASTX
                   g2281334
NCBI GI
BLAST score
                   359
E value
                   3.0e - 34
Match length
                   133
% identity
                   54
                   (U83619) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
                   212465
Seq. No.
                   LIB3145-053-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g710626
                   154
                   4.0e-10
                   43
```

NCBI GI BLAST score E value Match length 60 % identity

(D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941 NCBI Description (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi\_3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

212466 Seq. No.

Seq. ID LIB3145-053-Q1-K1-D7

BLASTX Method g4558591 NCBI GI BLAST score 286 1.0e-25 E value 76 Match length 75 % identity

(AC006555) putative beta-1,3-glucanase [Arabidopsis NCBI Description

thaliana]

212467 Seq. No.

Seq. ID LIB3145-053-Q1-K1-D8

Method BLASTX q2583081 NCBI GI BLAST score 217 1.0e-17 E value Match length 93



% identity (AF026977) microsomal glutathione S-transferase 3 [Homo NCBI Description sapiens] 212468 Seq. No. LIB3145-053-Q1-K1-D9 Seq. ID BLASTX Method q4490321 NCBI GI 460 BLAST score 5.0e-46E value 105 Match length % identity 85 (AJ011604) nitrate transporter [Arabidopsis thaliana] NCBI Description 212469 Seq. No. LIB3145-053-Q1-K1-E1 Seq. ID Method BLASTN g1907378 NCBI GI BLAST score 38 6.0e-12 E value Match length 100 % identity 90 NCBI Description Nymphaea nouchali 28S ribosomal RNA gene, partial sequence Seq. No. 212470 LIB3145-053-Q1-K1-E3 Seq. ID Method BLASTX NCBI GI q2736387 BLAST score 163 3.0e-11 E value Match length 111 % identity 36 (AF039041) No definition line found [Caenorhabditis NCBI Description elegans] 212471 Seq. No. Seq. ID LIB3145-053-Q1-K1-E4 Method BLASTX g1354849 NCBI GI 328 BLAST score 1.0e-30 E value Match length 133 51 % identity (U57350) epoxide hydrolase [Nicotiana tabacum] NCBI Description 212472 Seq. No. Seq. ID LIB3145-053-Q1-K1-E7 BLASTN Method NCBI GI

g3821780 BLAST score 33 E value 5.0e-09 33 Match length 58 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 212473

LIB3145-053-Q1-K1-E9 Seq. ID



```
BLASTN
Method
                  g2828187
NCBI GI
                  36
BLAST score
                  9.0e-11
E value
                  44
Match length
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21C13, complete sequence [Arabidopsis thaliana]
                  212474
Seq. No.
Seq. ID
                  LIB3145-053-Q1-K1-F12
                  BLASTX
Method
                  q1220196
NCBI GI
                  575
BLAST score
                  2.0e-59
E value
Match length
                  122
% identity
                  89
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
Seq. No.
                  212475
Seq. ID
                  LIB3145-053-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1173256
                  646
BLAST score
                  7.0e-68
E value
                  124
Match length
                  99
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                  212476
Seq. No.
Seq. ID
                  LIB3145-053-Q1-K1-F5
                  BLASTX
Method
NCBI GI
                  g2558654
BLAST score
                  170
E value
                  4.0e-12
                  129
Match length
                  29
% identity
                  (AC002354) No definition line found [Arabidopsis thaliana]
NCBI Description
                  212477
Seq. No.
Seq. ID
                  LIB3145-053-Q1-K1-F8
Method
                  BLASTX
                  q4455237
NCBI GI
BLAST score
                  437
                  2.0e-43
E value
                  135
Match length
% identity
                   62
                   (AL035523) ubiquitin activating enzyme-like protein
NCBI Description
```

[Arabidopsis thaliana]

Seq. No. 212478

LIB3145-053-Q1-K1-F9 Seq. ID

Method BLASTX NCBI GI g3461848



```
BLAST score
                  2.0e-64
E value
                  127
Match length
                  94
% identity
NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]
                  212479
Seq. No.
                  LIB3145-053-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  g2765817
NCBI GI
BLAST score
                  368
                  3.0e-35
E value
                  134
Match length
                  52
% identity
                  (Z95352) AtMlo-h1 [Arabidopsis thaliana]
NCBI Description
                  >gi 3892049 gb AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                  [Arabidopsis thaliana]
                  212480
Seq. No.
                  LIB3145-053-Q1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4262174
BLAST score
                  262
                  7.0e-23
E value
                  62
Match length
                  77
% identity
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
                  212481
Seq. No.
                  LIB3145-053-Q1-K1-G11
Seq. ID
                  BLASTX
Method
                  g4455171
NCBI GI
BLAST score
                  523
                  2.0e-53
E value
                  128
Match length
                  72
% identity
NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]
                  212482
Seq. No.
Seq. ID
                  LIB3145-053-Q1-K1-G12
                  BLASTX
Method
                   g2780194
NCBI GI
BLAST score
                   305
                   5.0e-28
E value
Match length
                  88
                  74
% identity
NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]
                   212483
Seq. No.
                  LIB3145-053-Q1-K1-G2
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g462013
BLAST score 628
E value 9.0e-66
Match length 135
% identity 92

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

Seq. No.

212489

```
periwinkle >gi 348696 (L14594) heat shock protein 90
                  [Catharanthus roseus]
                  212484
Seq. No.
Seq. ID
                  LIB3145-053-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2088646
BLAST score
                  263
                  6.0e-23
E value
Match length
                  48
% identity
                  90
                  (AF002109) Sulp isolog [Arabidopsis thaliana]
NCBI Description
                  212485
Seq. No.
                  LIB3145-053-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281334
BLAST score
                   394
E value
                   3.0e-38
Match length
                   122
                   59
% identity
                  (U83619) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
                  212486
Seq. No.
                  LIB3145-053-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2947069
BLAST score
                   151
                   8.0e-10
E value
Match length
                   41
                   63
% identity
                  (AC002521) putative pectate lyase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212487
                   LIB3145-053-Q1-K1-G8
Seq. ID
Method
                   BLASTX
                   q4191784
                                                                       . 4,
NCBI GI
                   346
BLAST score
                   9.0e-33
E value
                   72
Match length
                   90
% identity
                   (AC005917) putative WD-40 repeat protein [Arabidopsis
NCBI Description
                   thaliana]
                   212488
Seq. No.
                   LIB3145-053-Q1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1001379
BLAST score
                   160
                   2.0e-11
E value
                   77
Match length
                   40
% identity
                   (D64006) aspartate beta-semialdehyde dehydrogenese
NCBI Description
                   [Synechocystis sp.]
```

>gi 542022 pir S39558 HSP90 homolog - Madagascar

```
LIB3145-053-Q1-K1-H3
Seq. ID
                  BLASTN
Method
                  g450548
NCBI GI
                  40
BLAST score
                  3.0e-13
E value
Match length
                  60
                  92
% identity
                  O.sativa (pRSAM-1) gene for S-adenosyl methionine
NCBI Description
                  synthetase
                  212490
Seq. No.
Seq. ID
                  LIB3145-053-Q1-K1-H6
                  BLASTX
Method
                  g2290532
NCBI GI
BLAST score
                  190
                  2.0e-14
E value
Match length
                  77
                  49
% identity
                  (U94748) AN11 [Petunia x hybrida]
NCBI Description
                  212491
Seq. No.
Seq. ID
                  LIB3145-054-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2529678
BLAST score
                  351
E value
                  3.0e - 33
Match length
                  96
% identity
                  29
NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]
                  212492
Seq. No.
Seq. ID
                  LIB3145-054-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4262242
BLAST score
                  537
E value
                  4.0e-55
Match length
                  131
                  82
% identity
                  (AC006200) NADC homolog [Arabidopsis thaliana]
NCBI Description
                  212493
Seq. No.
Seq. ID
                  LIB3145-054-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  609
                  2.0e-63
E value
Match length
                  135
                  84
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  212494
Seq. No.
Seq. ID
                  LIB3145-054-Q1-K1-A7
Method
                  BLASTX
                  g2492952
NCBI GI
BLAST score
                  507
E value
                  1.0e-51
Match length
                  122
```



% identity NCBI Description

CHORISMATE SYNTHASE 1 PRECURSOR

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)

>gi\_542026\_pir\_\_S40410 chorismate synthase (EC 4.6.1.4) 1

precursor - tomato >gi\_410482\_emb\_CAA79859\_ (Z21796)

chorismate synthase 1 [Lycopersicon esculentum]

Seq. No. 212495

Seq. ID LIB3145-054-Q1-K1-A9

Method BLASTX
NCBI GI g3913008
BLAST score 584
E value 1.0e-60
Match length 130
% identity 85

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi 3021338\_emb\_CAA06308\_ (AJ005041) cytosolic

fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No. 212496

Seq. ID LIB3145-054-Q1-K1-B10

Method BLASTX
NCBI GI g1498053
BLAST score 436
E value 3.0e-43
Match length 107
% identity 82

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 212497

Seq. ID LIB3145-054-Q1-K1-B11

Method BLASTX
NCBI GI g1335862
BLAST score 437
E value 2.0e-43
Match length 94
% identity 86

NCBI Description (U42608) clathrin heavy chain [Glycfine max]

Seq. No. 212498

Seq. ID LIB3145-054-Q1-K1-B4

Method BLASTX
NCBI GI g3913416
BLAST score 539
E value 3.0e-55
Match length 135
% identity 76

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi\_2129920\_pir\_\_S68990 adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle

>gi\_758695 (U12573) S-adenosyl-L-methionine decarboxylase proenzyme [Catharanthus roseus] >gi\_1094441\_prf\_\_2106177A

Met(S-adenosyl) decarboxylase [Catharanthus roseus]

Seq. No. 212499

Seq. ID LIB3145-054-Q1-K1-B5

Method BLASTX



```
NCBI GI
                  g3913419
                  158
BLAST score
                  3.0e-14
E value
Match length
                  70
                  61
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi_1531765_emb_CAA69076_ (Y07768)
                  S-adenosylmethionine decarboxylase [Datura stramonium]
Seq. No.
                  212500
Seq. ID
                  LIB3145-054-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q99809
                  559
BLAST score
                  1.0e-57
E value
                  131
Match length
% identity
                  75
                  gene Bp10 protein - rape >gi 17795 emb CAA47177_ (X66608)
NCBI Description
                  Bplo [Brassica napus]
Seq. No.
                  212501
Seq. ID
                  LIB3145-054-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g498906
BLAST score
                  162
E value
                  1.0e-11
Match length
                  65
% identity
                  53
                  (U10046) ribosomal protein L27 homolog [Pisum sativum]
NCBI Description
                  212502
Seq. No.
Seq. ID
                  LIB3145-054-Q1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2138088
BLAST score
                  78
                   6.0e-36
E value
                  78
Match length
                  100
% identity
NCBI Description Ehretia cymosa 18S ribosomal RNA gene, partial sequence
Seq. No.
                  212503
Seq. ID
                  LIB3145-054-Q1-K1-C7
Method
                  BLASTX
                  g3850821
NCBI GI
BLAST score
                   654
E value
                  8.0e-69
                  130
Match length
                  96
% identity
                   (Y18350) U2 snRNP auxiliary factor, large subunit
NCBI Description
                   [Nicotiana plumbaginifolia]
Seq. No.
                  212504
```

LIB3145-054-Q1-K1-C9 Seq. ID

Method BLASTX NCBI GI g1346485 BLAST score 437 2.0e-43 E value



Match length 113 % identity 77

NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT

MALIC ENZYME) (NADP-ME) >gi\_20469\_emb\_CAA39690\_ (X56233) malic enzyme [Populus balsamifera subsp. trichocarpa]

Seq. No. 212505

Seq. ID LIB3145-054-Q1-K1-D1

Method BLASTX
NCBI GI g1362115
BLAST score 597
E value 4.0e-62
Match length 132
% identity 83

NCBI Description pyruvate decarboxylase (EC 4.1.1.1) 1 - common tobacco

(fragment)

Seq. No. 212506

Seq. ID LIB3145-054-Q1-K1-D4

Method BLASTX
NCBI GI g267069
BLAST score 624
E value 3.0e-65
Match length 117
% identity 100

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183\_pir\_\_JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi 166914

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 212507

Seq. ID LIB3145-054-Q1-K1-D6

Method BLASTX
NCBI GI g4263792
BLAST score 348
E value 5.0e-33
Match length 70
% identity 79

NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]

Seq. No. 212508

Seq. ID LIB3145-054-Q1-K1-D8

Method BLASTX
NCBI GI g2498732
BLAST score 498
E value 1.0e-50
Match length 127
% identity 76

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2

>gi\_1362014\_pir\_\_S57612 zeta-crystallin homolog Arabidopsis thaliana >gi\_886430\_emb\_CAA89262\_ (Z49268)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 212509

Seq. ID LIB3145-054-Q1-K1-D9

Method BLASTX NCBI GI g2832672



BLAST score 508
E value 1.0e-51
Match length 124
% identity 81
NCBL Description (AL0217)

NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 212510

Seq. ID LIB3145-054-Q1-K1-E10

Method BLASTX
NCBI GI g1749676
BLAST score 161
E value 5.0e-11
Match length 118
% identity 37

NCBI Description (D89234) similar to Saccharomyces cerevisiae ORF YGR205W, EMBL Accession Number Z72990 [Schizosaccharomyces pombe]

Seq. No. 212511

Seq. ID LIB3145-054-Q1-K1-E11

Method BLASTX
NCBI GI 94415929
BLAST score 228
E value 7.0e-19
Match length 64
% identity 55

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 212512

Seq. ID LIB3145-054-Q1-K1-E12

Method BLASTX
NCBI GI g3334405
BLAST score 480
E value 2.0e-48
Match length 102
% identity 98

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)

>gi 2267583 (AF009338) vacuolar H+-ATPase subunit E

[Gossypium hirsutum]

Seq. No. 212513

Seq. ID LIB3145-054-Q1-K1-E3

Method BLASTX
NCBI GI g3334259
BLAST score 352
E value 2.0e-33
Match length 69
% identity 93

NCBI Description WD-40 REPEAT PROTEIN MSI4 >gi 2599092 (AF028711) WD-40

repeat protein MSI4 [Arabidopsis thaliana]

Seq. No. 212514

Seq. ID LIB3145-054-Q1-K1-E4

Method BLASTX
NCBI GI g3334259
BLAST score 307
E value 4.0e-28
Match length 67



% identity 84
NCBI Description WD-40 REPEAT PROTEIN MSI4 >gi\_2599092 (AF028711) WD-40
repeat protein MSI4 [Arabidopsis thaliana]
Seq. No. 212515

 Seq. ID
 LIB3145-054-Q1-K1-F1

 Method
 BLASTX

 NCBI GI
 g1619300

 BLAST score
 335

 E value
 2.0e-31

 Match length
 77

 % identity
 78

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 212516

Seq. ID LIB3145-054-Q1-K1-F11

Method BLASTX
NCBI GI g4033424
BLAST score 243
E value 1.0e-20
Match length 79
% identity 77

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi\_2668746 (AF034947) inorganic

pyrophosphatase [Zea mays]

Seq. No. 212517

Seq. ID LIB3145-054-Q1-K1-F2

Method BLASTX
NCBI GI g4006932
BLAST score 151
E value 8.0e-10
Match length 98
% identity 44

NCBI Description (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit

[Bos taurus]

Seq. No. 212518

Seq. ID LIB3145-054-Q1-K1-F4

Method BLASTX
NCBI GI g3341468
BLAST score 260
E value 1.0e-22
Match length 65
% identity 72

NCBI Description (AJ009594) Dof zinc finger protein [Nicotiana tabacum]

Seq. No. 212519

Seq. ID LIB3145-054-Q1-K1-F8

Method BLASTX
NCBI GI g2961358
BLAST score 215
E value 2.0e-17
Match length 52
% identity 79

NCBI Description (AL022140) serine/threonine protein kinase like protein

[Arabidopsis thaliana]



212520 Seq. No. Seq. ID LIB3145-054-Q1-K1-G1 BLASTX Method NCBI GI g2983642 BLAST score 250 2.0e-21 E value Match length 134 % identity 40 NCBI Description (AE000728) diaminopimelate decarboxylase [Aquifex aeolicus] Seq. No. 212521 Seq. ID LIB3145-054-Q1-K1-H1 Method BLASTX NCBI GI q4454051 BLAST score 559 E value 1.0e-57 Match length 133 % identity 76 NCBI Description (AL035394) putative polygalacturonase [Arabidopsis thaliana] Seq. No. 212522 Seq. ID LIB3145-054-Q1-K1-H11 Method BLASTX NCBI GI q4454033 BLAST score 505 E value 2.0e-51 Match length 124 % identity 74 (AL035394) putative potassium transport protein NCBI Description [Arabidopsis thaliana] 212523 Seq. No. Seq. ID LIB3145-054-Q1-K1-H12 Method BLASTX NCBI GI q3643602 BLAST score 150 8.0e-10 E value Match length 80 42 % identity (AC005395) putative tonoplast intrinsic protein NCBI Description [Arabidopsis thaliana] 212524 Seq. No. Seq. ID LIB3145-054-Q1-K1-H5 Method BLASTX NCBI GI g3142300 BLAST score 163 2.0e-11 E value

100 Match length 44 % identity

(AC002411) Contains similarity to pre-mRNA processing NCBI Description

protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb\_T88158, gb\_N38703 and gb\_AA651043 come from this

gene. [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  LIB3145-054-Q1-K1-H7
                  BLASTX
Method
                  g3776577
NCBI GI
BLAST score
                   382
E value
                  7.0e-37
Match length
                  129
                  57
% identity
                  (AC005388) T22H22.24 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212526
Seq. ID
                  LIB3145-055-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  g2780193
BLAST score
                  43
E value
                   4.0e-15
Match length
                  59
% identity
                  93
NCBI Description Lupinus albus mRNA for adenine nucleotide translocator
Seq. No.
                  212527
Seq. ID
                  LIB3145-055-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2137490
BLAST score
                   320
E value
                  1.0e-29
Match length
                  130
% identity
                   48
NCBI Description
                  lymphocyte specific helicase - mouse >qi 805296 (U25691)
                  lymphocyte specific helicase [Mus musculus]
                  212528
Seq. No.
Seq. ID
                  LIB3145-055-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2673917
                  297
BLAST score
                   4.0e-27
E value
Match length
                  84
% identity
                  67
                   (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  212529
Seq. ID
                  LIB3145-055-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3281869
BLAST score
                  202
```

8.0e-16 E value 126 Match length 43 % identity

(AL031004) RSZp22 splicing factor [Arabidopsis thaliana] NCBI Description

>gi 3435094 (AF033586) 9G8-like SR protein [Arabidopsis

thaliana]

212530 Seq. No.

Seq. ID LIB3145-055-Q1-K1-B1

Method BLASTX



```
NCBI GI g266346
BLAST score 644
E value 1.0e-67
Match length 139
% identity 90
```

NCBI Description KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID

REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE) >gi\_81509\_pir\_\_S17180 ketol-acid reductoisomerase (EC 1.1.1.86) precursor - spinach

>gi\_21234\_emb\_CAA40356\_ (X57073) ketol-acid

reductoisomerase [Spinacia oleracea]

```
Seq. No. 212531
```

Seq. ID LIB3145-055-Q1-K1-B10

Method BLASTX
NCBI GI g3287832
BLAST score 747
E value 1.0e-79
Match length 143
% identity 99

NCBI Description (+)-DELTA-CADINENE SYNTHASE (D-CADINENE SYNTHASE)

>gi 1843647 (U88318) (+)-delta-cadinene synthase [Gossypium

hirsutum]

Seq. No. 212532

Seq. ID LIB3145-055-Q1-K1-B8

Method BLASTX
NCBI GI g2833388
BLAST score 504
E value 3.0e-51
Match length 126
% identity 76

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi\_629660\_pir\_\_S43341 ADPglucose--starch

glucosyltransferase (EC 2.4.1.21) precursor - cassava
>gi\_437042\_emb\_CAA52273\_ (X74160) starch (bacterial

glycogen) synthase [Manihot esculenta]

Seq. No. 212533

Seq. ID LIB3145-055-Q1-K1-B9

Method BLASTX
NCBI GI g4469023
BLAST score 611
E value 9.0e-64
Match length 131
% identity 85

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 212534

Seq. ID LIB3145-055-Q1-K1-C1

Method BLASTX
NCBI GI g2780194
BLAST score 364
E value 9.0e-35
Match length 75
% identity 97

NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]



```
212535
   Seq. No.
   Seq. ID
                      LIB3145-055-Q1-K1-C11
   Method
                      BLASTX
   NCBI GI
                      g3264759
                      473
   BLAST score
                      2.0e-47
   E value
                      130
   Match length
% identity
                      64
   NCBI Description
                     (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
                      212536
   Seq. No.
   Seq. ID
                      LIB3145-055-Q1-K1-C12
   Method
                      BLASTX
                      g2769696
   NCBI GI
   BLAST score
                      175
                      1.0e-12
   E value
                      84
   Match length
   % identity
                      46
                      (AC003982) unknown function; 60% similar to Z50177
   NCBI Description
                      (PID:g927403) (PID:g927402) [Homo sapiens]
   Seq. No.
                      212537
                      LIB3145-055-Q1-K1-C2
   Seq. ID
   Method
                      BLASTX
                      g3702331
   NCBI GI
   BLAST score
                      292
                      2.0e-26
   E value
                      129
   Match length
                      50
   % identity
   NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
   Seq. No.
                      212538
   Seq. ID
                      LIB3145-055-Q1-K1-C3
                      BLASTX
   Method
                      g125271
   NCBI GI
   BLAST score
                      494
                      6.0e-50
   E value
                      121
   Match length
                      77
    % identity
                      CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA)
   NCBI Description
                      >gi 100860 pir S19726 casein kinase II (EC 2.7.1.-) alpha
                      chain - maize >gi 3318993 pdb 1A60 Protein Kinase Ck2
                       (Catalytic Subunit) From Zea Mays >gi_22117_emb_CAA43659_
                       (X61387) casein kinase II alpha subunit [Zea mays]
                      212539
    Seq. No.
   Seq. ID
                      LIB3145-055-Q1-K1-C8
                      BLASTX
   Method
   NCBI GI
                      g1694976
   BLAST score
                      410
   E value
                      4.0e-40
   Match length
                      119
                      67
    % identity
   NCBI Description
                      (Y09482) HMG1 [Arabidopsis thaliana]
```

29521

thaliana]

>gi\_2832361\_emb\_CAA74402\_ (Y14073) HMG protein [Arabidopsis



```
Seq. No.
                    212540
Seq. ID
                    LIB3145-055-Q1-K1-C9
Method
                    BLASTX
NCBI GI
                    g1705463
BLAST score
                    663
                    8.0e-70
E value
Match length
                    142
% identity
                    84
NCBI Description
                    BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >qi 2129547 pir S71201
                    biotin sythase - Arabidopsis thaliana >gi_10453\overline{16} (\overline{U2}4147) biotin sythase [Arabidopsis thaliana] >gi_11403662 (\overline{U3}1806)
                    BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)
                    biotin synthase [Arabidopsis thaliana] >gi 2288983
                    (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                    >gi 1589016 prf 2209438A biotin synthase [Arabidopsis
                    thaliana]
                    212541
Seq. No.
Seq. ID
                    LIB3145-055-Q1-K1-D12
Method
                    BLASTX
NCBI GI
                    g3860250
BLAST score
                    584
E value
                    6.0e-61
Match length
                    142
% identity
                    85
                    (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    212542
Seq. ID
                    LIB3145-055-Q1-K1-D4
Method
                    BLASTX
```

NCBI GI g4105798 BLAST score 390 6.0e-38 E value Match length 105 % identity 58

(AF049930) PGP237-11 [Petunia x hybrida] NCBI Description

Seq. No. 212543

Seq. ID LIB3145-055-Q1-K1-D9

Method BLASTX NCBI GI g3367521 BLAST score 272 E value 6.0e-24 Match length 107 % identity 51

NCBI Description (AC004392) Similar to gb U08285 membrane-associated

> salt-inducible protein from Nicotiana tabacum. ESTs gb\_T44131 and gb\_T04378 come from this gene. [Arabidopsis

thaliana]

Seq. No. 212544

Seq. ID LIB3145-055-Q1-K1-E10

Method BLASTX NCBI GI g2388586 BLAST score 223

```
E value 3.0e-18
Match length 136
% identity 44
NCBI Description (AC000098) Similar to Saccharomyces RAD16 (gb_X78993).
[Arabidopsis thaliana]

Seq. No. 212545
Seq. ID LIB3145-055-Q1-K1-E11
Method BLASTX
```

Method BLASTX
NCBI GI g2388586
BLAST score 289
E value 5.0e-26
Match length 76
% identity 70

NCBI Description (AC000098) Similar to Saccharomyces RAD16 (gb X78993).

[Arabidopsis thaliana]

Seq. No. 212546

Seq. ID LIB3145-055-Q1-K1-E2

Method BLASTX
NCBI GI g2462762
BLAST score 376
E value 4.0e-36
Match length 139
% identity 58

NCBI Description (AC002292) Highly similar to auxin-induced protein

(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 212547

Seq. ID LIB3145-055-Q1-K1-E6

Method BLASTN
NCBI GI g4165340
BLAST score 41
E value 1.0e-13
Match length 147
% identity 86

NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 212548

Seq. ID LIB3145-055-Q1-K1-E7

Method BLASTX
NCBI GI g4467128
BLAST score 171
E value 1.0e-24
Match length 115
% identity 51

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 212549

Seq. ID LIB3145-055-Q1-K1-F10

Method BLASTN
NCBI GI g167346
BLAST score 79
E value 2.0e-36
Match length 312
% identity 82





```
NCBI Description Gossypium hirsutum Lea5-A late embryogenesis-abundant protein (Lea5-A) gene, complete cds
```

Seq. No. 212550

Seq. ID LIB3145-055-Q1-K1-F11

Method BLASTX
NCBI GI g2244965
BLAST score 219
E value 2.0e-23
Match length 134
% identity 54

NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No. 212551

Seq. ID LIB3145-055-Q1-K1-F2

Method BLASTX
NCBI GI g2702269
BLAST score 217
E value 1.0e-17
Match length 101
% identity 49

NCBI Description (AC003033) hypothetical protein [Arabidopsis thaliana]

Seq. No. 212552

Seq. ID LIB3145-055-Q1-K1-F7

Method BLASTX
NCBI GI g2879867
BLAST score 394
E value 3.0e-38
Match length 115
% identity 66

NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces

pombe]

Seq. No. 212553

Seq. ID LIB3145-055-Q1-K1-F9

Method BLASTX
NCBI GI g1350680
BLAST score 398
E value 9.0e-39
Match length 110
% identity 73

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 212554

Seq. ID LIB3145-055-Q1-K1-G10

Method BLASTX
NCBI GI g3552013
BLAST score 202
E value 9.0e-16
Match length 71
% identity 63

NCBI Description (AF086759) proline-rich protein precursor [Glycine max]

Seq. No. 212555

Seq. ID LIB3145-055-Q1-K1-G6

Method BLASTX

```
q2832664
NCBI GI
BLAST score
                  234
                  1.0e-19
E value
Match length
                  101
                  47
% identity
                  (AL021710) pollen-specific protein - like [Arabidopsis
NCBI Description
                  thaliana]
                  212556
Seq. No.
Seq. ID
                  LIB3145-055-Q1-K1-G8
                  BLASTX
Method
                  g3552013
NCBI GI
BLAST score
                  207
                  2.0e-16
E value
                  71
Match length
                  65
% identity
                  (AF086759) proline-rich protein precursor [Glycine max]
NCBI Description
                  212557
Seq. No.
Seq. ID
                  LIB3145-055-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3552013
BLAST score
                  160
                  6.0e-11
E value
                  68
Match length
                  59
% identity
NCBI Description (AF086759) proline-rich protein precursor [Glycine max]
                  212558
Seq. No.
Seq. ID
                  LIB3145-055-Q1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3776559
BLAST score
                  143
                  6.0e-15
E value
                  82
Match length
                  55
% identity
                  (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
                  gene. [Arabidopsis thaliana]
                  212559
Seq. No.
Seq. ID
                  LIB3145-055-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  q3757520
BLAST score
                  236
E value
                  9.0e-20
Match length
                  70
% identity
NCBI Description
                  (AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.
                  212560
```

Seq. ID LIB3145-055-Q1-K1-H12

Method BLASTX
NCBI GI g3757520
BLAST score 194
E value 7.0e-15



Match length 122 % identity 40

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 212561

Seq. ID LIB3145-055-Q1-K1-H2

Method BLASTX
NCBI GI g2829751
BLAST score 188
E value 3.0e-14
Match length 102
% identity 39

NCBI Description MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF)

>gi\_1850559 (U88035) macrophage migration inhibitory factor
[Brugia malayi] >gi 2190976 (AF002699) macrophage migration

inhibitory factor [Brugia malayi]

Seq. No. 212562

Seq. ID LIB3145-055-Q1-K1-H4

Method BLASTX
NCBI GI g533256
BLAST score 371
E value 1.0e-35
Match length 125
% identity 58

NCBI Description (L27101) pectinesterase [Petunia inflata]

Seq. No. 212563

Seq. ID LIB3145-055-Q1-K1-H7

Method BLASTX
NCBI GI g289920
BLAST score 585
E value 9.0e-61
Match length 115
% identity 94

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 212564

Seq. ID LIB3145-055-Q1-K1-H8

Method BLASTX
NCBI GI g3047114
BLAST score 309
E value 2.0e-28
Match length 83
% identity 59

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.

212565

Seq. ID LIB3145-055-Q1-K1-H9

Method BLASTX
NCBI GI g4467157
BLAST score 212
E value 6.0e-17
Match length 123
% identity 40

NCBI Description (AL035540) disease resistance response like protein



## [Arabidopsis thaliana]

```
Seq. No.
                  212566
                  LIB3145-056-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738306
BLAST score
                  244
                  1.0e-20
E value
Match length
                  140
                  46
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  212567
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  g2499542
BLAST score
                  470
                  3.0e-47
E value
Match length
                  134
                  64
% identity
NCBI Description
                  IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP)
                  >gi 1218042 (U48448) secreted purple acid phosphatase
                  precursor [Arabidopsis thaliana]
                  212568
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-A6
                  BLASTX
Method
NCBI GI
                  g3128218
BLAST score
                  551
E value
                  2.0e-56
                  142
Match length
% identity
                  77
NCBI Description
                  (AC004077) putative end13 protein [Arabidopsis thaliana]
                  212569
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-A8
Method
                  BLASTN
NCBI GI
                  q3985934
BLAST score
                  53
E value
                  7.0e-21
Match length
                  216
% identity
                  84
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJE7, complete sequence [Arabidopsis thaliana]
                  212570
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q346685
BLAST score
                  470
                  4.0e-47
E value
Match length
                  121
% identity
NCBI Description
                  developmentally-regulated GTP-binding protein - mouse
```

Seq. No. 212571

Seq. ID LIB3145-056-Q1-K1-B11

```
Method
                  BLASTX
NCBI GI
                  g3024386
BLAST score
                  299
                  7.0e-35
E value
Match length
                  110
% identity
                  69
NCBI Description
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
                  >gi_2129500_pir__S52006 polygalacturonase - upland cotton
                  >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  212572
Seq. ID
                  LIB3145-056-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q1694976
BLAST score
                  207
E value
                  2.0e-16
Match length
                  45
% identity
                  84
                  (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                  >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis
                  thaliana]
Seq. No.
                  212573
Seq. ID
                  LIB3145-056-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q4090533
BLAST score
                  316
E value
                  3.0e-29
Match length
                  116
                  53
% identity
NCBI Description
                  (U68215) ACC oxidase [Carica papaya]
Seq. No.
                  212574
Seq. ID
                  LIB3145-056-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2196542
BLAST score
                  169
E value
                  5.0e-12
Match length
                  45
% identity
                  73
NCBI Description (AF001894) glycine-rich protein [Oryza sativa]
```

Seq. No. 212575

Seq. ID LIB3145-056-Q1-K1-B5

Method BLASTX NCBI GI g3075402 BLAST score 150 1.0e-09 E value Match length 91 % identity 38

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 212576

Seq. ID LIB3145-056-Q1-K1-B7

Method BLASTX NCBI GI g2827655 BLAST score 166

BLAST score

% identity

NCBI Description

E value Match length 212 7.0e-17

55

```
E value
                   1.0e-11
Match length
                   67
                  24
% identity
                  (AL021637) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212577
                  LIB3145-056-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3452497
BLAST score
                   658
                  3.0e-69
E value
Match length
                  136
% identity
                   93
                  (Y17796) ketol-acid reductoisomerase [Pisum sativum]
NCBI Description
                  212578
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2245134
BLAST score
                  153
                   5.0e-10
E value
Match length
                   116
% identity
                   37
NCBI Description
                   (Z97344) heat shock transcription factor HSF1 [Arabidopsis
                  thaliana]
Seq. No.
                  212579
Seq. ID
                  LIB3145-056-Q1-K1-C11
Method
                  BLASTN
NCBI GI
                   g407800
BLAST score
                   286
                   1.0e-160
E value
Match length
                  374
                   94
% identity
                  G.hirsutum mRNA for ribosomal protein 41, large subunit
NCBI Description
                   (RL41)
                  212580
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-C2
                  BLASTX
Method
NCBI GI
                  g2982251
BLAST score
                  234
                  1.0e-19
E value
Match length
                   97
                   57
% identity
                  (AF051208) putative RNA-binding protein [Picea mariana]
NCBI Description
Seq. No.
                  212581
Seq. ID
                  LIB3145-056-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4567250
```

29529

(AC007070) hypothetical protein [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

Match length

% identity

g4454480

192 1.0e-14

63

59

```
Seq. No.
                  212582
Seq. ID
                  LIB3145-056-Q1-K1-C6
                  BLASTX
Method
                  g3559816
NCBI GI
BLAST score
                  242
                  2.0e-20
E value
                  63
Match length
                  73
% identity
                  (Y15782) transketolase 2 [Capsicum annuum]
NCBI Description
Seq. No.
                  212583
Seq. ID
                  LIB3145-056-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  q417360
BLAST score
                  352
E value
                  2.0e-33
Match length
                  120
% identity
                  56
                  HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
NCBI Description
                  >gi_2131280_pir__S67767 high mobility group-like protein
                  NHP2 - yeast (Saccharomyces cerevisiae)
                  >gi 666101 emb CAA40885 (X57714) high mobility group-like
                  nuclear protein 2 [Saccharomyces cerevisiae]
                  >gi 1429348 emb CAA67483 (X99000) high-mobility-group-like
                  protein [Saccharomyces cerevisiae]
                  >gi 1431346 emb CAA98786 (Z74256) ORF YDL208w
                  [Saccharomyces cerevisiae]
Seq. No.
                  212584
                  LIB3145-056-Q1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512658
BLAST score
                  172
                  2.0e-12
E value
Match length
                  102
% identity
                  38
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212585
                  LIB3145-056-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g2495699
NCBI GI
BLAST score
                  277
                  1.0e-24
E value
                  136
Match length
% identity
                  HYPOTHETICAL PROTEIN KIAA0032 >gi 517115 dbj BAA04945
NCBI Description
                  (D25215) KIAA0032 [Homo sapiens]
                  212586
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-D3
                  BLASTX
Method
```

29530

```
(AC006234) putative (1-4)-beta-mannan endohydrolase
 NCBI Description
                    [Arabidopsis thaliana]
                   212587
 Seq. No.
                   LIB3145-056-Q1-K1-D4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2342735
                   364
 BLAST score
                   7.0e-35
 E value
                   92
 Match length
 % identity
                   78
 NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
                   212588
 Seq. No.
                   LIB3145-056-Q1-K1-D6
 Seq. ID
                   BLASTN
 Method
                    g3821780
 NCBI GI
 BLAST score
                    33
                    5.0e-09
 E value
                    49
 Match length
                    41
 % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                    212589
                    LIB3145-056-Q1-K1-D7
 Seq. ID
                    BLASTX
 Method
                    q1771158
 NCBI GI
                    177
 BLAST score
                    7.0e-13
 E value
                    86
 Match length
                    42
 % identity
 NCBI Description (Y07861) MFP1 protein [Lycopersicon esculentum]
                    212590
 Seq. No.
                    LIB3145-056-Q1-K1-D8
 Seq. ID
 Method
                    BLASTX
                    q2982251
 NCBI GI
BLAST score
                    238
                    5.0e-20
 E value
                    58
 Match length
                    74
 % identity
 NCBI Description (AF051208) putative RNA-binding protein [Picea mariana]
                    212591
 Seq. No.
                    LIB3145-056-Q1-K1-D9
 Seq. ID
                    BLASTX
 Method
                    g2827665
 NCBI GI
                    388
 BLAST score
                    5.0e-38
 E value
                    77
 Match length
                    82
 % identity
```

NCBI Description (AL021637) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

Seq. No. 212592

Seq. ID LIB3145-056-Q1-K1-E1

Method BLASTX

29531



```
NCBI GI
                  q2815246
BLAST score
                  218
                  9.0e-18
E value
Match length
                  55
% identity
                  71
NCBI Description
                  (X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.
                  212593
                  LIB3145-056-Q1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245394
BLAST score
                  290
E value
                  4.0e-26
Match length
                  146
% identity
                  45
NCBI Description
                  (U89771) ARF1-binding protein [Arabidopsis thaliana]
Seq. No.
                  212594
Seq. ID
                  LIB3145-056-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3024386
BLAST score
                  255
E value
                  3.0e-22
Match length
                  74
                  73
% identity
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                  >gi 2129500 pir S52006 polygalacturonase - upland cotton
                  >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  212595
Seq. ID
                  LIB3145-056-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3309243
BLAST score
                  617
E value
                  2.0e-64
Match length
                  133
% identity
                  89
NCBI Description
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
                  limon]
Seq. No.
                  212596
Seq. ID
                  LIB3145-056-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g3075394
BLAST score
                  518
E value
                  7.0e-53
Match length
                  125
% identity
                  77
                  (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
```

212597 Seq. No.

Seq. ID LIB3145-056-Q1-K1-F11

Method BLASTX NCBI GI g3075394 BLAST score 188



E value Match length 106 % identity 46

(ACO04484) putative beta-ketoacyl-CoA synthase [Arabidopsis NCBI Description

thaliana] >gi 3559809 emb\_CAA09311\_ (AJ010713) fiddlehead

protein [Arabidopsis thaliana]

Seq. No. 212598

Seq. ID LIB3145-056-Q1-K1-F5

Method BLASTX NCBI GI q1332579 BLAST score 602 E value 9.0e-63 Match length 124

% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 212599

Seq. ID LIB3145-056-Q1-K1-G4

Method BLASTX NCBI GI g3097266 BLAST score 431 E value 7.0e-43Match length 96

% identity 88

NCBI Description (Y17186) translation initiation factor [Pisum sativum]

Seq. No. 212600

Seq. ID LIB3145-056-Q1-K1-G5

Method BLASTX NCBI GI g3097266 BLAST score 327 E value 1.0e-30 Match length 115 % identity 60

NCBI Description (Y17186) translation initiation factor [Pisum sativum]

Seq. No. 212601

Seq. ID LIB3145-056-Q1-K1-G6

Method BLASTX NCBI GI g3097266 BLAST score 357 E value 2.0e-34 Match length 76 % identity 92

(Y17186) translation initiation factor [Pisum sativum] NCBI Description

Seq. No. 212602

Seq. ID LIB3145-056-Q1-K1-G7

Method BLASTN NCBI GI g18511 BLAST score 410 E value 0.0e + 00Match length 418 % identity 100

NCBI Description G.hirsutum light regulated unknown reading frame DNA

Match length

NCBI Description

% identity

114

thaliana]

61



```
Seq. No.
                   212603
Seq. ID
                  LIB3145-056-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3377843
BLAST score
                   378
E value
                  2.0e-36
Match length
                  126
                  63
% identity
                   (AF076274) contains similarity to rat p47 protein
NCBI Description
                   (GB:AB002086) [Arabidopsis thaliana]
Seq. No.
                  212604
Seq. ID
                  LIB3145-056-Q1-K1-H1
Method
                  BLASTX
                  g294845
NCBI GI
BLAST score
                  252
                  1.0e-21
E value
Match length
                  100
% identity
                  47
NCBI Description
                  (L13655) membrane protein [Saccharum hybrid cultivar
                  H65-7052]
Seq. No.
                  212605
                  LIB3145-056-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q231573
BLAST score
                  436
                  3.0e-43
E value
Match length
                  124
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                  >gi 99970_pir S24757 asparaginase (EC 3.5.1.1) -
                  narrow-leaved blue lupine >gi_19135_emb_CAA43099_ (X60691)
                  developing seed L-asparaginase [Lupinus angustifolius]
                  212606
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1352316
BLAST score
                  356
E value
                  3.0e - 34
Match length
                  82
% identity
                  82
NCBI Description
                  DR1 PROTEIN HOMOLOG >gi 633026 dbj BAA07288 (D38110) Dr1
                   [Arabidopsis thaliana]
Seq. No.
                  212607
Seq. ID
                  LIB3145-056-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3549681
BLAST score
                  378
E value
                  2.0e-36
```

29534

(AL031394) male sterility 2-like protein [Arabidopsis

BLAST score

E value

281 1.0e-157

```
Seq. No.
                  212608
Seq. ID
                  LIB3145-056-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4158232
BLAST score
                  618
E value
                  2.0e-64
Match length
                  121
                  93
% identity
                  (Y18626) reversibly glycosylated polypeptide [Triticum
NCBI Description
                  aestivum]
Seq. No.
                  212609
Seq. ID
                  LIB3145-056-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  q4105097
BLAST score
                  598
E value
                  3.0e-62
Match length
                  129
% identity
                  88
                  (AF043255) MADS box protein 26 [Cucumis sativus]
NCBI Description
                  212610
Seq. No.
Seq. ID
                  LIB3145-056-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4105097
BLAST score
                  461
                  4.0e-46
E value
Match length
                  124
% identity
                  70
NCBI Description
                  (AF043255) MADS box protein 26 [Cucumis sativus]
Seq. No.
                  212611
Seq. ID
                  LIB3145-056-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3044218
BLAST score
                  151
                  6.0e-10
E value
Match length
                  58
% identity
                  52
                  (AF057144) signal peptidase [Arabidopsis thaliana]
NCBI Description
                  212612
Seq. No.
Seq. ID
                  LIB3145-057-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1944403
BLAST score
                  394
                  2.0e-38
E value
Match length
                  126
% identity
                  63
                  (D86590) cinnamyl alcohol dehydrogenase [Zinnia elegans]
NCBI Description
Seq. No.
                  212613
Seq. ID
                  LIB3145-057-Q1-K1-A10
Method
                  BLASTN
NCBI GI
                  g2687434
```

29535

```
Match length
                   97
% identity
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                   212614
                  LIB3145-057-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3935138
BLAST score
                   412
                   2.0e-40
E value
Match length
                   128
% identity
                   58
                  (AC005106) T25N20.2 [Arabidopsis thaliana]
NCBI Description
                   212615
Seq. No.
                   LIB3145-057-Q1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2707336
                   355
BLAST score
                   3.0e-35
E value
                   96
Match length
% identity
                   77
                  (AF037442) histone acetyltransferase [Arabidopsis thaliana]
NCBI Description
                   212616
Seq. No.
                   LIB3145-057-Q1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q717142
                   313
BLAST score
                   8.0e-29
E value
Match length
                   107
% identity
                   60
                   (U21801) alcohol dehydrogenase homolog [Solanum
NCBI Description
                   lycopersicum]
                   212617
Seq. No.
                   LIB3145-057-Q1-K1-B12
Seq. ID
Method
                   BLASTX
                   g2707336
NCBI GI
BLAST score
                   328
                   2.0e-31
E value
                   96
Match length
% identity
                   73
                  (AF037442) histone acetyltransferase [Arabidopsis thaliana]
NCBI Description
                   212618
Seq. No.
Seq. ID
                   LIB3145-057-Q1-K1-B4
Method
                   BLASTX
                   g541816
NCBI GI
                   332
BLAST score
                   5.0e-31
E value
```

protein kinase - common ice plant >gi\_457689\_emb\_CAA82990\_

(Z30329) protein kinase [Mesembryanthemum crystallinum]

110

60

Match length

NCBI Description

% identity



```
Seq. No.
                  212619
                  LIB3145-057-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567278
BLAST score
                  336
E value
                  1.0e-31
Match length
                  84
                  77
% identity
                  (AC006841) putative anthracycline associated resistance ARX
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  212620
Seq. ID
                  LIB3145-057-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g228210
BLAST score
                  221
                  3.0e-18
E value
Match length
                  50
% identity
                  granule-bound starch synthase [Solanum tuberosum]
NCBI Description
                  212621
Seq. No.
Seq. ID
                  LIB3145-057-Q1-K1-B9
Method
                  BLASTX
                  q548653
NCBI GI
BLAST score
                  156
                  2.0e-10
E value
Match length
                  61
% identity
                  62
                  50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)
NCBI Description
                  >gi 541895 pir A53394 ribosomal protein L12.A, chloroplast
                   - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046)
                  ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                  212622
Seq. ID
                  LIB3145-057-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q2826842
BLAST score
                  262
                   6.0e-23
E value
Match length
                  73
% identity
                   68
                  (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
NCBI Description
Seq. No.
                  212623
Seq. ID
                  LIB3145-057-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q1362093
BLAST score
                  121
E value
                  3.0e-09
Match length
                  81
                   43
% identity
                  hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                  >gi_924632 (U20595) unknown [Solanum lycopersicum]
```

Seq. No. 212624

Seq. ID LIB3145-057-Q1-K1-C12

29537

机。

NCBI Description

```
Method
NCBI GI
                  q3915089
BLAST score
                  399
E value
                  3.0e-39
                  92
Match length
                  78
% identity
NCBI Description
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
                  4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_2144269_pir__JC5129 trans-cinnamate 4-monooxygenase (EC
                  1.14.13.11) A - Populus kitakamiensis
                  >gi_1139561_dbj_BAA11579_ (D82815) cinnamic acid
                  4-hydroxylase [Populus kitakamiensis]
                  >gi 1777370 dbj BAA11576 (D82812) cinnamic acid
                  4-hydroxylase [Populus kitakamiensis]
Seq. No.
                  212625
                  LIB3145-057-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  g3097266
NCBI GI
BLAST score
                  283
E value
                  3.0e-25
Match length
                  60
                  90
% identity
NCBI Description
                  (Y17186) translation initiation factor [Pisum sativum]
Seq. No.
                  212626
Seq. ID
                  LIB3145-057-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q2342690
BLAST score
                  505
E value
                  2.0e-51
Match length
                  127
% identity
                  75
NCBI Description
                  (AC000106) Similar to Homo copine I (gb U83246).
                   [Arabidopsis thaliana]
Seq. No.
                  212627
Seq. ID
                  LIB3145-057-Q1-K1-C7
Method
                  BLASTN
NCBI GI
                  q899609
BLAST score
                  38
E value
                  6.0e-12
Match length
                  82
% identity
                  87
                  Zea mays acidic ribosomal protein P2 (RPA-2A1) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  212628
Seq. ID
                  LIB3145-057-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1362093
BLAST score
                  477
                  4.0e-48
E value
Match length
                  112
% identity
                  77
```

hypothetical protein (clone TPP15) - tomato (fragment)

>gi\_924632 (U20595) unknown [Solanum lycopersicum]

% identity

NCBI Description

90



```
Seq. No.
                   212629
Seq. ID
                   LIB3145-057-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   g1729891
BLAST score
                   176
E value
                   8.0e-13
Match length
                   102
% identity
                   36
                   TEGT PROTEIN (TESTIS ENHANCED GENE TRANSCRIPT)
NCBI Description
                   >gi 2136254 pir I38334 TEGT (testis enhanced gene
                   transcript) - human >gi_458545_emb_CAA53472_ (X75861) TEGT [Homo sapiens] >gi_4507433_ref_NP_003208.1_pTEGT_ testis
                   enhanced gene transcript
Seq. No.
                   212630
Seq. ID
                   LIB3145-057-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g2980795
BLAST score
                   211
E value
                   5.0e-17
Match length
                   72
% identity
                   60
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212631
Seq. ID
                   LIB3145-057-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g1439631
                   438
BLAST score
                   2.0e-43
E value
Match length
                   136
% identity
                   63
                   (U64598) similar to helicases of the SNF2/RAD54 family.
NCBI Description
                   Does not contain the bromodomain. [Caenorhabditis elegans]
Seq. No.
                   212632
Seq. ID
                   LIB3145-057-Q1-K1-D5
                   BLASTX
Method
                   g4220535
NCBI GI
BLAST score
                   581
E value
                   3.0e-60
Match length
                   136
% identity
                   81
NCBI Description
                   (AL035356) clathrin coat assembly like protein [Arabidopsis
                   thaliana]
Seq. No.
                   212633
Seq. ID
                   LIB3145-057-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   g3915083
BLAST score
                   654
E value
                   8.0e-69
Match length
                   135
```

29539

beta-tubulin [Cicer arietinum]

TUBULIN BETA CHAIN >gi\_1403143 emb CAA67056 (X98406)

Method

NCBI GI

BLASTX

q2760834



```
212634
Seq. No.
Seq. ID
                  LIB3145-057-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g629846
BLAST score
                  143
                  7.0e-09
E value
Match length
                  103
% identity
                  40
NCBI Description
                  initiator-binding protein - maize >gi 483444 emb CAA55693
                  (X79086) initiator-binding protein [Zea mays]
Seq. No.
                  212635
Seq. ID
                  LIB3145-057-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1658197
BLAST score
                  649
E value
                  3.0e-68
Match length
                  134
% identity
                  87
NCBI Description
                  (U74630) calreticulin [Ricinus communis] >qi 1763297
                  (U74631) calreticulin [Ricinus communis]
Seq. No.
                  212636
Seq. ID
                  LIB3145-057-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q2853076
BLAST score
                  275
                  2.0e-24
E value
Match length
                  74
% identity
                  77
                 (AL021768) putative protein [Arabidopsis thaliana]
NCBI Description
                  212637
Seq. No.
                  LIB3145-057-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454026
                  378
BLAST score
                  2.0e-36
E value
                  106
Match length
                  70
% identity
                  (AL035394) phosphatase like protein [Arabidopsis thaliana]
NCBI Description
                  212638
Seq. No.
Seq. ID
                  LIB3145-057-Q1-K1-E4
Method
                  BLASTN
NCBI GI
                  g2570118
BLAST score
                  55
                  4.0e-22
E value
Match length
                  83
                  92
% identity
NCBI Description S.latifolia mRNA, clone CCLS
                  212639
Seq. No.
Seq. ID
                  LIB3145-057-Q1-K1-E5
```

29540



BLAST score 377 E value 2.0e-36 Match length 111 % identity 69

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis

thaliana]

Seq. No. 212640

Seq. ID LIB3145-057-Q1-K1-E7

Method BLASTX
NCBI GI g543867
BLAST score 516
E value 1.0e-52
Match length 132
% identity 78

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_1076684\_pir\_\_A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi\_303626\_dbj\_BAA03526\_ (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

Seq. No. 212641

Seq. ID LIB3145-057-Q1-K1-E9

Method BLASTX
NCBI GI g4008156
BLAST score 613
E value 5.0e-64
Match length 129
% identity 86

NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

Seq. No. 212642

Seq. ID LIB3145-057-Q1-K1-F3

Method BLASTX
NCBI GI g4218121
BLAST score 245
E value 7.0e-21
Match length 110
% identity 50

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 212643

Seq. ID LIB3145-057-Q1-K1-F4

Method BLASTN
NCBI GI g2564044
BLAST score 37
E value 2.0e-11
Match length 242
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 212644

Seq. ID LIB3145-057-Q1-K1-F7

Method BLASTX
NCBI GI g3551983
BLAST score 671



E value 9.0e-71
Match length 129
% identity 98

NCBI Description

(AF085073) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551985 (AF085074) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551987 (AF085075) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551989 (AF085076) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140602 (AF090150) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140612

alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140612 (AF090155) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140614 (AF090156) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140616 (AF090157) alcohol dehydrogenase A

[Gossypium hirsutum]

Seq. No. 212645

Seq. ID LIB3145-057-Q1-K1-F8

Method BLASTN
NCBI GI g1418705
BLAST score 141
E value 2.0e-73
Match length 353
% identity 95

NCBI Description G.hirsutum metallothionein-like gene

Seq. No. 212646

Seq ID LIB3145-057-Q1-K1-F9

Method BLASTX
NCBI GI g533692
BLAST score 210
E value 1.0e-16
Match length 72
% identity 62

NCBI Description (U12150) protease inhibitor [Glycine max]

Seq. No. 212647

Seq. ID LIB3145-057-Q1-K1-G1

Method BLASTX
NCBI GI g2088651
BLAST score 405
E value 1.0e-39
Match length 125
% identity 62

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 212648

Seq. ID LIB3145-057-Q1-K1-G4

Method BLASTX
NCBI GI g4038034
BLAST score 162
E value 2.0e-11
Match length 43
% identity 70

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 212649

Seq. ID LIB3145-057-Q1-K1-G9



```
Method
NCBI GI
                  q3063396
BLAST score
                   527
E value
                   6.0e-54
Match length
                  114
% identity
                  86
NCBI Description
                  (AB012947) vcCyP [Vicia faba]
Seq. No.
                  212650
                  LIB3145-057-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529665
BLAST score
                  186
                  4.0e-14
E value
Match length
                  100
% identity
                  56
NCBI Description
                   (AC002535) putative ribosomal protein L7A [Arabidopsis
                  thaliana]
                  212651
Seq. No.
                  LIB3145-057-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529665
BLAST score
                  187
E value
                  2.0e-14
Match length
                  78
% identity
                  36
NCBI Description
                  (AC002535) putative ribosomal protein L7A [Arabidopsis
                  thaliana]
Seq. No.
                  212652
Seq. ID
                  LIB3145-058-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g122006
BLAST score
                  280
E value
                  5.0e-25
Match length
                  83
                  69
% identity
NCBI Description HISTONE H2A >gi 81906 pir JQ1183 histone H2A - garden pea
Seq. No.
                  212653
Seq. ID
                  LIB3145-058-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2267567
BLAST score
                  163
                  3.0e-11
E value
Match length
                  39
                  74
```

% identity

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium

x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

Seq. No.

212654

Seq. ID

LIB3145-058-Q1-K1-A3

Method BLASTX NCBI GI g1730107 BLAST score 529



E value Match length 125 % identity 72

LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN NCBI Description

HYDROXYLASE) >gi\_421870\_pir\_\_S33144 anthocyanidin hydroxylase - apple tree >gi\_296844\_emb\_CAA50498\_ (X71360)

anthocyanidin hydroxylase [Malus sp.]

Seq. No. 212655

Seq. ID LIB3145-058-Q1-K1-A6

Method BLASTX NCBI GI q3320379 BLAST score 483 E value 7.0e-49 Match length 103 92 % identity

(AF014375) putative JUN kinase activation domain binding NCBI Description

protein [Medicago sativa]

212656 Seq. No.

Seq. ID LIB3145-058-Q1-K1-A8

Method BLASTX NCBI GI q1352668 BLAST score 197 3.0e-15 E value Match length 72 % identity 61

SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT NCBI Description

>gi 17848 emb CAA40687 (X57439) phosphatase 2A [Brassica

napus]

Seq. No. 212657

Seq. ID LIB3145-058-Q1-K1-A9

Method BLASTX NCBI GI g1169586 BLAST score 571 E value 5.0e-59 Match length 131 % identity

FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC NCBI Description

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi\_542079\_pir\_\_S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi\_440591\_emb\_CAA54265\_ (X76946)

fructose-1,6-bisphosphatase [Solanum tuberosum]

212658 Seq. No.

Seq. ID LIB3145-058-Q1-K1-B1

Method BLASTX q2440044 NCBI GI BLAST score 218 3.0e-18 E value Match length 45 89 % identity

(AJ001293) major intrinsic protein PIPB [Craterostigma NCBI Description

plantagineum]

Seq. No. 212659

```
LIB3145-058-Q1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4127878
BLAST score
                  147
                  2.0e-09
E value
Match length
                  111
% identity
                  35
                  (AJ011831) NDX1 homeobox protein [Glycine max]
NCBI Description
Seq. No.
                  212660
                  LIB3145-058-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q99807
BLAST score
                  500
E value
                  8.0e-51
Match length
                  116
% identity
NCBI Description
                  gene Bp10 protein - rape >gi 17782 emb CAA47176 (X66607)
                  Bplo [Brassica napus]
                  212661
Seq. No.
Seq. ID
                  LIB3145-058-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                  466
E value
                  9.0e-47
Match length
                  112
                  79
% identity
NCBI Description (AB012947) vcCyP [Vicia faba]
                  212662
Seq. No.
                  LIB3145-058-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1943751
BLAST score
                  636
                  1.0e-66
E value
Match length
                  135
% identity
                  87
NCBI Description
                  (U93845) Arabidopsis thaliana ER-type calcium pump
                  protein, complete sequence >gi 2078292 (U96455) ER-type
                  Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                  212663
Seq. No.
                  LIB3145-058-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4098129
BLAST score
                   604
                  5.0e-63
E value
Match length
                  119
                  97
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
```

Seq. No.

212664

Seq. ID LIB3145-058-Q1-K1-C9

Method BLASTX NCBI GI g1483563 BLAST score 614



```
E value
                  134
Match length
                  84
% identity
                  (X99825) leucine aminopeptidase [Petroselinum crispum]
NCBI Description
                  212665
Seq. No.
Seq. ID
                  LIB3145-058-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4105097
BLAST score
                  538
                  3.0e-55
E value
Match length
                  114
% identity
                  89
                  (AF043255) MADS box protein 26 [Cucumis sativus]
NCBI Description
```

212666 Seq. No. Seq. ID LIB3145-058-Q1-K1-D11 Method BLASTX g132944 NCBI GI

297 BLAST score 4.0e-27 E value Match length 72 % identity 78

60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal NCBI Description

protein L3 (ARP2) - Arabidopsis thaliana >gi\_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 212667 Seq. ID LIB3145-058-Q1-K1-D12 Method BLASTX

g132944 NCBI GI BLAST score 335 E value 1.0e-31 Match length 81 % identity 78

60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal NCBI Description

protein L3 (ARP2) - Arabidopsis thaliana >gi\_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

212668 Seq. No.

Seq. ID LIB3145-058-Q1-K1-D4

BLASTX Method NCBI GI g4163997 268 BLAST score 7.0e-43 E value Match length 120 % identity 76

(AF087483) alpha-xylosidase precursor [Arabidopsis NCBI Description

thaliana]

212669 Seq. No.

Seq. ID LIB3145-058-Q1-K1-D5

Method BLASTX NCBI GI g2118220 BLAST score 405 1.0e-39 E value Match length 116



% identity

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>gi\_3096941\_emb\_CAA18851.1\_ (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana] >qi 4539311 emb CAB38812.1 (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]

Seq. No. 212670

Seq. ID LIB3145-058-Q1-K1-D7

Method BLASTX NCBI GI q125568 BLAST score 529 4.0e-54 E value Match length 133 % identity 76

PROTEIN KINASE PVPK-1 >gi\_100013\_pir\_\_A30311 protein kinase NCBI Description

C (EC 2.7.1.-) homolog - kidney bean >gi\_169361 (J04555)

PVPK-1 protein [Phaseolus vulgaris]

Seq. No. 212671

Seq. ID LIB3145-058-Q1-K1-D8

Method BLASTX NCBI GI q132944 BLAST score 553 E value 5.0e-57 Match length 107 95 % identity

60S RIBOSOMAL PROTEIN L3 >gi\_81658\_pir\_\_JQ0772 ribosomal NCBI Description

protein L3 (ARP2) - Arabidopsis thaliana >gi\_806279

(M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 212672

Seq. ID LIB3145-058-Q1-K1-E1

Method BLASTX NCBI GI q3914136 BLAST score 166 E value 9.0e-12 Match length 60 % identity 50

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)

>gi 2632171 emb CAA05771 (AJ002958) lipid transfer protein

[Cicer arietinum]

Seq. No. 212673

Seq. ID LIB3145-058-Q1-K1-E2

Method BLASTX q1871192 NCBI GI BLAST score 319 2.0e-29 E value Match length 121 % identity

(U90439) Cys3His zinc finger protein isolog [Arabidopsis NCBI Description

thaliana]



```
212674
Seq. No.
Seq. ID
                  LIB3145-058-Q1-K1-E5
                  BLASTX
Method
NCBI GI
                  g3914006
                  370
BLAST score
                  2.0e-35
E value
                  107
Match length
% identity
                  70
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1816588
NCBI Description
                  (U85495) LON2 [Zea mays]
Seq. No.
                  212675
                  LIB3145-058-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024386
BLAST score
                  655
E value
                  6.0e-69
Match length
                  127
% identity
                  99
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                  >gi 2129500 pir S52006 polygalacturonase - upland cotton
                  >qi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  212676
                  LIB3145-058-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1850546
BLAST score
                  234
E value
                  1.0e-19
Match length
                  86
                  59
% identity
NCBI Description
                  (U88045) syntaxin related protein AtVam3p [Arabidopsis
                  thaliana]
                  212677
Seq. No.
Seq. ID
                  LIB3145-058-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g1620970
BLAST score
                  531
                  2.0e-54
E value
Match length
                  116
% identity
                  92
                  (Y08887) L-lactate dehydrogenase [Lycopersicon esculentum]
NCBI Description
                  >gi 1806117 emb CAA71611 (Y10602) L-lactate dehydrogenase
                  [Lycopersicon esculentum]
Seq. No.
                  212678
Seq. ID
                  LIB3145-058-Q1-K1-F10
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4105696
BLAST score 552
E value 7.0e-57
Match length 109
% identity 93

NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]

```
Seq. No.
                   212679
Seq. ID
                  LIB3145-058-Q1-K1-F2
Method
                  BLASTN
NCBI GI
                   g2564046
BLAST score
                   47
E value
                   2.0e-17
Match length
                   257
% identity
                  82
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MGI19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  212680
Seq. ID
                  LIB3145-058-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q2605621
BLAST score
                   366
E value
                   3.0e-35
Match length
                   92
                  73
% identity
NCBI Description
                 (D88619) OSMYB3 [Oryza sativa]
Seq. No.
                  212681
Seq. ID
                  LIB3145-058-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2641638
BLAST score
                  424
                  5.0e-42
E value
Match length
                  98
% identity
                  82
NCBI Description
                 (AF032883) AtJ3 [Arabidopsis thaliana]
Seq. No.
                  212682
Seq. ID
                  LIB3145-058-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2501449
BLAST score
                  175
E value
                  8.0e-13
Match length
                  33
% identity
                  100
NCBI Description
                  UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773_emb_CAA67922_
                   (X99608) ubiquitin-like protein [Oryza sativa]
Seq. No.
                  212683
Seq. ID
                  LIB3145-058-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q1109830
BLAST score
                  306
E value
                  4.0e-28
Match length
                  109
% identity
                  59
NCBI Description
                  (U41534) coded for by C. elegans cDNA CEESI42F; Similar to
                  helicases of SNF2/RAD54 family. [Caenorhabditis elegans]
```

Seq. No. Seq. ID LIB3145-058-Q1-K1-F8

212684

Method BLASTX NCBI GI g4056432

29549



BLAST score 557 E value 2.0e-57 Match length 127 % identity 76

NCBI Description (AC005990) Similar to gi\_2245014 glucosyltransferase

homolog from Arabidopsis thaliana chromosome 4 contig gb Z97341. ESTs gb T20778 and gb AA586281 come from this

gene. [Arabidopsis thaliana]

Seq. No. 212685

Seq. ID LIB3145-058-Q1-K1-F9

Method BLASTX
NCBI GI g4056432
BLAST score 404
E value 2.0e-39
Match length 107
% identity 68

NCBI Description (AC005990) Similar to gi 2245014 glucosyltransferase

homolog from Arabidopsis thaliana chromosome 4 contig gb\_Z97341. ESTs gb\_T20778 and gb\_AA586281 come from this

gene. [Arabidopsis thaliana]

Seq. No. 212686

Seq. ID LIB3145-058-Q1-K1-G1

Method BLASTX
NCBI GI g2351380
BLAST score 164
E value 2.0e-11
Match length 113
% identity 32

NCBI Description (U54559) translation initiation factor eIF3 p40 subunit

[Homo sapiens] >gi\_4503515\_ref\_NP\_003747.1\_pEIF3S3\_ UNKNOWN

Seq. No. 212687

Seq. ID LIB3145-058-Q1-K1-G3

Method BLASTX
NCBI GI g3063396
BLAST score 369
E value 1.0e-35
Match length 74
% identity 91

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 212688

Seq. ID LIB3145-058-Q1-K1-G4

Method BLASTX
NCBI GI g2443757
BLAST score 318
E value 1.0e-29
Match length 76
% identity 79

NCBI Description (AF020434) cyclophilin [Arabidopsis thaliana]

Seq. No. 212689

Seq. ID LIB3145-058-Q1-K1-G7

Method BLASTX NCBI GI g267069



BLAST score E value 8.0e-52 Match length 94 99 % identity

TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 212690

Seq. ID LIB3145-058-Q1-K1-G9

Method BLASTX NCBI GI q100010 BLAST score 394 E value 2.0e-38 Match length 117 % identity

NCBI Description pectinesterase (EC 3.1.1.11) - kidney bean (fragment)

>gi 21062 emb CAA48169 (X68028) pectinesterase [Phaseolus

vulgaris]

212691\* Seq. No.

Seq. ID LIB3145-058-Q1-K1-H1

Method BLASTX NCBI GI g1346701 BLAST score 218 7.0e-18 E value Match length 97 % identity 49

EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG) NCBI Description

(PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi\_421831\_pir\_\_S34199 exopolygalacturonase (clone GBGe184) - Arabidopsis thaliana >gi\_313682\_emb\_CAA51032\_ (X72291)

exopolygalacturonase [Arabidopsis thaliana]

>gi\_3004440\_emb\_CAA76127\_ (Y16230) polygalacturonase

[Arabidopsis thaliana]

Seq. No. 212692

Seq. ID LIB3145-058-Q1-K1-H10

Method BLASTN NCBI GI q2618602 BLAST score 35 3.0e-10 E value Match length 150 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 212693

Seq. ID LIB3145-058-Q1-K1-H11

Method BLASTX NCBI GI q4263715 BLAST score 444 E value 4.0e-44 Match length 129 % identity 63

NCBI Description (AC006223) putative alanine acetyl transferase [Arabidopsis

NCBI GI

E value

BLAST score

g461729

1.0e-40

414



## thaliana]

```
212694
Seq. No.
                  LIB3145-058-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  q3893079
NCBI GI
BLAST score
                  566
                  2.0e-58
E value
Match length
                  122
                  85
% identity
                  (Y18432) glucose-1-phosphate adenylyltransferase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  212695
                  LIB3145-058-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g1346701
NCBI GI
                  213
BLAST score
E value
                  3.0e-17
                  86
Match length
                  49
% identity
                  EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG)
NCBI Description
                  (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 421831_pir__S34199 exopolygalacturonase (clone GBGe184)
                  - Arabidopsis thaliana >gi_313682_emb_CAA51032_ (X72291)
                  exopolygalacturonase [Arabidopsis thaliana]
                  >gi 3004440 emb CAA76127 (Y16230) polygalacturonase
                   [Arabidopsis thaliana]
Seq. No.
                  212696
Seq. ID
                  LIB3145-058-Q1-K1-H5
Method
                  BLASTX
                  g2160166
NCBI GI
BLAST score
                  164
                  2.0e-11
E value
Match length
                  93
% identity
                  43
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212697
                  LIB3145-058-01-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3912988
BLAST score
                  424
E value
                  5.0e-42
                  99
Match length
                  87
% identity
                  FLORAL HOMEOTIC PROTEIN AGL9 >qi 2345158 (AF015552) AGL9
NCBI Description
                   [Arabidopsis thaliana] >gi 2829878 (AC002396) AGL9
                   [Arabidopsis thaliana]
Seq. No.
                  212698
                  LIB3145-058-Q1-K1-H7
Seq. ID
Method
                  BLASTX
```



Match length % identity 77 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) NCBI Description >gi\_2146744\_pir\_\_S65597 probable chaperonin, 10K -Arabidopsis thaliana >gi 166662 (L02843) 10 kDa chaperonin [Arabidopsis thaliana] Seq. No. 212699 LIB3145-058-Q1-K1-H8 Seq. ID Method BLASTX g729051 NCBI GI BLAST score 510 E value 7.0e-52 Match length 104 % identity 59 CALTRACTIN (CENTRIN) >gi 444342 prf 1906390A NCBI Description caltractin-like protein [Atriplex nummularia] 212700 Seq. No. LIB3145-058-Q1-K1-H9 Seq. ID BLASTX Method g2129579 NCBI GI BLAST score 186 E value 4.0e-14 Match length 38 95 % identity NCBI Description Dwarf1 protein - Arabidopsis thaliana >gi 516043 (U12400) Dwarfl [Arabidopsis thaliana] Seq. No. 212701 LIB3146-001-P1-K2-A10 Seq. ID Method BLASTX g3068713 NCBI GI BLAST score 580 5.0e-60 E value Match length 135 84 % identity (AF049236) unknown [Arabidopsis thaliana] NCBI Description Seq. No. 212702 LIB3146-001-P1-K2-A11 Seq. ID Method BLASTX NCBI GI g4115379 BLAST score 230 E value 4.0e-19

Match length 83 % identity 51

(AC005967) putative carbonyl reductase [Arabidopsis NCBI Description

thaliana]

Seq. No. 212703

Seq. ID LIB3146-001-P1-K2-A3

Method BLASTX NCBI GI g416922 BLAST score 143 2.0e-09 E value Match length 45



% identity 78

NCBI Description

DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) (DUTP PYROPHOSPHATASE) (P18) >gi 282947\_pir\_\_JQ1599 dUTP

pyrophosphatase (EC 3.6.1.23) - tomato

>gi 251897 bbs 109276 (S40549) deoxyuridine triphosphatase, dUTPase, PI8 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar

LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No. 212704

Seq. ID LIB3146-001-P1-K2-A5

Method BLASTN
NCBI GI g4519187
BLAST score 33
E value 3.0e-09
Match length 49

% identity 92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K1G2, complete sequence

Seq. No. 212705

Seq. ID LIB3146-001-P1-K2-A8

Method BLASTX
NCBI GI g2342686
BLAST score 143
E value 4.0e-09
Match length 54
% identity 44

NCBI Description (AC000106) Similar to Saccharomyces hypothetical protein

YDR051c (gb Z49209). ESTs gb T44436,gb\_42252 come from this

gene. [Arabidopsis thaliana]

Seq. No. 212706

Seq. ID LIB3146-001-P1-K2-B1

Method BLASTX
NCBI GI g4539291
BLAST score 277
E value 1.0e-24
Match length 70
% identity 73

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 212707

Seq. ID LIB3146-001-P1-K2-B10

Method BLASTX
NCBI GI g4531443
BLAST score 339
E value 8.0e-32
Match length 88
% identity 76

NCBI Description (AC006224) putative 50s ribosomal protein L3 [Arabidopsis

thaliana]

Seq. No. 212708

Seq. ID LIB3146-001-P1-K2-B11

Method BLASTX NCBI GI g3043432 BLAST score 243

```
1.0e-20
E value
Match length
                  48
% identity
                  94
                  (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]
NCBI Description
Seq. No.
                  212709
                  LIB3146-001-P1-K2-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982303
BLAST score
                  659
                  2.0e-69
E value
Match length
                  138
% identity
                  91
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
                  212710
Seq. No.
Seq. ID
                  LIB3146-001-P1-K2-B2
Method
                  BLASTX
NCBI GI
                  g2529662
BLAST score
                  492
E value
                  1.0e-49
Match length
                  104
% identity
                  92
NCBI Description
                  (AC002535) putative small nuclear ribonucleoprotein, Sm D2
                   [Arabidopsis thaliana] >gi_3738278 (AC005309) putative
                  small nuclear ribonucleoprotein, Sm D2 [Arabidopsis
                  thaliana]
Seq. No.
                  212711
Seq. ID
                  LIB3146-001-P1-K2-B7
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                  172
E value
                  8.0e-13
Match length
                  34
                  79
% identity
                 (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 212712

Seq. ID LIB3146-001-P1-K2-B8

Method BLASTX NCBI GI g3355474 BLAST score 562 E value 5.0e-58 Match length 118 89 % identity

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 212713

Seq. ID LIB3146-001-P1-K2-B9

Method BLASTX NCBI GI g2564237 BLAST score 610 1.0e-63 E value 123 Match length 88 % identity

(Y10112) omega-6 desatúrase [Gossypium hirsutum] NCBI Description

Method

NCBI GI

BLASTX

g3746059



```
Seq. No.
                  212714
Seq. ID
                  LIB3146-001-P1-K2-C11
Method
                  BLASTX
NCBI GI
                  g3063467
BLAST score
                  395
E value
                  2.0e-38
                  121
Match length
% identity
                  64
NCBI Description
                  (AC003981) F22013.29 [Arabidopsis thaliana]
                  212715
Seq. No.
Seq. ID
                  LIB3146-001-P1-K2-C12
Method
                  BLASTX
NCBI GI
                  g4454468
BLAST score
                  290
                  4.0e-26
E value
Match length
                  110
                  52
% identity
NCBI Description
                   (AC006234) putative NADH dehydrogenase [Arabidopsis
                  thaliana]
                  212716
Seq. No.
Seq. ID
                  LIB3146-001-P1-K2-C2
Method
                  BLASTX
                  q4376099
NCBI GI
BLAST score
                  225
                  1.0e-18
E value
Match length
                  54
% identity
                  85
NCBI Description
                  (X95690) Histone H2b homologue [Allium cepa]
Seq. No.
                  212717
                  LIB3146-001-P1-K2-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1326163
BLAST score
                  282
E value
                  4.0e-25
Match length
                  66
                  80
% identity
NCBI Description (U54704) stress related protein PvSRP [Phaseolus vulgaris]
Seq. No.
                  212718
Seq. ID
                  LIB3146-001-P1-K2-C5
Method
                  BLASTX
NCBI GI
                  q2645971
BLAST score
                  520
E value
                  4.0e-53
Match length
                  102
% identity
                  92
NCBI Description
                  (AF034255) reversibly glycosylated polypeptide-3
                  [Arabidopsis thaliana]
Seq. No.
                  212719
Seq. ID
                  LIB3146-001-P1-K2-C6
```

29556



```
BLAST score
                   2.0e-16
E value
                   86
Match length
% identity
                   51
                   (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi 4432812 gb AAD20662_ (AC006593) putative
                   cysteinyl-tRNA synthetase [Arabidopsis thaliana]
                   212720
Seq. No.
Seq. ID
                   LIB3146-001-P1-K2-C7
Method
                   BLASTX
NCBI GI
                   g1326163
BLAST score
                   172
E value
                   1.0e-12
Match length
                   63
                   54
% identity
                  (U54704) stress related protein PvSRP [Phaseolus vulgaris]
NCBI Description
                   212721
Seq. No.
Seq. ID
                   LIB3146-001-P1-K2-C8
Method
                   BLASTX
NCBI GI
                   q1694621
BLAST score
                   307
E value
                   3.0e-28
                   66
Match length
                   89
% identity
                  (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
NCBI Description
Seq. No.
                   212722
                   LIB3146-001-P1-K2-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1841870
BLAST score
                   391
                   7.0e-38
E value
Match length
                   87
% identity
                   87
                  (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
NCBI Description
Seq. No.
                   212723
                   LIB3146-001-P1-K2-D11
Seq. ID
                   BLASTX
Method
                   g3953471
NCBI GI
BLAST score
                   327
                   2.0e-30
E value
                   95
Match length
                   62
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212724
                   LIB3146-001-P1-K2-D12
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g4580384
BLAST score 450
E value 8.0e-45
Match length 92
% identity 99

NCBI Description (AC007184) putative histone H2B [Arabidopsis thaliana]



Seq. No.

212725

```
LIB3146-001-P1-K2-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g629735
                  248
BLAST score
                   4.0e-21
E value
                   71
Match length
                   66
% identity
                  fill protein - garden snapdragon >gi_406309_emb_CAA40553_
NCBI Description
                   (X57296) FIL1 [Antirrhinum majus]
                   212726
Seq. No.
                  LIB3146-001-P1-K2-E10
Seq. ID
                  BLASTX
Method
                   g2245098
NCBI GI
BLAST score
                   511
                   1.0e-59
E value
                   149
Match length
                   79
% identity
                  (Z97343) ribosomal protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212727
                   LIB3146-001-P1-K2-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4469003
BLAST score
                   157
E value
                   2.0e-10
Match length
                   71
% identity
                   44
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212728
Seq. ID
                   LIB3146-001-P1-K2-F1
Method
                   BLASTX
                   g1199772
NCBI GI
BLAST score
                   331
                   3.0e-31
E value
                   89
Match length
                   75
% identity
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                   >gi 1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                   212729
Seq. No.
                   LIB3146-001-P1-K2-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2388577
BLAST score
                   182
                   2.0e-13
E value
                   102
Match length
                   41
% identity
                   (AC000098) Similar to Arabidopsis putative ion-channel
NCBI Description
                   PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]
                   212730
Seq. No.
                   LIB3146-001-P1-K2-F12
Seq. ID
```

```
Method
NCBI GI
                  q4249417
BLAST score
                  192
E value
                  1.0e-14
Match length
                  88
                  43
% identity
NCBI Description
                  (AC006072) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  212731
                  LIB3146-001-P1-K2-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629693
BLAST score
                  369
                  2.0e-35
E value
Match length
                  141
% identity
                  50
NCBI Description
                  probable integrase - common tobacco (fragment)
                  >gi 530742 emb CAA56791 (X80830) integrase [Nicotiana
                  tabacum]
Seq. No.
                  212732
                  LIB3146-001-P1-K2-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4102111
BLAST score
                  200
                  1.0e-15
E value
Match length
                  40
                  100
% identity
NCBI Description
                  (AF009126) NAP1-1 [Nicotiana tabacum]
                  212733
Seq. No.
Seq. ID
                  LIB3146-001-P1-K2-F4
Method
                  BLASTX
NCBI GI
                  q2815246
BLAST score
                  218
E value
                  1.0e-17
Match length
                  55
% identity
                  71
NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.
                  212734
Seq. ID
                  LIB3146-001-P1-K2-F5
Method
                  BLASTX
NCBI GI
                  g3738290
BLAST score
                  221
E value
                  4.0e-18
Match length
                  106
% identity
                  45
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212735
```

Seq. ID LIB3146-001-P1-K2-F8

Method BLASTX NCBI GI g464986 BLAST score 574 2.0e-59 E value Match length 108



% identity NCBI Description

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)

>gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana

>gi 297884 emb\_CAA78714\_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi\_4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

212736 Seq. No.

LIB3146-001-P1-K2-G3 Seq. ID

Method BLASTX NCBI GI g2224911 BLAST score 208 E value 2.0e-16 Match length 111 % identity

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]

212737 Seq. No.

LIB3146-001-P1-K2-G5 Seq. ID

Method BLASTX NCBI GI q3063439 BLAST score 159 8.0e-11 E value Match length 52 % identity 62

NCBI Description (AC003981) F22013.1 [Arabidopsis thaliana]

Seq. No. 212738

LIB3146-001-P1-K2-G8 Seq. ID

BLASTX Method g2244792 NCBI GI BLAST score 651 2.0e-68 E value 151 Match length 48 % identity

NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

212739 Seq. No.

LIB3146-001-P1-K2-H12 Seq. ID

BLASTX Method NCBI GI q1352821 BLAST score 199 2.0e-15 E value 42 Match length 88 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >qi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

NCBI GI

E value

BLAST score

g3264766

42 2.0e-14



```
212740
  Seq. No.
  Seq. ID
                     LIB3146-001-P1-K2-H5
  Method
                     BLASTX
  NCBI GI
                     g2559012
  BLAST score
                     600
  E value
                     2.0e-62
  Match length
                     142
  % identity
                     (AF026293) chaperonin containing t-complex polypeptide 1,
  NCBI Description
                     beta subunit; CCT-beta [Homo sapiens] >gi_4090929
                     (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                     [Homo sapiens]
  Seq. No.
                     212741
                     LIB3146-001-P1-K2-H6
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q3182981
  BLAST score
                     652
                     2.0e-68
  E value
  Match length
                     145
                     83
  % identity.
                     CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_
  NCBI Description
                     (D86494) diminuto [Pisum sativum]
  Seq. No.
                     212742
                     LIB3146-002-P1-K1-E10
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q1170747
  BLAST score
                     151
                     2.0e-10
  E value
                     42
  Match length
  % identity
                     81
  NCBI Description
                     LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                     (M88324) late embryogenesis-abundant protein [Gossypium
                     hirsutum] >gi_167347 (M37697) Lea5-A late
                     embryogenesis-abundant protein [Gossypium hirsutum]
  Seq. No.
                     212743
  Sea. ID
                     LIB3146-002-P1-K1-G12
  Method
                     BLASTX
  NCBI GI
                     q417073
  BLAST score
                     513
  E value
                     3.0e-52
  Match length
                     140
  % identity
  NCBI Description
                     GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
                     >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC
                     1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate
                     synthase [Medicago sativa]

∴ Seq. No.

                     212744
  Seq. ID
                     LIB3146-002-P1-K2-A11
  Method
                     BLASTN
```



Match length 87 % identity

Prunus armeniaca AP2 domain containing protein (AP2DCP) NCBI Description

mRNA, partial cds

212745 Seq. No.

Seq. ID LIB3146-002-P1-K2-A12

Method BLASTX NCBI GI g4567304 BLAST score 342 4.0e-32 E value Match length 108 % identity 68

(AC005956) unknown protein [Arabidopsis thaliana] NCBI Description

212746 Seq. No.

Seq. ID LIB3146-002-P1-K2-A3

Method BLASTX NCBI GI g2947063 BLAST score 238 3.0e-20 E value Match length 90

% identity 57

(AC002521) putative Ser/Thr protein kinase [Arabidopsis NCBI Description

thaliana]

212747 Seq. No.

Seq. ID LIB3146-002-P1-K2-A6

Method BLASTX NCBI GI g4151068 BLAST score 581 E value 4.0e-60 Match length 126

87 % identity

NCBI Description (Y10862) ribonucleotide reductase [Nicotiana tabacum]

212748 Seq. No.

Seq. ID LIB3146-002-P1-K2-A9

Method BLASTX NCBI GI g2760837 BLAST score 236 E value 8.0e-20 Match length 121 45 % identity

NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

212749 Seq. No.

Seq. ID LIB3146-002-P1-K2-B10

Method BLASTX NCBI GI g3355486 BLAST score 462 E value 3.0e-46 Match length 149 % identity 62

(AC004218) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 212750

```
LIB3146-002-P1-K2-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129579
                  309
BLAST score
                   9.0e-34
E value
                  88
Match length
                  82
% identity
                  Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
NCBI Description
                  Dwarfl [Arabidopsis thaliana]
                  212751
Seq. No.
                  LIB3146-002-P1-K2-B2
Seq. ID
Method
                  BLASTX
                  q3024020
NCBI GI
BLAST score
                   496
                  2.0e-58
E value
Match length
                  123
% identity
                  93
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation
                   factor 5A3 [Solanum tuberosum]
Seq. No.
                   212752
Seq. ID
                  LIB3146-002-P1-K2-B4
Method
                  BLASTX
NCBI GI
                  g3320120
BLAST score
                  159
E value
                   4.0e-11
Match length
                  89
% identity
                   40
NCBI Description
                  (U66669) 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo
                  sapiens]
                   212753
Seq. No.
Seq. ID
                  LIB3146-002-P1-K2-B6
Method
                  BLASTX
NCBI GI
                  q3355477
BLAST score
                   415
                   1.0e-40
E value
                   112
Match length
% identity
                   40
                   (AC004218) putative P-glycoprotein, pgpl [Arabidopsis
NCBI Description
                   thaliana]
                   212754
Seq. No.
Seq. ID
                  LIB3146-002-P1-K2-B9
Method
                  BLASTX
NCBI GI
                   q4376158
                   596
BLAST score
                   6.0e-62
E value
Match length
                  136
                   82
% identity
```

NCBI Description (X98873) aspartate kinase [Arabidopsis thaliana]

212755 Seq. No.

Seq. ID LIB3146-002-P1-K2-C1

Method BLASTX

```
NCBI GI
                  q4107343
BLAST score
                  356
                  8.0e-34
E value
Match length
                  142
% identity
                  48
NCBI Description (AJ224922) ATP citrate lyase [Sordaria macrospora]
                  212756
Seq. No.
                  LIB3146-002-P1-K2-C12
Seq. ID
                  BLASTX
```

Method BLASTX
NCBI GI g1220196
BLAST score 492
E value 9.0e-50
Match length 115
% identity 78

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

 Seq. No.
 212757

 Seq. ID
 LIB3146-002-P1-K2-C3

 Method
 BLASTX

 NCBI GI
 g2497486

NCBI GI g2497486
BLAST score 170
E value 2.0e-12
Match length 41
% identity 78

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP

KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis

thaliana]

Seq. No. 212758

Seq. ID LIB3146-002-P1-K2-C4

Method BLASTX

NCBI GI g4115337

BLAST score 400

E value 6.0e-39

Match length 88

% identity 16

NCBI Description (L81141) ubiquitin [Pisum sativum]

Seq. No. 212759

Seq. ID LIB3146-002-P1-K2-C5

Method BLASTX
NCBI GI g3021344
BLAST score 257
E value 3.0e-22
Match length 61
% identity 77

NCBI Description (AJ004959) hypothetical protein [Cicer arietinum]

Seq. No. 212760

Seq. ID LIB3146-002-P1-K2-C7

Method BLASTX
NCBI GI g2498464
BLAST score 224
E value 3.0e-18
Match length 74

% identity 62



28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF NCBI Description

ASSOCIATED PROTEIN) >gi\_1136584 (U41745) PDGF associated

protein [Homo sapiens] >gi\_1589642\_prf\_\_2211382B

platelet-derived growth factor-associated protein [Homo

sapiens]

212761 Seq. No.

Seq. ID LIB3146-002-P1-K2-D5

Method BLASTX NCBI GI g3355617 BLAST score 387 2.0e-37 E value Match length 90 % identity 81

NCBI Description (AJ000229) unnamed protein product [Hordeum vulgare]

212762 Seq. No.

LIB3146-002-P1-K2-D6 Seq. ID

Method BLASTX g3395938 NCBI GI BLAST score 392 E value 3.0e-50 Match length 151 51 % identity

NCBI Description (AF076924) polypyrimidine tract-binding protein homolog

[Arabidopsis thaliana]

212763 Seq. No.

LIB3146-002-P1-K2-D7 Seq. ID

Method BLASTX g3402752 NCBI GI BLAST score 210 8.0e-17 E value Match length 87

% identity 57

NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

212764 Seq. No.

Seq. ID LIB3146-002-P1-K2-D8

Method BLASTX NCBI GI a2429280 740 BLAST score 9.0e-79 E value 160 Match length % identity

(AF014055) asparagine synthetase [Triphysaria versicolor] NCBI Description

>gi\_2429282 (AF014056) asparagine synthetase [Triphysaria versicolor] >gi\_2429284 (AF014057) asparagine synthetase

[Triphysaria versicolor]

Seq. No. 212765

Seq. ID LIB3146-002-P1-K2-D9

Method BLASTX NCBI GI g549063 BLAST score 332 5.0e-31 E value 86 Match length



% identity 73
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)
21kd polypeptide [Oryza sativa]

Seq. No. 212766

Seq. ID LIB3146-002-P1-K2-E10

Method BLASTX
NCBI GI g1170747
BLAST score 423
E value 1.0e-41
Match length 97
% identity 86

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 212767

Seq. ID LIB3146-002-P1-K2-E11

Method BLASTX
NCBI GI g1617272
BLAST score 425
E value 6.0e-42
Match length 128
% identity 64

NCBI Description (Z72151) AMP-binding protein [Brassica napus]

Seq. No. 212768

Seq. ID LIB3146-002-P1-K2-E2

Method BLASTX
NCBI GI g2760836
BLAST score 282
E value 4.0e-25
Match length 119
% identity 26

NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 212769

Seq. ID LIB3146-002-P1-K2-E9

Method BLASTX
NCBI GI g2980770
BLAST score 698
E value 7.0e-74
Match length 144
% identity 87

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 212770

Seq. ID LIB3146-002-P1-K2-F10

Method BLASTX
NCBI GI g629735
BLAST score 249
E value 2.0e-21
Match length 71



Seq. No. 212771

Seq. ID LIB3146-002-P1-K2-F11

Method BLASTX
NCBI GI g4538939
BLAST score 437
E value 2.0e-43
Match length 136
% identity 67

NCBI Description (AL049483) Col-O casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No. 212772

Seq. ID LIB3146-002-P1-K2-F3

Method BLASTX
NCBI GI g4455366
BLAST score 386
E value 3.0e-37
Match length 128
% identity 65

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 212773

Seq. ID LIB3146-002-P1-K2-F4

Method BLASTX
NCBI GI g3152880
BLAST score 617
E value 2.0e-64
Match length 158
% identity 69

NCBI Description (AF063246) cell wall invertase; beta-fructofuranosidase

[Pisum sativum]

Seq. No. 212774

Seq. ID LIB3146-002-P1-K2-F5

Method BLASTX
NCBI GI 94467126
BLAST score 371
E value 1.0e-35
Match length 141
% identity 48

NCBI Description (AL035538) guanine nucleotide-exchange protein-like

[Arabidopsis thaliana]

Seq. No. 212775

Seq. ID LIB3146-002-P1-K2-F7

Method BLASTX
NCBI GI g549010
BLAST score 630
E value 6.0e-66
Match length 132
% identity 92

NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)

(OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)





>gi\_322554\_pir\_\_S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi\_16514\_emb\_CAA49172\_(X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi\_1402882\_emb\_CAA66813\_(X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No. LIB3146-002-P1-K2-F8 Seq. ID Method BLASTX NCBI GI g2529707 BLAST score 391 E value 7.0e-38 Match length 157 50 % identity NCBI Description (AF001434) Hpast [Homo sapiens]

212776

Seq. No. 212777 Seq. ID LIB3146-002-P1-K2-F9

Method BLASTX NCBI GI q2252634 BLAST score 192 E value 1.0e-14 Match length 70

% identity

NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

212778 Seq. No.

LIB3146-002-P1-K2-G10 Seq. ID

Method BLASTX NCBI GI g4467144 380 BLAST score E value 1.0e-36 100 Match length % identity 70

(AL035540) putative phosphatidylinositol synthase NCBI Description

[Arabidopsis thaliana]

212779 Seq. No.

Seq. ID LIB3146-002-P1-K2-G11

Method BLASTX NCBI GI g3334144 445 BLAST score E value 4.0e-48 Match length 126 75 % identity

NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >qi 1695698 dbj BAA13181

(D86925) C-type cyclin [Oryza sativa]

Seq. No. 212780

Seq. ID LIB3146-002-P1-K2-G12

Method BLASTX NCBI GI g417073 BLAST score 618 E value 2.0e-64



Match length 152 % identity 76

NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)

>gi\_484529\_pir\_\_JQ1977 glutamate synthase (NADH) (EC
1.4.1.14) - alfalfa >gi\_166412 (L01660) NADH-glutamate

synthase [Medicago sativa]

Seq. No. 212781

Seq. ID LIB3146-002-P1-K2-G7

Method BLASTX
NCBI GI g2970654
BLAST score 363
E value 1.0e-34
Match length 99

% identity 72

NCBI Description (AF052058) ferritin subunit cowpea2 precursor [Vigna

unguiculata]

Seq. No. 212782

Seq. ID LIB3146-002-P1-K2-G8

Method BLASTX
NCBI GI g2144183
BLAST score 361
E value 2.0e-34
Match length 93
% identity 73

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) chain III -

Ecotype Columbia >gi 1184686 (U35049) RNA polymerase I(A)

and III(C) 14 kDa subunit [Arabidopsis thaliana]

>gi\_1184688 (U35050) Arabidopsis thaliana RNA polymerase I(A) and III(C) 14 kDa subunit [Arabidopsis thaliana] >gi\_3980382 (AC004561) RNA polymerase I(A) and III(C) 14

kDa subunit (AtRPAC14) [Arabidopsis thaliana]

Seq. No. 212783

Seq. ID LIB3146-002-P1-K2-H10

Method BLASTN
NCBI GI g2244733
BLAST score 119
E value 2.0e-60
Match length 305
% identity 90

NCBI Description Cotton mRNA for actin, clone CF456, partial cds

Seq. No. 212784

Seq. ID LIB3146-002-P1-K2-H8

Method BLASTX
NCBI GI g114682
BLAST score 340
E value 4.0e-32
Match length 98
% identity 70

NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)

>gi\_100471\_pir\_\_A35227 H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, mitochondrial - sweet
potato >gi\_168270 (J05397) F-1-ATPase delta subunit

Match length

% identity

114

67





## precursor (EC 3.6.1.3) [Ipomoea batatas]

```
212785
Seq. No.
Seq. ID
                  LIB3146-003-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2062172
BLAST score
                  419
                  3.0e-41
E value
Match length
                  134
% identity
                  61
NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]
                  212786
Seq. No.
Seq. ID
                  LIB3146-003-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4204575
BLAST score
                  356
                  8.0e-34
E value
Match length
                  109
% identity
                  66
NCBI Description
                 (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
Seq. No.
                  212787
Seq. ID
                  LIB3146-003-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  625
E value
                  2.0e-65
Match length
                  118
                  97
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  212788
Seq. ID
                  LIB3146-003-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g544184
BLAST score
                  196
                  3.0e-15
E value
Match length
                  51
% identity
                  71
NCBI Description
                  4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)
                  (DISPROPORTIONATING ENZYME) (D-ENZYME)
                  >gi 322785 pir A45049 4-alpha-glucanotransferase (EC
                  2.4.1.25) - potato >gi 296692 emb CAA48630 (X68664)
                  4-alpha-glucanotransferase [Solanum tuberosum]
Seq. No.
                  212789
Seq. ID
                  LIB3146-003-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4204575
BLAST score
                  387
E value
                  2.0e-37
```





```
NCBI Description
                  (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
                  212790
Seq. No.
Seq. ID
                  LIB3146-003-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3176726
BLAST score
                  317
E value
                  3.0e-29
Match length
                  128
% identity
                  48
                  (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  212791
Seq. ID
                  LIB3146-003-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g927428
                  375
BLAST score
                  5.0e-36
E value
Match length
                  75
% identity
                  89
NCBI Descriptton
                  (X86733) fis1 [Linum usitatissimum]
Seq. No.
                  212792
Seq. ID
                  LIB3146-003-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2388689
BLAST score
                  524
E value
                  2.0e-53
Match length
                  129
                  79
% identity
NCBI Description
                  (AF016633) GH1 protein [Glycine max]
Seq. No.
                  212793
Seq. ID
                  LIB3146-003-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g1658197
BLAST score
                  645
                  1.0e-67
E value
Match length
                  133
                  89
% identity
NCBI Description
                  (U74630) calreticulin [Ricinus communis] >gi 1763297
                  (U74631) calreticulin [Ricinus communis]
Seq. No.
                  212794
Seq. ID
                  LIB3146-003-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g3860318
BLAST score
                  34
E value
                  2.0e-09
```

Match length 126 % identity 82

NCBI Description Cicer arietinum mRNA for nucleolar protein, partial

Seq. No. 212795

Seq. ID LIB3146-003-P1-K1-C3

Method BLASTX



```
q2344901
NCBI GI
BLAST score
                  546
                  5.0e-56
E value
                  142
Match length
                  78
% identity
                   (AC002388) serine/threonine protein kinase isolog
NCBI Description
                   [Arabidopsis thaliana]
                  212796
Seq. No.
                  LIB3146-003-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1173256
BLAST score
                  242
                  2.0e-20
E value
                  58
Match length
% identity
                  83
                  40S RIBOSOMAL PROTEIN S4 >gi 629496 pir_ S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
Seq. No.
                  212797
Seq. ID
                  LIB3146-003-P1-K1-D1
Method
                  BLASTX
                  g2739000
NCBI GI
BLAST score
                  306
                  5.0e-28
E value
Match length
                  145
% identity
                   42
                  (AF022459) CYP71D10p [Glycine max]
NCBI Description
Seq. No.
                  212798
Seq. ID
                  LIB3146-003-P1-K1-D5
Method
                  BLASTX
                  g4566614
NCBI GI
                   477
BLAST score
                   4.0e-48
E value
Match length
                  102
                   87
% identity
                   (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                  Populus tremula]
                  212799
Seq. No.
                  LIB3146-003-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q125887
BLAST score
                   196
E value
                   5.0e-15
                  101
Match length
                   45
% identity
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
```

>gi 82092 pir S04765 LAT52 protein precursor - tomato >gi\_295812\_emb\_CAA33854\_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 212800

LIB3146-003-P1-K1-D7 Seq. ID

```
Method
                  BLASTX
                  g3915082
NCBI GI
                  219
BLAST score
                  9.0e-18
E value
                  44
Match length
% identity
                  98
                  TUBULIN ALPHA CHAIN >gi 1220545 (M97956) alpha tubulin
NCBI Description
                   [Trypanosoma cruzi] >gi 1220548 (M96849) alpha tubulin
                  [Trypanosoma cruzi]
                  212801
Seq. No.
Seq. ID
                  LIB3146-003-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g112717
BLAST score
                  268
E value
                  1.0e-23
Match length
                  115
% identity
                  44
NCBI Description
                  21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911
                  hypothetical protein precursor - carrot
                  >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA
                  -22 to 171) [Daucus carota]
Seq. No.
                  212802
Seq. ID
                  LIB3146-003-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q3334144
BLAST score
                  508
E value
                  1.0e-51
Match length
                  125
% identity
                  80
                  G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698 dbj BAA13181
NCBI Description
                  (D86925) C-type cyclin [Oryza sativa]
Seq. No.
                  212803
Seq. ID
                  LIB3146-003-P1-K1-E2
Method
                  BLASTX
                  q4510430
NCBI GI
BLAST score
                  543
                  1.0e-55
E value
Match length
                  116
                  85
% identity
                  (AC006929) unknown protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 212804

Seq. ID LIB3146-003-P1-K1-E3

Method BLASTX
NCBI GI g1170373
BLAST score 626
E value 2.0e-65
Match length 134

% identity 90

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi\_1072473\_pir\_\_S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi\_397482 emb\_CAA52684 (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

NCBI Description

212810

Seq. No.



```
212805
Seq. No.
                  LIB3146-003-P1-K1-E4
Seq. ID
                  BLASTX
Method
                  g2980770
NCBI GI
BLAST score
                  366
E value
                  5.0e-35
Match length
                  121
% identity
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212806
                  LIB3146-003-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3449321
BLAST score
                  45
                   4.0e-16
E value
Match length
                  117
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  212807
Seq. ID
                  LIB3146-003-P1-K1-F1
Method
                  BLASTN
                  q3821780
NCBI GI
BLAST score
                   36
E value
                   8.0e-11
Match length
                   37
                   61
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                   212808
                   LIB3146-003-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   161
                   1.0e-19
E value
Match length
                   123
% identity
                   56
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   212809
Seq. ID
                   LIB3146-003-P1-K1-F11
                   BLASTX
Method
NCBI GI
                   q3218467
                   176
BLAST score
                   1.0e-12
E value
                   129
Match length
                   33
% identity
```

29574

(AJ006529) putative phosphatase [Gallus gallus]

```
LIB3146-003-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g2979545
NCBI GI
                  235
BLAST score
                  1.0e-19
E value
                  96
Match length
                  53
% identity
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.
                  212811
                  LIB3146-003-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1771160
BLAST score
                  464
E value
                  2.0e-46
                  142
Match length
% identity
                  63
                  (X98929) SBT1 [Lycopersicon esculentum]
NCBI Description
                  >gi 3687305 emb CAA06999 (AJ006378) subtilisin-like
                  protease [Lycopersicon esculentum]
Seq. No.
                  212812
Seq. ID
                  LIB3146-003-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q2739387
BLAST score
                  191
E value
                  2.0e-14
Match length
                  96
% identity
                  43
NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  212813
Seq. ID
                  LIB3146-003-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g1439608
                  39
BLAST score
                  2.0e-12
E value
Match length
                  51
% identity
                  94
                  Gossypium hirsutum delta-tonoplast intrinsic protein mRNA,
NCBI Description
                  complete cds
                  212814
Seq. No.
                  LIB3146-003-P1-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4539405
BLAST score
                   449
                  7.0e-45
E value
Match length
                  108
                  78
% identity
                   (ALO49524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  212815
Seq. ID
                  LIB3146-003-P1-K1-G12
```

29575

BLASTX

g1046373

Method NCBI GI



```
BLAST score
                  2.0e-13
E value
Match length
                  41
                  71
% identity
                  (U37336) SAG12 protein [Arabidopsis thaliana]
NCBI Description
                  212816
Seq. No.
                  LIB3146-003-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585350
BLAST score
                  490
                  6.0e-58
E value
Match length
                  123
                  93
% identity
                  CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
NCBI Description
                  >gi 419753 pir S31099 casein kinase II (EC 2.7.1.-)
                  alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
                  >gi 391605 dbj BAA01091 (D10247) casein kinase II
                  catalytic subunit [Arabidopsis thaliana]
                  212817
Seq. No.
Seq. ID
                  LIB3146-003-P1-K1-G3
Method
                  BLASTX
                  q2499967
NCBI GI
                  227
BLAST score
                  9.0e-19
E value
                  52
Match length
% identity
                  83
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E
NCBI Description
                  B) >gi 632724 bbs_151002 (S72358) photosystem I subunit
                  PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,
                  143 aa] [Nicotiana sylvestris]
Seq. No.
                  212818
Seq. ID
                  LIB3146-003-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q3927827
BLAST score
                  190
E value
                  1.0e-14
                  46
Match length
                  72
% identity
                  (AC005727) osmotin-like protein precursor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  212819
Seq. ID
                  LIB3146-003-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4455159
BLAST score
                  204
```

6.0e-16 E value Match length 147 36 % identity

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 212820

Seq. ID LIB3146-003-P1-K1-H11

Method BLASTX

Match length

% identity

131

41

```
g2924520
NCBI GI
                   466
BLAST score
                  8.0e-47
E value
                  105
Match length
                   87
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                  212821
Seq. No.
                  LIB3146-004-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g4322327
NCBI GI
                   142
BLAST score
E value
                   3.0e-09
                   58
Match length
                   45
% identity
                  (AF080545) peptide transporter [Nepenthes alata]
NCBI Description
                   212822
Seq. No.
                   LIB3146-004-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g4325338
NCBI GI
BLAST score
                   239
                   7.0e-33
E value
Match length
                   90
                   83
% identity
NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]
                   212823
Seq. No.
                   LIB3146-004-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   g4455158
NCBI GI
BLAST score
                   192
E value
                   1.0e-15
Match length
                   56
                   79
% identity
                  (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
                   212824
Seq. No.
                   LIB3146-004-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   q2245021
NCBI GI
                   177
BLAST score
                   2.0e-13
E value
Match length
                   56
                   57
% identity
                   (Z97341) heat shock protein 110 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   212825
Seq. No.
                   LIB3146-004-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2760326
BLAST score
                   244
E value
                   1.0e-20
```

E value Match length

% identity

NCBI Description





```
(AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                    212826
Seq. No.
                    LIB3146-004-P1-K1-B6
Seq. ID
Method
                    BLASTX
NCBI GI
                     g3335375
BLAST score
                     339
                     1.0e-36
E value
                     123
Match length
                     72
% identity
                    (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                     212827
                    LIB3146-004-P1-K1-B9
Seq. ID
Method
                     BLASTX
                     q1408473
NCBI GI
BLAST score
                     441
E value
                     7.0e-44
                     101
Match length
% identity
                     81
                     (U48939) actin depolymerizing factor 2 [Arabidopsis
NCBI Description
                     thaliana]
Seq. No.
                     212828
                     LIB3146-004-P1-K1-C1
Seq. ID
Method
                     BLASTX
                     q1708794
NCBI GI
                     301
BLAST score
E value
                     2.0e-27
                     98
Match length
                     60
% identity
                    GTP-BINDING PROTEIN LEPA >gi_1122398_emb_CAA62842 (X91655) lepA [Bacillus subtilis] >gi_1303804_dbj_BAA12460 (D84432) YqeQ [Bacillus subtilis] >gi_2634997_emb_CAB14493 (Z99117)
NCBI Description
                     GTP-binding protein [Bacillus subtilis]
Seq. No.
                     212829
                     LIB3146-004-P1-K1-C12
Seq. ID
Method
                     BLASTX
NCBI GI
                     g3924599
                     177
BLAST score
                     7.0e-13
E value
Match length
                     111
% identity
                     40
                    (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                     212830
                     LIB3146-004-P1-K1-C6
Seq. ID
                     BLASTX
Method
NCBI GI
                     q3319882
BLAST score
                     654
```

(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer

8.0e-69

arietinum]



```
212831
Seq. No.
                  LIB3146-004-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  q4490297
NCBI GI
                  332
BLAST score
                  4.0e-31
E value
                  115
Match length
                  55
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  212832
Seq. No.
                  LIB3146-004-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  g1351206
NCBI GI
                  568
BLAST score
                  8.0e-59
E value
                  115
Match length
                  93
% identity
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                  4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_629663_pir__S44169 trans-cinnamate 4-monooxygenase (EC
                  1.14.13.11) cytochrome P450 73 - Madagascar periwinkle
                  >gi_2129922_pir__S68204 trans-cinnamate 4-monooxygenase (EC
                  1.14.13.11) - Madagascar periwinkle
                  >gi_473229_emb_CAA83552_ (Z32563) cinnamate 4-hydroxylase
                  (CYP73) [Catharanthus roseus]
                  212833
Seq. No.
                  LIB3146-004-P1-K1-D1
Seq. ID
Method
                  BLASTX
                  q1732511
NCBI GI
BLAST score
                  421
                  6.0e-46
E value
                  108
Match length
% identity
                  (U62742) Ran binding protein 1 homolog [Arabidopsis
NCBI Description
                  thaliana]
                  212834
Seq. No.
Seq. ID
                  LIB3146-004-P1-K1-D12
                  BLASTX
Method
                  q115768
NCBI GI
BLAST score
                   504
                   4.0e-51
E value
Match length
                   98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
```

(CAB) (LHCP) >gi 72743 pir CDKV chlorophyll a/b-binding protein precursor - cucumber (fragment) >gi\_167523 (M16057)

chlorophyll a/b-binding protein [Cucumis sativus]

212835 Seq. No.

LIB3146-004-P1-K1-D3 Seq. ID

BLASTX Method NCBI GI g3482918 640 BLAST score 4.0e-67 E value

```
Match length
                    92
 % identity
                    (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
 NCBI Description
                   thaliana]
                    212836
 Seq. No.
                   LIB3146-004-P1-K1-D6
 Seq. ID
                   BLASTX
 Method
                    q2708749
 NCBI GI
                    274
 BLAST score
                    2.0e-24
 E value
                    88
 Match length
                    57
 % identity
                   (AC003952) putative senescence-assoc. rhodanese-like
 NCBI Description
                    protein [Arabidopsis thaliana]
                    212837
 Seq. No.
                    LIB3146-004-P1-K1-D7
 Seq. ID
Method
                    BLASTX
                    g2495365
 NCBI GI
 BLAST score
                    491
                    1.0e-49
 E value
                    133
 Match length
                    74
 % identity
                    HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf 1908431B
 NCBI Description
                    heat shock protein HSP81-2 [Arabidopsis thaliana]
                    212838
 Seq. No.
                    LIB3146-004-P1-K1-E1
 Seq. ID
 Method
                    BLASTX
                    g1173027
 NCBI GI
                    452
 BLAST score
                    4.0e-45
 E value
 Match length
                    120
 % identity
                    60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
 NCBI Description
                    protein L31 [Nicotiana glutinosa]
                    212839
 Seq. No.
                    LIB3146-004-P1-K1-E3
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2995990
                    375
 BLAST score
 E value
                    4.0e-36
 Match length
                    117
                    63
  % identity
```

(AF053746) dormancy-associated protein [Arabidopsis NCBI Description thaliana] >gi 2995992 (AF053747) dormancy-associated

protein [Arabidopsis thaliana]

212840 Seq. No.

LIB3146-004-P1-K1-E5 Seq. ID

BLASTX Method g4490704 NCBI GI BLAST score 344 1.0e-32E value 118 Match length



```
% identity
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                  212841
Seq. No.
                  LIB3146-004-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3582333
                  179
BLAST score
                  5.0e-13
E value
                  98
Match length
                  42
% identity
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212842
                  LIB3146-004-P1-K1-F10
Seq. ID
Method
                  BLASTX
                  q4557060
NCBI GI
BLAST score
                   466
E value
                   5.0e-49
                   147
Match length
                   74
% identity
                  (AC007154) putative chromosome-associated polypeptide, 5'
NCBI Description
                  partial [Arabidopsis thaliana]
Seq. No.
                   212843
Seq. ID
                   LIB3146-004-P1-K1-F12
Method
                   BLASTX
                   q4126399
NCBI GI
BLAST score
                   563
E value
                   4.0e-58
                   137
Match length
                   80
% identity
                  (AB011794) chalcone isomerase [Citrus sinensis]
NCBI Description
                   212844
Seq. No.
                   LIB3146-004-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g559684
BLAST score
                   582
E value
                   2.0e-60
Match length
                   137
                   82
% identity
                  (L36097) aquaporin [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                   212845
                   LIB3146-004-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914024
BLAST score
                   212
                   6.0e-17
E value
                   61
Match length
                   61
% identity
                   (R)-MANDELONITRILE LYASE ISOFORM 2 PRECURSOR
NCBI Description
                   (HYDROXYNITRILE LYASE 2) ((R)-OXYNITRILASE 2) >gi_2773274
```

29581

(AF040078) (R)-(+)-mandelonitrile lyase isoform MDL2 precursor [Prunus serotina] >gi\_2773276 (AF040079)

(R)-(+)-mandelonitrile lyase isoform MDL2 precursor [Prunus



Seq. No. 212846

Seq. ID LIB3146-004-P1-K1-F5

Method BLASTX
NCBI GI g3668088
BLAST score 295
E value 1.0e-26
Match length 145
% identity 41

NCBI Description (AC004667) G9a-like protein [Arabidopsis thaliana]

Seq. No. 212847

Seq. ID LIB3146-004-P1-K1-F6

Method BLASTX
NCBI GI g2462754
BLAST score 428
E value 3.0e-42
Match length 146
% identity 62

NCBI Description (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No. 212848

Seq. ID LIB3146-004-P1-K1-F7

Method BLASTX
NCBI GI g1174162
BLAST score 648
E value 4.0e-68
Match length 126
% identity 90

NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis

thaliana] >gi\_3746915 (AF091106) E2

ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No. 212849

Seq. ID LIB3146-004-P1-K1-G5

Method BLASTX
NCBI GI g4128197
BLAST score 184
E value 1.0e-13
Match length 68
% identity 46

NCBI Description (U75273) acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No. 212850

Seq. ID LIB3146-004-P1-K1-G6

Method BLASTX
NCBI GI g3080398
BLAST score 179
E value 4.0e-13
Match length 47
% identity 40

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 212851

Seq. ID LIB3146-004-P1-K1-G9

Method BLASTX



q1170555 NCBI GI BLAST score 6.0e-33 E value Match length 114 55 % identity

MYO-INOSITOL 4-O-METHYLTRANSFERASE >gi 282822\_pir\_\_S22696 NCBI Description methyltransferase - common ice plant  $>gi_1672\overline{6}2$  ( $\overline{M8}7340$ )

myo-inositol O-methyl transferase [Mesembryanthemum

crystallinum] >gi\_1488237 (U63634) inositol methyltransferase [Mesembryanthemum crystallinum]

212852 Seq. No.

Seq. ID LIB3146-004-P1-K1-H1

Method BLASTX g3386618 NCBI GI 216 BLAST score 2.0e-17 E value 97 Match length 51 % identity

(AC004665) hypothetical protein [Arabidopsis thaliana] NCBI Description

212853 Seq. No.

LIB3146-004-P1-K1-H11 Seq. ID

BLASTX Method g586145 NCBI GI BLAST score 529 3.0e-54 E value 116 Match length 82 % identity

UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT NCBI Description

PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)

>gi\_488848\_emb\_CAA55894\_ (X79332) Rieske iron sulphur

protein [Solanum tuberosum]

212854 Seq. No.

Seq. ID LIB3146-004-P1-K1-H2

Method BLASTX NCBI GI q282950 144 BLAST score 3.0e-09 E value 48 Match length 50 % identity

protein 108 precursor - tomato >gi\_19152\_emb\_CAA78466\_ NCBI Description

(Z14088) 108 protein [Lycopersicon esculentum]

212855 Seq. No.

LIB3146-004-P1-K1-H6 Seq. ID

BLASTX Method NCBI GI q3695021 BLAST score 364 4.0e-35 E value Match length 91

77 % identity

(AF055849) hypothetical protein [Arabidopsis thaliana] NCBI Description

212856 Seq. No.

LIB3146-004-P1-K1-H7 Seq. ID

```
Method
                   BLASTX
NCBI GI
                   g4455174
BLAST score
                   303
E value
                   1.0e-27
                   95
Match length
                   65
% identity
NCBI Description
                  (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   212857
Seq. ID
                  LIB3146-004-P1-K1-H9
Method
                  BLASTX
NCBI GI
                   g4335750
BLAST score
                   181
                   2.0e-13
E value
                   52
Match length
% identity
                   56
NCBI Description
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
                   thaliana]
Seq. No.
                   212858
Seq. ID
                   LIB3146-005-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                   g100481
BLAST score
                   247
E value
                   5.0e-21
                   69
Match length
% identity
                   67
NCBI Description
                  fil1 protein - garden snapdragon
                   212859
Seq. No.
                   LIB3146-005-Q1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2262172
BLAST score
                   170
E value
                   4.0e-12
Match length
                   121
                   38
% identity
                   (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   212860
Seq. No.
Seq. ID
                   LIB3146-005-Q1-K1-A5
```

Method BLASTX NCBI GI g1800281

BLAST score 613 E value 5.0e-64 125 Match length 22 % identity

NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]

212861 Seq. No.

Seq. ID LIB3146-005-Q1-K1-A6

Method BLASTX g3885884 NCBI GI BLAST score 169 E value 6.0e-12 Match length 56



% identity NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa] 212862 Seq. No. LIB3146-005-Q1-K1-B12 Seq. ID Method BLASTX NCBI GI g2980788 229 BLAST score 6.0e-19 E value Match length 122 % identity 50 NCBI Description (AL022197) putative protein [Arabidopsis thaliana] Seq. No. 212863 LIB3146-005-Q1-K1-B2 Seq. ID Method BLASTX g477280 NCBI GI BLAST score 272 5.0e-24 E value Match length 63 76 % identity mitochondrial processing peptidase (EC 3.4.99.41) 55K NCBI Description protein precursor - potato >gi\_410633\_bbs\_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa] Seq. No. 212864 LIB3146-005-Q1-K1-B3 Seq. ID Method BLASTX NCBI GI q4539345 BLAST score 463 2.0e-46 E value Match length 124 % identity 73 NCBI Description (AL035539) hypothetical protein [Arabidopsis thaliana] Seq. No. 212865 LIB3146-005-Q1-K1-B4 Seq. ID Method BLASTX q3763916 NCBI GI 333 BLAST score 4.0e-31 E value Match length 106 % identity 61 (AC004450) unknown protein [Arabidopsis thaliana] NCBI Description >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown protein [Arabidopsis thaliana] Seq. No. 212866 Seq. ID LIB3146-005-Q1-K1-B6

Method BLASTN NCBI GI g2224750 BLAST score 35 E value 4.0e-10 Match length 51 % identity 92





```
212867
Seq. No.
Seq. ID
                  LIB3146-005-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3746069
BLAST score
                  180
E value
                  3.0e-13
Match length
                  122
% identity
                  34
                   (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  212868
                  LIB3146-005-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1209703
BLAST score
                  459
E value
                  6.0e-46
Match length
                  121
% identity
                   69
NCBI Description
                  (U40489) maize gl1 homolog [Arabidopsis thaliana]
Seq. No.
                  212869
Seq. ID
                  LIB3146-005-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2129927
BLAST score
                  302
E value
                   6.0e-45
Match length
                  108
% identity
                  83
NCBI Description
                  zeta-carotene desaturase precursor - pepper
                  >gi 1176437 bbs 171885 zeta-carotene desaturase,
                  CapZDS=phytoene desaturase homolog [Capsicum annuum, early
                  ripening fruit, Peptide, 588 aa]
                  212870
Seq. No.
Seq. ID
                  LIB3146-005-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2961358
BLAST score
                   217
E value
                  1.0e-17
                  50
Match length
                  84
% identity
                   (AL022140) serine/threonine protein kinase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  212871
Seq. ID
                  LIB3146-005-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  g167358
BLAST score
                  37
E value
                  2.0e-11
Match length
                  61
                  90
% identity
NCBI Description
                  Cotton 2S albumin storage protein (Mat5-A) gene, complete
```

NCBI Description Arabidopsis thaliana mRNA for ribosomal protein S6

cds



```
212872
Seq. No.
                  LIB3146-005-Q1-K1-C5
Seq. ID
                  BLASTX
Method
                  g3355490
NCBI GI
                  229
BLAST score
                  6.0e-19
E value
Match length
                  104
% identity
                  49
NCBI Description
                  (AC004218) putative dolichyl-phosphate
                  beta-glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                  212873
                  LIB3146-005-Q1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738320
BLAST score
                  281
E value
                  3.0e-30
Match length
                  102
                  72
% identity
                  (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  212874
                  LIB3146-005-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3393062
BLAST score
                  358
E value
                  5.0e - 34
Match length
                  136
% identity
                   51
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                  212875
Seq. No.
                  LIB3146-005-Q1-K1-C9
Seq. ID
Method
                  BLASTN
                  q1019945
NCBI GI
BLAST score
                   281
                   1.0e-157
E value
                   336
Match length
                   96
% identity
                  Gossypium hirsutum ascorbate peroxidase mRNA, complete cds
NCBI Description
                   212876
Seq. No.
Seq. ID
                  LIB3146-005-Q1-K1-D1
Method
                  BLASTX
                   g2880043
NCBI GI
BLAST score
                   306
E value
                   5.0e-28
                   115
Match length
```

50 % identity

(AC002340) putative 3-hydroxyisobutyryl-coenzyme A NCBI Description

hydrolase [Arabidopsis thaliana]

212877 Seq. No.

Seq. ID LIB3146-005-Q1-K1-D12

Method BLASTX

```
g4490317
NCBI GI
                  191
BLAST score
                  2.0e-14
E value
                  100
Match length
                  39
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                  212878
Seq. No.
                  LIB3146-005-Q1-K1-D4
Seq. ID
Method
                  BLASTX
                  q3702641
NCBI GI
BLAST score
                  187
                   5.0e-14
E value
Match length
                  79
                   42
% identity
                   (AL031825) similar to human 75k autoantigen
NCBI Description
                   [Schizosaccharomyces pombe]
                                                                       -20
Seq. No.
                   212879
                   LIB3146-005-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3043428
BLAST score
                   498
                   2.0e-50
E value
                   105
Match length
                   95
% identity
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.
                   212880
                   LIB3146-005-Q1-K1-D7
Seq. ID
Method
                   BLASTX
                   g4455207
NCBI GI
BLAST score
                   440
                   9.0e-44
E value
Match length
                   95
% identity
                   91
                  (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212881
                   LIB3146-005-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g123656
NCBI GI
BLAST score
                   415
                   6.0e-41
E value
                   107
Match length
                   79
% identity
                   CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED
NCBI Description
                   PROTEIN >gi 285407_pir__A42582 heat shock protein SCE70 -
```

spinach >gi 21338 emb CAA43711 (X61491) 70 kDa heat shock

protein [Spinacia oleracea]

212882 Seq. No.

Seq. ID LIB3146-005-Q1-K1-E5

BLASTX Method g2244926 NCBI GI BLAST score 154 4.0e-10 E value



```
Match length 84
% identity 38
NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]
Seq. No. 212883
```

 Seq. No.
 212883

 Seq. ID
 LIB3146-005-Q1-K1-E6

 Method
 BLASTX

 NCBI GI
 g2062167

 BLAST score
 294

 F value
 1 0e-26

BLAST score 294
E value 1.0e-26
Match length 120
% identity 45

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 212884

Seq. ID LIB3146-005-Q1-K1-E7

Method BLASTX
NCBI GI g2584806
BLAST score 433
E value 7.0e-43
Match length 96
% identity 81

NCBI Description (Y15253) phospholipase C [Pisum sativum]

Seq. No. 212885

Seq. ID LIB3146-005-Q1-K1-F1

Method BLASTX
NCBI GI g3915169
BLAST score 153
E value 3.0e-10
Match length 76
% identity 38

NCBI Description PROBABLE TRNA (GUANOSINE-2'-O-)-METHYLTRANSFERASE (TRNA

[GM18] METHYLTRANSFERASE) >gi 2983982 (AE000749) rRNA

methylase SpoU [Aquifex aeolicus]

Seq. No. 212886

Seq. ID LIB3146-005-Q1-K1-F11

Method BLASTX
NCBI GI g3962377
BLAST score 522
E value 2.0e-53
Match length 121
% identity 85

NCBI Description (AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No. 212887

Seq. ID LIB3146-005-Q1-K1-F12

Method BLASTX
NCBI GI g543905
BLAST score 306
E value 5.0e-28
Match length 85
% identity 66

NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi\_347459 (L22162)

brassinosteroid-regulated protein [Glycine max]

NCBI Description



```
212888
Seq. No.
                  LIB3146-005-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1103318
BLAST score
                   447
                   2.0e-44
E value
Match length
                   137
% identity
                   60
                   (X78818) casein kinase I [Arabidopsis thaliana]
NCBI Description
                   >qi 2244791 emb CAB10213.1 (Z97336) casein kinase I
                   [Arabidopsis thaliana]
Seq. No.
                   212889
                   LIB3146-005-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3202042
BLAST score
                   243
                   1.0e-20
E value
Match length
                   82
                   60
% identity
                   (AF069324) 26S proteasome regulatory subunit S5A
NCBI Description
                   [Mesembryanthemum crystallinum]
                   212890
Seq. No.
                   LIB3146-005-Q1-K1-G1
Seq. ID.
Method
                   BLASTX
NCBI GI
                   q2462748
BLAST score
                   156
E value
                   1.0e-10
Match length
                   31
                   94
% identity
NCBI Description
                   (AC002292) putative Clathrin Coat Assembly protein
                   [Arabidopsis thaliana]
                   212891
Seq. No.
                   LIB3146-005-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q511497
                   675
BLAST score
                   3.0e-71
E value
                   136
Match length
                   88
% identity
                   (L20978) oleoyl-acyl carrier protein thioesterase
NCBI Description
                   [Coriandrum sativum]
                   212892
Seq. No.
Seq. ID
                   LIB3146-005-Q1-K1-G4
                   BLASTX
Method
                   g3128168
NCBI GI
BLAST score
                   456
                   1.0e-45
E value
Match length
                   118
                   65
% identity
                   (AC004521) putative carboxyl-terminal peptidase
```

[Arabidopsis thaliana]

Seq. ID

Method

```
Seq. No.
Seq. ID
                  LIB3146-005-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  a3360289
                  573
BLAST score
                  3.0e-59
E value
Match length
                  142
                  77
% identity
                  (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  1 [Zea mays]
Seq. No.
                  212894
Seq. ID
                  LIB3146-005-Q1-K1-G7
                  BLASTN
Method
                  q3821780
NCBI GI
                  36
BLAST score
E value
                  1.0e-10
Match length
                  48
% identity
                  67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  212895
Seq. No.
                  LIB3146-005-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g3757517
NCBI GI
BLAST score
                  357
                  6.0e-34
E value
                  140
Match length
% identity
                  (AC005167) putative salt-inducible protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  212896
Seq. ID
                  LIB3146-005-Q1-K1-H11
                  BLASTX
Method
NCBI GI
                  q3334346
BLAST score
                   212
                   6.0e-17
E value
                   43
Match length
% identity
                   98
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
NCBI Description
                   >gi 2852445 dbj_BAA24697_ (AB003378) SUI1 homolog [Salix
                  bakko]
Seq. No.
                   212897
Seq. ID
                   LIB3146-005-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   g3128192
BLAST score
                   490
E value
                   1.0e-49
                   109
Match length
% identity
                   80
                  (AC004521) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   212898
```

29591

LIB3146-005-Q1-K1-H5

BLASTX

```
q4097915
NCBI GI
BLAST score
                  170
                  4.0e-12
E value
Match length
                  127
                  33
% identity
NCBI Description (U72147) unknown [Anabaena sp. CA]
                  212899
Seq. No.
                  LIB3146-005-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915083
BLAST score
                  629
E value
                  6.0e-66
                  122
Match length
                  98
% identity
                  TUBULIN BETA CHAIN >qi 1403143 emb CAA67056 (X98406)
NCBI Description
                  beta-tubulin [Cicer arietinum]
Seq. No.
                  212900
                  LIB3146-006-Q1-K1-A5
Seq. ID
                  BLASTX
Method
                  q1314712
NCBI GI
BLAST score
                   557
E value
                   2.0e-57
Match length
                  130
% identity
                   83
                   (U54615) calcium-dependent protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   212901
                   LIB3146-006-Q1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4508073
BLAST score
                   322
E value
                   5.0e-30
Match length
                   103
% identity
                   62
                  (AC005882) 43220 [Arabidopsis thaliana]
NCBI Description
                   212902
Seq. No.
                   LIB3146-006-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   g3122671
NCBI GI
BLAST score
                   578
                   6.0e-60
E value
Match length
                   123
% identity
                   83
                   HYPOTHETICAL RAE1-LIKE PROTEIN >gi 2129676_pir__S71241
NCBI Description
                   probable export protein - Arabidopsis thaliana >gi_1297188
                   (U53501) Theoretical protein with similarity to Swiss-Prot
                   Accession Number P41838 poly A+ RNA export protein
                   [Arabidopsis thaliana]
```

Seq. No. 212903

Seq. ID LIB3146-006-Q1-K1-A9

Method BLASTX NCBI GI g1931655



```
BLAST score
                   7.0e-49
E value
                   122
Match length
                   75
% identity
                   (U95973) receptor-kinase isolog [Arabidopsis thaliana]
NCBI Description
                   212904
Seq. No.
Seq. ID
                   LIB3146-006-Q1-K1-B11
                   BLASTX
Method
NCBI GI
                   q1170714
BLAST score
                   670
                   1.0e-70
E value
                   128
Match length
                   94
% identity
                   SHAGGY RELATED PROTEIN KINASE ASK-GAMMA
NCBI Description
                   >qi 541850 pir S41597 protein kinase ASK-gamma (EC
                   2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_
                   (X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
                   [Arabidopsis thaliana] >gi 2059329 emb CAA73247 (Y12710)
                   shaggy-like kinase gamma [Arabidopsis thaliana]
Seq. No.
                   212905
Seq. ID
                   LIB3146-006-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   q3193316
BLAST score
                   555
E value
                   3.0e-57
Match length
                   129
% identity
                   82
NCBI Description
                   (AF069299) contains similarity to nucleotide sugar
                   epimerases [Arabidopsis thaliana]
Seq. No.
                   212906
                   LIB3146-006-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                   g462195
NCBI GI
BLAST score
                   323
                   6.0e-30
E value
                   73
Match length
                   88
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi 3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
Seq. No.
                   212907
```

Seq. ID LIB3146-006-Q1-K1-B7

Method BLASTX NCBI GI q4103963 292 BLAST score 2.0e-26 E value 57 Match length 100 % identity

(AF030035) calmodulin [Phaseolus vulgaris] NCBI Description

Seq. No. 212908

NCBI Description

212913

Seq. No.



```
LIB3146-006-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g3928097
NCBI GI
                  166
BLAST score
                  1.0e-11
E value
                  102
Match length
                   41
% identity
                  (AC005770) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  212909
Seq. No.
                  LIB3146-006-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                   g1362086
NCBI GI
BLAST score
                   651
                   2.0e-68
E value
                   143
Match length
                   87
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 2129919 pir__S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
                   212910
Seq. No.
                   LIB3146-006-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   g2822483
NCBI GI
                   554
BLAST score
                   4.0e-57
E value
                   135
Match length
                   81
% identity
                  (AF039709) 14-3-3 protein homolog [Maackia amurensis]
NCBI Description
                   212911
Seq. No.
                   LIB3146-006-Q1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4138583
                   360
BLAST score
                   2.0e-34
E value
Match length
                   97
                   74
% identity
                  (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
NCBI Description
                   212912
Seq. No.
                   LIB3146-006-Q1-K1-C9
Seq. ID
Method
                   BLASTX
                   q1946358
NCBI GI
BLAST score
                   522
E value
                   3.0e-53
                   114
Match length
                   76
 % identity
                   (U93215) unknown protein [Arabidopsis thaliana]
```

```
LIB3146-006-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                  g1345785
NCBI GI
BLAST score
                  701
                  3.0e-74
E value
                  141
Match length
% identity
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                  >qi 567935 dbj BAA05640 (D26593) chalcone synthase
                  [Camellia sinensis]
                  212914
Seq. No.
                  LIB3146-006-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3688600
BLAST score
                  376
E value
                  4.0e-36
Match length
                  95
% identity
                  (AB009030) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
Seq. No.
                  212915
                  LIB3146-006-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g3287695
NCBI GI
BLAST score
                   492
E value
                   1.0e-49
Match length
                   150
% identity
                   (AC003979) Similar to hypothetical protein C34B7.2
NCBI Description
                   gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
                   212916
Seq. No.
                  LIB3146-006-Q1-K1-D3
Seq. ID
Method
                  BLASTX
                   g4432867
NCBI GI
BLAST score
                   176
                   1.0e-12
E value
                   98
Match length
                   35
% identity
                   (AC006300) putative dnaJ-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   212917
Seq. No.
                   LIB3146-006-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1161167
BLAST score
                   303
E value
                   1.0e-27
Match length
                   96
% identity
                   54
```

212918 Seq. No.

Seq. ID LIB3146-006-Q1-K1-D5

Method BLASTX

NCBI Description (L42466) ethylene-forming enzyme [Picea glauca]



```
g2780194
NCBI GI
                   461
BLAST score
                   4.0e-46
E value
                  94
Match length
                   56
% identity
                  (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
                   212919
Seq. No.
                  LIB3146-006-Q1-K1-D7
Seq. ID
Method
                   BLASTX
                   q2618721
NCBI GI
BLAST score
                   496
                   3.0e-50
E value
                   126
Match length
                   75
% identity
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
                   212920
Seq. No.
                   LIB3146-006-Q1-K1-D8
Seq. ID
                   BLASTX
Method
                   q3892059
NCBI GI
BLAST score
                   197
                   4.0e-15
E value
                   146
Match length
                   34
% identity
                   (AC002330) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   212921
Seq. No.
                   LIB3146-006-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   g1408471
NCBI GI
BLAST score
                   332
                   3.0e-31
E value
Match length
                   71
                   83
% identity
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   212922
Seq. No.
                   LIB3146-006-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   g3914442
NCBI GI
                   441
BLAST score
                   9.0e-44
E value
Match length
                   121
% identity
                   71
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
                   212923
Seq. No.
Seq. ID
                   LIB3146-006-Q1-K1-E2
                   {\tt BLASTX}
Method
```

29596

g3850581

436

NCBI GI BLAST score



```
2.0e-43
E value
Match length
                  119
                  68
% identity
                  (AC005278) EST gb_N96383 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  212924
                  LIB3146-006-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g2935450
NCBI GI
BLAST score
                  290
E value
                  4.0e-26
Match length
                  58
% identity
                  100
NCBI Description (AF048824) histone H2B [Malus domestica]
                  212925
Seq. No.
                  LIB3146-006-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g1363492
NCBI GI
BLAST score
                  471
                                                30 -
                  2.0e-47
E value
                  127
Match length
                  69
% identity
                  outer envelope membrane protein OEP75 precursor - garden
NCBI Description
                  pea >gi 576507 (L36858) outer membrane protein [Pisum
                  sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic
                  outer envelope membrane protein (OEP75) [Pisum sativum]
                  212926
Seq. No.
                  LIB3146-006-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                  q1125691
NCBI GI
BLAST score
                   388
                  1.0e-37
E value
Match length
                   112
                   66
% identity
                  (X94301) DnaJ protein [Solanum tuberosum]
NCBI Description
                   212927
Seq. No.
                  LIB3146-006-Q1-K1-E7
Seq. ID
                   BLASTX
Method
                   q4490342
NCBI GI
                   424
BLAST score
E value
                   8.0e-42
                   122
Match length
% identity
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
                   212928
Seq. No.
Seq. ID
                   LIB3146-006-Q1-K1-F10
Method
                   BLASTN
```

Method BLASTN
NCBI GI g2558961
BLAST score 54
E value 1.0e-21
Match length 105
% identity 92



```
NCBI Description Gossypium hirsutum histone H2B1 mRNA, complete cds
                  212929
Seq. No.
                  LIB3146-006-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                  q349379
NCBI GI
BLAST score
                  257
                  2.0e-22
E value
                  106
Match length
                   62
% identity
NCBI Description
                  (L22847) HAHB-1 [Helianthus annuus]
Seq. No.
                  212930
                  LIB3146-006-Q1-K1-F2
Seq. ID
                  BLASTN
Method
                  a3738177
NCBI GI
BLAST score
                   45
                   2.0e-16
E value
Match length
                   53
                  19
% identity
NCBI Description S.pombe chromosome II cosmid c337
                   212931
Seq. No.
Seq. ID
                  LIB3146-006-Q1-K1-F3
Method
                  BLASTX
                   g1084321
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   118
Match length
                   64
% identity
                  protochlorophyllide reductase (EC 1.3.1.33) - cucumber
NCBI Description
                   >gi 2244614 dbj BAA21089 (D50085)
                   NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]
                   212932
Seq. No.
Seq. ID
                   LIB3146-006-Q1-K1-F7
Method
                   BLASTX
                   q4106538
NCBI GI
BLAST score
                   390
E value
                   7.0e-38
                   119
Match length
% identity
                   66
                   (AF104220) gamma-tocopherol methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   212933
Seq. No.
                   LIB3146-006-Q1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539394
BLAST score
                   241
```

Method BLASTX
NCBI GI g4539394
BLAST score 241
E value 2.0e-20
Match length 79
% identity 56

NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 212934

Seq. ID LIB3146-006-Q1-K1-G3

% identity

NCBI Description

66



```
BLASTX
Method
NCBI GI
                  q3912927
BLAST score
                  155
                  2.0e-10
E value
                  115
Match length
% identity
                  11
                  (AF001308) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  212935
Seq. No.
                  LIB3146-006-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1402888
BLAST score
                  156
                  2.0e-10
E value
                  66
Match length
% identity
                  45
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212936
                  LIB3146-006-Q1-K1-G6
Seq. ID
Method
                  BLASTX
                  q3075394
NCBI GI
BLAST score
                  526
E value
                  1.0e-53
Match length
                  146
% identity
                  73
                  (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
Seq. No.
                  212937
                  LIB3146-006-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1351983
                   312
BLAST score
E value
                  1.0e-28
Match length
                  85
                  74
% identity
                  ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) 1
NCBI Description
                   (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 1)
                   >gi 2147131 pir S57931 asparagine synthase
                   (glutamine-hydrolysing) (EC 6.3.5.4) - Lotus japonicus
                   >gi 2147133 pir__S69182 asparagine synthase
                   (glutamine-hydrolysing) (EC 6.3.5.4) 1 - Lotus japonicus
                   >gi 897771 emb CAA61589 (X89409) asparagine synthase
                   (glutamine-hydrolysing) [Lotus japonicus]
                   212938
Seq. No.
Seq. ID
                   LIB3146-006-Q1-K1-H11
Method
                   BLASTX
NCBI GI
                   g2191136
BLAST score
                   372
E value
                   6.0e-36
Match length
                   103
```

29599

(AF007269) Similar to UTP-Glucose Glucosyltransferase;

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

```
      Seq. No.
      212939

      Seq. ID
      LIB3146-006-Q1-K1-H3

      Method
      BLASTX

      NCBI GI
      g3901014

      BLAST score
      235
```

E value 1.0e-19
Match length 55
% identity 76

NCBI Description (AJ130886) metallothionein-like protein class II [Fagus

sylvatica]

Seq. No. 212940

Seq. ID LIB3146-006-Q1-K1-H7
Method BLASTX
NCBI GI q2316016

NCBI GI g231601 BLAST score 502 E value 5.0e-51 Match length 127 % identity 74

NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 212941

Seq. ID LIB3146-006-Q1-K1-H8

Method BLASTX
NCBI GI g3335169
BLAST score 565
E value 3.0e-58
Match length 148
% identity 67

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi\_4455197\_emb\_CAB36520\_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 212942

Seq. ID LIB3146-006-Q1-K1-H9

Method BLASTX
NCBI GI g120669
BLAST score 528
E value 5.0e-54
Match length 107
% identity 93

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 212943

Seq. ID LIB3146-007-Q1-K1-A1

Method BLASTX
NCBI GI g1706958
BLAST score 200
E value 5.0e-16
Match length 41

```
% identity
                   (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   212944
Seq. No.
                   LIB3146-007-Q1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829275
                   400
BLAST score
                                               . 32
                   5.0e-39
E value
                   90
Match length
% identity
                   (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
NCBI Description
                   thaliana] >gi_3513740 (AF080118) contains similarity to
                   nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
                   301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
                    (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                    [Arabidopsis thaliana]
Seq. No.
                   212945
                   LIB3146-007-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464854
BLAST score
                    231
E value
                    6.0e-21
Match length
                    55
% identity
                    92
                   TUBULIN BETA CHAIN >gi_323075_pir__S30514 tubulin beta chain - Naegleria gruberi >gi_9737_emb_CAA78362_ (Z13961)
NCBI Description
                    beta-tubulin [Naegleria gruberi]
Seq. No.
                    212946
                    LIB3146-007-Q1-K1-A4
Seq. ID
                    BLASTX
Method
NCBI GI
                    q3319341
                    211
BLAST score
E value
                    5.0e-17
Match length
                    90
                    48
% identity
```

Seq. No. 212947

NCBI Description

Seq. ID LIB3146-007-Q1-K1-A5

Method BLASTX
NCBI GI g3687251
BLAST score 263
E value 4.0e-23
Match length 59
% identity 81

NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 212948

Seq. ID LIB3146-007-Q1-K1-A9

Method BLASTX
NCBI GI g2829275
BLAST score 444
E value 4.0e-44

(AF077407) similar to Medicago sativa nucleic acid binding

protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]



```
Match length
                  89
% identity
                  (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
NCBI Description
                  thaliana] >gi_3513740 (AF080118) contains similarity to
                  nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
                  301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
                   (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                  [Arabidopsis thaliana]
Seq. No.
                  212949
                  LIB3146-007-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3319882
                  444
BLAST score
                  2.0e-44
E value
Match length
                  90
                  94
% identity
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                  arietinum]
                  212950
Seq. No.
                  LIB3146-007-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1293688
                  303
BLAST score
                  7.0e-28
E value
                  90
Match length
                   64
% identity
                   (U53827) STA1-2 [Silene latifolia ssp. alba] >gi_1293692
NCBI Description
                   (U53829) STA1-18 [Silene latifolia ssp. alba]
                   212951
Seq. No.
Seq. ID
                  LIB3146-007-Q1-K1-B6
Method
                  BLASTX
                   g2317906
NCBI GI
                   204
BLAST score
                   3.0e-16
E value
                   40
Match length
% identity
                   97
                  (U89959) ARA-5 [Arabidopsis thaliana]
NCBI Description
                   212952
Seq. No.
                   LIB3146-007-Q1-K1-B7
Seq. ID
Method
                   BLASTX
                   g2642158
NCBI GI
BLAST score
                   313
                   5.0e-29
E value
                   87
Match length
                   71
% identity
```

Seq. No. 212953

NCBI Description

Seq. ID LIB3146-007-Q1-K1-C2

Method BLASTX
NCBI GI g3386604
BLAST score 240
E value 2.0e-20

(AC003000) hypothetical protein [Arabidopsis thaliana]

```
Match length
% identity
                  53
                  (AC004665) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  212954
Seq. No.
Seq. ID
                  LIB3146-007-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q421929
BLAST score
                  163
E value
                  2.0e-11
Match length
                  85
% identity
                  ubiquitin - tomato >gi 312160_emb CAA51679_ (X73156)
NCBI Description
                  ubiquitin [Lycopersicon esculentum]
                  212955
Seq. No.
                  LIB3146-007-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                  q2245127
NCBI GI
                  205
BLAST score
```

NCBI GI g2245127
BLAST score 205
E value 2.0e-16
Match length 78
% identity 54
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

NCBI Description (25/544) hypothetical protein (Mastaopsis charitana)

 Seq. No.
 212956

 Seq. ID
 LIB3146-007-Q1-K1-D1

 Method
 BLASTX

 NCBI GI
 g2388571

 BLAST score
 366

 E value
 3.0e-35

Match length 98 % identity 72

NCBI Description (AC000098) Strong similarity to Arabidopsis peroxidase
ATPEROX7A (gb\_X98321). [Arabidopsis thaliana] >gi\_2738254

(U97684) peroxidase precursor [Arabidopsis thaliana]

Seq. No. 212957

Seq. ID LIB3146-007-Q1-K1-D11

Method BLASTX
NCBI GI g3850585
BLAST score 306
E value 6.0e-28
Match length 125
% identity 53

NCBI Description (AC005278) ESTs gb\_H36966, gb\_R65511, gb\_T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]

Seq. No. 212958

Seq. ID LIB3146-007-Q1-K1-D2

Method BLASTX
NCBI GI g2245127
BLAST score 217
E value 9.0e-18
Match length 78
% identity 55

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]



```
212959
Seq. No.
Seq. ID
                  LIB3146-007-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3219769
                  149
BLAST score
                  5.0e-10
E value
                  77
Match length
% identity
                  38
NCBI Description ACTIN 42 >gi 1498380 (U60488) actin [Solanum tuberosum]
                  212960
Seq. No.
                  LIB3146-007-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g1053047
NCBI GI
BLAST score
                   447
                  9.0e-45
E value
                  91
Match length
                  98
% identity
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
                  212961
Seq. No.
Seq. ID
                  LIB3146-007-Q1-K1-D6
                  BLASTN
Method
NCBI GI
                  g2104680
BLAST score
                  36
                  7.0e-11
E value
                   67
Match length
                   96
% identity
NCBI Description V.faba mRNA for putative transciption factor (1556bp)
                  212962
Seq. No.
Seq. ID
                  LIB3146-007-Q1-K1-D7
                  BLASTX
Method
                   g2760330
NCBI GI
BLAST score
                   303
                   7.0e-28
E value
Match length
                   84
                   69
% identity
NCBI Description
                  (AC002130) F1N21.15 [Arabidopsis thaliana]
                   212963
Seq. No.
                  LIB3146-007-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1710587
                   227
BLAST score
                   6.0e-19
E value
                   86
Match length
% identity
NCBI Description
                   60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic
                   ribosomal protein PO [Glycine max]
```

Seq. No. 212964

Seq. ID LIB3146-007-Q1-K1-E11

Method BLASTX



NCBI GI g1351408 BLAST score 259 E value 1.0e-27 Match length 83 % identity 76

NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)

>gi\_1076563\_pir\_\_S51117 cystein proteinase - sweet orange >gi\_633185\_emb\_CAA87720\_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi\_1588548\_prf\_\_2208463A

vascular processing protease [Citrus sinensis]

Seq. No. 212965

Seq. ID LIB3146-007-Q1-K1-E2

Method BLASTX
NCBI GI g1332579
BLAST score 443
E value 1.0e-45
Match length 101
% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 212966

Seq. ID LIB3146-007-Q1-K1-E4

Method BLASTX
NCBI GI g2894600
BLAST score 345
E value 9.0e-33
Match length 89
% identity 70

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 212967

Seq. ID LIB3146-007-Q1-K1-E9

Method BLASTX
NCBI GI g625547
BLAST score 475
E value 6.0e-48
Match length 107
% identity 86

NCBI Description chlorophyll a/b-binding protein type I - common tobacco

>gi 493723 emb CAA45523 (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

Seq. No. 212968

Seq. ID LIB3146-007-Q1-K1-G1

Method BLASTX
NCBI GI g3335355
BLAST score 429
E value 1.0e-42
Match length 88
% identity 25

NCBI Description (AC004512) Match to polyubiquitin DNA gb\_L05401 from A.

thaliana. Contains insertion of mitochondrial NADH

dehydrogenase gb\_X82618 and gb\_X98301. May be a pseudogene with an expressed insert. EST gb\_AA586248 comes from this

region. [Arabi

NCBI Description



```
212969
Seq. No.
                  LIB3146-007-Q1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618701
BLAST score
                  213
                  3.0e-17
E value
Match length
                  88
                  49
% identity
                  (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212970
Seq. ID
                  LIB3146-007-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3334115
BLAST score
                   410
E value
                  2.0e-40
Match length
                   90
                  86
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                   212971
Seq. No.
                  LIB3146-007-Q1-K1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4455318
BLAST score
                   144
E value
                   7.0e-20
Match length
                   72
                   74
% identity
                   (AL035528) glycine hydroxymethyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   212972
Seq. No.
                   LIB3146-007-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1477428
BLAST score
                   473
                   8.0e-48
E value
Match length
                   90
% identity
                   97
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
NCBI Description
                   212973
Seq. No.
Seq. ID
                   LIB3146-007-Q1-K1-H1
Method
                   BLASTX
                   g2129929
NCBI GI
BLAST score
                   498
                   1.0e-50
E value
                   101
Match length
                   92
% identity
```

[Solanum lycopersicum]

DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -

tomato >gi 1049068 (U28403) RNA polymerase II subunit 2

NCBI GI

BLAST score



```
212974
Seq. No.
                  LIB3146-007-Q1-K1-H4
Seq. ID
                  BLASTX
Method
                  g4204265
NCBI GI
                   243
BLAST score
                   8.0e-21
E value
                   96
Match length
                   53
% identity
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
                   212975
Seq. No.
                   LIB3146-007-Q1-K1-H5
Seq. ID
                   BLASTX
Method
                   g4099131
NCBI GI
BLAST score
                   203
                   4.0e-16
E value
                   75
Match length
                   51
% identity
                  (U83902) mitotic checkpoint component Mad2 [Mus musculus]
NCBI Description
                   212976
Seq. No.
                   LIB3146-008-Q1-K1-A1
Seq. ID
                   BLASTN
Method
                   g3702735
NCBI GI
                   51
BLAST score
                   9.0e-20
E value
                   119
Match length
% identity
                   86
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQL5, complete sequence [Arabidopsis thaliana]
                   212977
Seq. No.
                   LIB3146-008-Q1-K1-A3
Seq. ID
                   BLASTX
Method
                   g4204912
NCBI GI
                   486
BLAST score
                   3.0e-49
E value
                   109
Match length
                   83
% identity
                   (U58918) MEK kinase [Arabidopsis thaliana]
NCBI Description
                   212978
Seq. No.
                   LIB3146-008-Q1-K1-A4
Seq. ID
                   BLASTX
Method
                   q2062167
NCBI GI
                   183
BLAST score
                   1.0e-13
E value
                   83
Match length
                   47
% identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   212979
Seq. No.
                   LIB3146-008-Q1-K1-A7
Seq. ID
                   BLASTX
Method
```

29607

g3264769 297



E value 6.0e-27 Match length 74 % identity 73

NCBI Description (AF071894) late embryogenesis-like protein [Prunus

armeniaca]

Seq. No. 212980

Seq. ID LIB3146-008-Q1-K1-A8

Method BLASTX
NCBI GI g3901014
BLAST score 223
E value 3.0e-18
Match length 55
% identity 75

NCBI Description (AJ130886) metallothionein-like protein class II [Fagus

sylvatica]

Seq. No. 212981

Seq. ID LIB3146-008-Q1-K1-A9

Method BLASTX
NCBI GI g3126969
BLAST score 165
E value 2.0e-11
Match length 82
% identity 46

NCBI Description (AF061808) chalcone isomerase [Elaeagnus umbellata]

Seq. No. 212982

Seq. ID LIB3146-008-Q1-K1-B1

Method BLASTX
NCBI GI g2583123
BLAST score 514
E value 2.0e-52
Match length 128
% identity 77

NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis

thaliana]

Seq. No. 212983

Seq. ID LIB3146-008-Q1-K1-B2

Method BLASTX
NCBI GI g1771160
BLAST score 257
E value 8.0e-23
Match length 61
% identity 80

NCBI Description (X98929) SBT1 [Lycopersicon esculentum]

>gi 3687305 emb CAA06999 (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 212984

Seq. ID LIB3146-008-Q1-K1-B4

Method BLASTX
NCBI GI g124224
BLAST score 585
E value 1.0e-60
Match length 115



% identity 95

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi\_100345\_pir\_\_S21060 translation initiation factor eIF-5A

- common tobacco >gi\_19887\_emb\_CAA45105\_ (X63543)

eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 212985

Seq. ID LIB3146-008-Q1-K1-B5

Method BLASTX
NCBI GI g124224
BLAST score 316
E value 1.0e-29
Match length 85
% identity 82

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi\_100345\_pir\_\_S21060 translation initiation factor eIF-5A

- common tobacco >gi\_19887\_emb\_CAA45105\_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 212986

Seq. ID LIB3146-008-Q1-K1-B7

Method BLASTX
NCBI GI g3264769
BLAST score 587
E value 6.0e-61
Match length 134
% identity 80

NCBI Description (AF071894) late embryogenesis-like protein [Prunus

armeniaca]

Seq. No. 212987

Seq. ID LIB3146-008-Q1-K1-C11

Method BLASTN
NCBI GI g18502
BLAST score 38
E value 5.0e-12
Match length 138
% identity 83

NCBI Description G.hirsutum Lea5 gene for late embryogenesis abundant

protein

Seq. No. 212988

Seq. ID LIB3146-008-Q1-K1-C2

Method BLASTN
NCBI GI g437326
BLAST score 282
E value 1.0e-157
Match length 329
% identity 98

NCBI Description Cotton DNA-binding domain mRNA

Seq. No. 212989

Seq. ID LIB3146-008-Q1-K1-C3

Method BLASTX
NCBI GI g4107099
BLAST score 462
E value 3.0e-46



Match length 64 % identity

(AB015141) AHP1 [Arabidopsis thaliana] NCBI Description

>gi 4156245\_dbj\_BAA37112\_ (AB012570) ATHP3 [Arabidopsis

thaliana]

212990 Seq. No.

Seq. ID LIB3146-008-Q1-K1-C4

BLASTX Method q4193382 NCBI GI BLAST score 249 7.0e-22 E value 55 Match length 85 % identity

(AF083336) ribosomal protein S27 [Arabidopsis thaliana] NCBI Description

>gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis

thaliana]

Seq. No.

212991

LIB3146-008-Q1-K1-C7 Seq. ID Method BLASTX

NCBI GI g4102861 BLAST score 564 3.0e-58 E value Match length 115 % identity 90

(AF016893) copper/zinc-superoxide dismutase [Populus NCBI Description

tremuloides]

212992 Seq. No.

Seq. ID LIB3146-008-Q1-K1-C9

BLASTX Method NCBI GI g2245069 BLAST score 430 1.0e-42 E value 114 Match length % identity 67

(Z97342) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 212993

Seq. ID LIB3146-008-Q1-K1-D4

BLASTX Method NCBI GI g2499611 BLAST score 443 3.0e-44E value 93 Match length 91 % identity

MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) NCBI Description

(ATMPK7) >gi\_629548\_pir\_\_S40473 mitogen-activated protein

kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis

thaliana]

Seq. No. 212994

Seq. ID LIB3146-008-Q1-K1-D7

BLASTX Method NCBI GI g3757520



```
BLAST score
                  4.0e-22
E value
Match length
                  132
                  48
% identity
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  212995
                  LIB3146-008-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g2467274
NCBI GI
BLAST score
                  315
E value
                  5.0e-29
Match length
                  108
% identity
                  63
                  (Z99759) rna binding protein [Schizosaccharomyces pombe]
NCBI Description
                  212996
Seq. No.
                  LIB3146-008-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1103712
BLAST score
                  496
E value
                  2.0e-50
                  114
Match length
% identity
                  92
                  (X83729) inorganic pyrophosphatase [Nicotiana tabacum]
NCBI Description
                  212997
Seq. No.
                  LIB3146-008-Q1-K1-E3
Seq. ID
Method
                  BLASTN
                  q3869074
NCBI GI
BLAST score
                  56
                  8.0e-23
E value
                  88
Match length
% identity
                  92
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMI9, complete sequence [Arabidopsis thaliana]
                  212998
Seq. No.
Seq. ID
                  LIB3146-008-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q266944
BLAST score
                  410
                  2.0e-40
E value
Match length
                  89
% identity
                  87
                  60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
NCBI Description
                  >gi 71078 pir R5TOL8 ribosomal protein L8, cytosolic -
                   tomato >gi 19343 emb CAA45863 (X64562) ribosomal protein
                  L2 [Lycopersicon esculentum]
                   212999
Seq. No.
```

Seq. ID LIB3146-008-Q1-K1-F1

Method BLASTX
NCBI GI g1928981
BLAST score 556
E value 2.0e-57
Match length 128

NCBI Description

complete cds

```
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                  213000
Seq. No.
Seq. ID
                  LIB3146-008-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1076274
BLAST score
                  350
                  3.0e-33
E value
Match length
                  104
% identity
                   61
                  cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)
NCBI Description
                  213001
Seq. No.
                  LIB3146-008-Q1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2695925
                   279
BLAST score
E value
                   8.0e-25
                   72
Match length
                   76
% identity
                  (AJ222776) hypothetical protein [Hordeum vulgare]
NCBI Description
                   213002
Seq. No.
Seq. ID
                   LIB3146-008-Q1-K1-F3
                   BLASTX
Method
                   q4545262
NCBI GI
BLAST score
                   239
                   4.0e-20
E value
                   44
Match length
                   100
% identity
                   (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                   hirsutum]
                   213003
Seq. No.
Seq. ID
                   LIB3146-008-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   g3915847
                   393
BLAST score
                   3.0e-38
E value
Match length
                   85
                   87
% identity
                   40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative
NCBI Description
                   40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                   213004
                   LIB3146-008-Q1-K1-F7
Seq. ID
                   BLASTN
Method
NCBI GI
                   q899609
                   38
BLAST score
                   6.0e-12
E value
                   82
Match length
                   87
% identity
                   Zea mays acidic ribosomal protein P2 (RPA-2A1) mRNA,
```



```
Seq. No.
                  213005
                  LIB3146-008-Q1-K1-G1
Seq. ID
Method
                  BLASTX
                  q4455208
NCBI GI
BLAST score
                  410
E value
                  3.0e-40
                  93
Match length
                  80
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  213006
Seq. No.
                  LIB3146-008-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352821
BLAST score
                  172
E value
                  3.0e-12
                  32
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  213007
                  LIB3146-008-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1899175
BLAST score
                  533
E value
                  1.0e-54
Match length
                  125
                  82
% identity
                  (U90262) calcium-dependent calmodulin-independent protein
NCBI Description
                  kinase CDPK [Cucurbita pepo]
Seq. No.
                  213008
Seq. ID
                  LIB3146-008-Q1-K1-H1
Method
                  BLASTX
                  q2129552
NCBI GI
BLAST score
                  583
                  2.0e-60
E value
                  132
Match length
% identity
NCBI Description
                  calcium-dependent protein kinase 19 - Arabidopsis thaliana
                   (fragment)
Seq. No.
                  213009
Seq. ID
                  LIB3146-008-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2829275
BLAST score
                   491
```

1.0e-49 E value 99 Match length 89 % identity

(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis NCBI Description thaliana] >gi 3513740 (AF080118) contains similarity to

nucleoside diphosphate kinases (Pfam: NDK.hmm, score:





301.12) [Arabidopsis thaliana] >gi\_4539375\_emb\_CAB40069.1\_(AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No. 213010

Seq. ID LIB3146-008-Q1-K1-H4

Method BLASTX
NCBI GI g2130017
BLAST score 304
E value 7.0e-28
Match length 69
% identity 78

NCBI Description hypothetical protein - common sunflower

>gi\_1040729\_emb CAA60621 (X87143) cytochrome b5 containing

fusion protein [Helianthus annuus]

Seq. No. 213011

Seq. ID LIB3146-009-Q1-K1-A3

Method BLASTX
NCBI GI 94467159
BLAST score 382
E value 5.0e-37
Match length 104
% identity 65

NCBI Description (AL035540) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213012

Seq. ID LIB3146-009-Q1-K1-A4

Method BLASTX
NCBI GI g1730109
BLAST score 468
E value 7.0e-50
Match length 124
% identity 72

NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN

HYDROXYLASE) >gi\_499022\_emb\_CAA53580\_ (X75966) leucoanthocyanidin dioxygenase [Vitis vinifera]

Seq. No. 213013

Seq. ID LIB3146-009-Q1-K1-A6

Method BLASTX
NCBI GI g3269284
BLAST score 381
E value 9.0e-37
Match length 126
% identity 63

NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No. 213014

Seq. ID LIB3146-009-Q1-K1-B1

Method BLASTX
NCBI GI g1906830
BLAST score 587
E value 7.0e-61
Match length 141
% identity 82

NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]



```
Seq. No.
                  213015
                  LIB3146-009-01-K1-B4
Seq. ID
Method
                  BLASTX
                  q2136140
NCBI GI
BLAST score
                  424
E value
                  9.0e-42
                  128
Match length
% identity
                  61
                  serine C-palmitoyltransferase (EC 2.3.1.50) - human
NCBI Description
                  (fragment) >gi_1001945 (U15555) serine palmitoyltransferase
                  [Homo sapiens]
Seq. No.
                  213016
                  LIB3146-009-Q1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  33
                  5.0e-09
E value
Match length
                  37
                  97
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213017
Seq. ID
                  LIB3146-009-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213018
                  LIB3146-009-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  620
                  9.0e-65
E value
Match length
                  140
% identity
                  83
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  213019
Seq. ID
                  LIB3146-009-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q4193388
```

Method BLASTX
NCBI GI g4193388
BLAST score 402
E value 3.0e-39
Match length 87
% identity 87

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]



```
213020
Seq. No.
Seq. ID
                  LIB3146-009-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                   g3212869
BLAST score
                   634
                   2.0e-66
E value
                   144
Match length
% identity
                   78
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   213021
                  LIB3146-009-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2429280
BLAST score
                   583
E value
                   2.0e-60
Match length
                   126
% identity
NCBI Description
                   (AF014055) asparagine synthetase [Triphysaria versicolor]
                   >gi 2429282 (AF014056) asparagine synthetase [Triphysaria
                   versicolor] >gi_2429284 (AF014057) asparagine synthetase
                   [Triphysaria versicolor]
                   213022
Seq. No.
                   LIB3146-009-Q1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1200205
BLAST score
                   421
E value
                   2.0e-41
Match length
                   89
                   85
% identity
NCBI Description
                  (X95753) DAG [Antirrhinum majus]
Seq. No.
                   213023
                   LIB3146-009-Q1-K1-D5
Seq. ID
Method
                   BLASTX
                   g2815246
NCBI GI
BLAST score
                   225
                   2.0e-18
E value
Match length
                   55
                   73
% identity
                  (X95709) class I type 2 metallothionein [Cicer arietinum]
NCBI Description
Seq. No.
                   213024
Seq. ID
                   LIB3146-009-Q1-K1-E1
Method
                   BLASTX
                   g2190551
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
                   88
Match length
                   50
% identity
```

NCBI Description

(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb\_Z71181). ESTs gb\_H36844,gb\_AA394956 come from

this gene. [Arabidopsis thaliana]

Seq. No.

```
LIB3146-009-Q1-K1-E7
Seq. ID
Method
                  BLASTX
                  q3885334
NCBI GI
                  665
BLAST score
                  4.0e-70
E value
Match length
                  138
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  213026
Seq. No.
                  LIB3146-009-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g3236258
NCBI GI
BLAST score
                  381
                  6.0e-37
E value
                  109
Match length
                  66
% identity
                  (AC004684) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  213027
Seq. No.
                  LIB3146-009-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  g3980254
NCBI GI
BLAST score
                  528
                  5.0e-54
E value
                  139
Match length
                   70
% identity
                   (AJ006053) peroxisomal membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                   213028
Seq. No.
Seq. ID
                   LIB3146-009-Q1-K1-G1
                   BLASTX
Method
NCBI GI
                   q3063691
BLAST score
                   491
                   1.0e-49
E value
                   140
Match length
% identity
                   66
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                   213029
Seq. No.
Seq. ID
                   LIB3146-009-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   g4098129
BLAST score
                   621
                   7.0e-65
E value
Match length
                   140
                   85
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                   213030
Seq. No.
                   LIB3146-009-Q1-K1-H5
Seq. ID
Method
                   BLASTX
```

29617

g1350930

196

NCBI GI BLAST score



E value 3.0e-15 Match length 39 % identity 97

NCBI Description 40S RIBOSOMAL PROTEIN S13

Seq. No. 213031

Seq. ID LIB3146-010-Q1-K1-A12

Method BLASTX
NCBI GI g1698548
BLAST score 401
E value 3.0e-39
Match length 104
% identity 76

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 213032

Seq. ID LIB3146-010-Q1-K1-A4

Method BLASTX
NCBI GI g122070
BLAST score 201
E value 3.0e-16
Match length 40
% identity 97

NCBI Description HISTONE H3 >gi 82483 pir A25564 histone H3 - rice

>gi 169793 (M15664) histone 3 [Oryza sativa] >gi\_940018

(U25664) histone H3 [Oryza sativa]

Seq. No. 213033

Seq. ID LIB3146-010-Q1-K1-A5

Method BLASTX
NCBI GI g456568
BLAST score 586
E value 6.0e-61
Match length 110
% identity 97

NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No. 213034

Seq. ID LIB3146-010-Q1-K1-A6

Method BLASTX
NCBI GI g2497738
BLAST score 200
E value 9.0e-16
Match length 62
% identity 55

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN A PRECURSOR (LTP A)

(WAX-ASSOCIATED PROTEIN 9A) >gi 500841 (L33904) lipid

transfer protein [Brassica oleracea]

Seq., No. 213035

Seq. ID LIB3146-010-Q1-K1-A7

Method BLASTX
NCBI GI g1684913
BLAST score 434
E value 4.0e-43
Match length 105
% identity 78



NCBI Description (U77888) receptor-like protein kinase [Ipomoea nil]

Seq. No. 213036

Seq. ID LIB3146-010-Q1-K1-B12

Method BLASTX
NCBI GI g1777443
BLAST score 171
E value 3.0e-12
Match length 108
% identity 44

NCBI Description (U28422) CCA1 [Arabidopsis thaliana] >gi\_3510263 (AC005310)

DNA-binding protein CCA1 [Arabidopsis thaliana] >gi\_4090569

(U79156) CCA1 [Arabidopsis thaliana]

Seq. No. 213037

Seq. ID LIB3146-010-Q1-K1-B3

Method BLASTX
NCBI GI g2865177
BLAST score 505
E value 2.0e-51
Match length 108
% identity 86

NCBI Description (AB010946) AtRerlB [Arabidopsis thaliana]

Seq. No. 213038

Seq. ID LIB3146-010-Q1-K1-B6

Method BLASTX
NCBI GI g1345882
BLAST score 174
E value 1.0e-12
Match length 37
% identity 84

NCBI Description CYTOCHROME B5

Seq. No. 213039

Seq. ID LIB3146-010-Q1-K1-B8

Method BLASTX
NCBI GI g3128168
BLAST score 400
E value 4.0e-39
Match length 110
% identity 62

NCBI Description (AC004521) putative carboxyl-terminal peptidase

[Arabidopsis thaliana]

Seq. No. 213040

Seq. ID LIB3146-010-Q1-K1-B9

Method BLASTX
NCBI GI g3776574
BLAST score 439
E value 1.0e-43
Match length 113
% identity 71

NCBI Description (AC005388) Similar to T11J7.13 gi 2880051 putative protein

kinase from Arabidopsis thaliana BAC gb\_AC002340.

[Arabidopsis thaliana]

BLAST score

E value

37

5.0e-12



```
213041
Seq. No.
Seq. ID
                  LIB3146-010-Q1-K1-C1
                  BLASTX
Method
                  g2980793
NCBI GI
BLAST score
                   499
                  9.0e-51
E value
                  113
Match length
                  77
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                  213042
Seq. No.
                  LIB3146-010-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  q4105262
NCBI GI
BLAST score
                  336
                   6.0e-34
E value
Match length
                  89
                  87
% identity
NCBI Description (AF044573) actin [Brassica oleracea]
Seq. No.
                   213043
Seq. ID
                  LIB3146-010-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                   q3928099
BLAST score
                   400
E value
                   4.0e-39
Match length
                   113
% identity
                   34
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
                   213044
Seq. No.
Seq. ID
                   LIB3146-010-Q1-K1-C12
Method
                  BLASTX
                   q2344898
NCBI GI
BLAST score
                   480
                   2.0e-48
E value
                   115
Match length
                   76
% identity
                   (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   213045
Seq. No.
Seq. ID
                   LIB3146-010-Q1-K1-C4
Method
                   BLASTX
                   g482230
NCBI GI
                   227
BLAST score
                   4.0e-19
E value
                   83
Match length
                   52
% identity
NCBI Description hypothetical protein K03H1.2 - Caenorhabditis elegans
Seq. No.
                   213046
Seq. ID
                   LIB3146-010-Q1-K1-C5
                   BLASTN
Method
NCBI GI
                   q451543
```



Match length 100 % identity

NCBI Description

Gossypium barbadense Sea Island proline-rich cell wall protein gene complete cds. >gi\_1598725\_gb\_I18370\_I18370

Sequence 25 from patent US

213047 Seq. No.

LIB3146-010-Q1-K1-C7 Seq. ID

BLASTX Method g136057 NCBI GI 402 BLAST score 2.0e-39 E value 109 Match length 73 % identity

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description

>gi\_99499\_pir\_\_A32187 (S)-tetrahydroberberine oxidase -

Coptis japonica >gi 556171 (J04121) triosephosphate

isomerase [Coptis japonica]

213048 Seq. No.

LIB3146-010-Q1-K1-C9 Seq. ID

BLASTX Method g1351271 NCBI GI 257 BLAST score 2.0e-22 E value 53 Match length 96 % identity

TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) NCBI Description

>gi\_1084309\_pir\_\_S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi\_806312 (L36387) triosephosphate isomerase, chloroplast isozyme

[Spinacia oleracea]

213049 Seq. No.

LIB3146-010-Q1-K1-D1 Seq. ID

BLASTX Method g3885339 NCBI GI BLAST score 181 2.0e-13 E value Match length 98 41 % identity

(AC005623) putative bzip protein [Arabidopsis thaliana] NCBI Description

213050 Seq. No.

LIB3146-010-Q1-K1-D10 Seq. ID

Method BLASTX NCBI GI g3880282 BLAST score 166 7.0e-12 E value Match length 54 % identity 56

(Z82059) similar to ABC transporters (2 domains); cDNA EST NCBI Description

EMBL:D73856 comes from this gene; cDNA EST EMBL:D73975 comes from this gene; cDNA EST EMBL: C09722 comes from this gene; cDNA EST yk428c4.5 comes from this gene; cDNA ES...

>gi 3881299 emb CAA21772 (AL032665) similar to ABC transporters (2 domains); cDNA EST EMBL:D73856 comes from

Seq. No.

213056

```
comes from this gene; cDNA
                  213051
Seq. No.
                  LIB3146-010-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  q3319882
NCBI GI
BLAST score
                   444
E value
                  3.0e-44
Match length
                  89
% identity
                  97
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                  arietinum]
                   213052
Seq. No.
Seq. ID
                  LIB3146-010-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                   g1710587
BLAST score
                   254
                   5.0e-22
E value
Match length
                   92
% identity
                   59
                   60S ACIDIC RIBOSOMAL PROTEIN PO >gi_1196897 (L46848) acidic
NCBI Description
                   ribosomal protein PO [Glycine max]
                   213053
Seq. No.
Seq. ID
                   LIB3146-010-Q1-K1-D3
Method
                   BLASTX
                   g537639
NCBI GI
BLAST score
                   145
                   3.0e-09
E value
Match length
                   65
% identity
                   42
                  (U14168) lipid transfer protein [Nicotiana tabacum]
NCBI Description
                   213054
Seq. No.
                   LIB3146-010-Q1-K1-D4
Seq. ID
Method
                   BLASTX
                   g3986110
NCBI GI
                   406
BLAST score
                   8.0e-40
E value
                   99
Match length
                   79
% identity
                  (AB012716) heat shock protein 70 cognate [Salix gilgiana]
NCBI Description
                   213055
Seq. No.
                   LIB3146-010-Q1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3935173
BLAST score
                   380
E value
                   8.0e-37
                   109
Match length
                   64
% identity
                  (AC004557) F17L21.16 [Arabidopsis thaliana]
NCBI Description
```

this gene; cDNA EST EMBL:D73975 comes from this gene; cDNA EST EMBL:C09722 comes from this gene; cDNA EST yk428c4.5



```
LIB3146-010-Q1-K1-D7
Seq. ID
Method
                  BLASTX
                  q3286691
NCBI GI
                  294
BLAST score
                  1.0e-26
E value
Match length
                  84
% identity
                  69
                  (AJ007450) auxilin-like protein [Arabidopsis thaliana]
NCBI Description
                  213057
Seq. No.
                  LIB3146-010-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3695021
BLAST score
                  448
                  9.0e-45
E value
Match length
                  110
% identity
                  77
NCBI Description
                  (AF055849) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  213058
                  LIB3146-010-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244763
BLAST score
                  183
E value
                  1.0e-13
Match length
                  88
% identity
                  47
NCBI Description
                  (Z97335) A6 anther-specific protein [Arabidopsis thaliana]
Seq. No.
                  213059
                  LIB3146-010-Q1-K1-E12
Seq. ID
Method
                  BLASTX
                  g3608179
NCBI GI
BLAST score
                  492
                  6.0e-50
E value
Match length
                  114
% identity
                  82
NCBI Description
                  (AB008188) cyclin D [Pisum sativum]
Seq. No.
                  213060
Seq. ID
                  LIB3146-010-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g119640
BLAST score
                  211
E value
                  5.0e-17
Match length
                  78
% identity
                  55
NCBI Description
                  1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
                  E8) >gi 82109 pir S01642 ripening protein E8 - tomato
                  >gi 19199 emb CAA31789 (X13437) E8 protein [Lycopersicon
                  esculentum]
```

Seq. No. 213061

Seq. ID LIB3146-010-Q1-K1-E7

Method BLASTX NCBI GI g4263722 BLAST score 278



```
.0e-25
E value
                   97
Match length
                   49
% identity
                   (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213062
Seq. ID
                   LIB3146-010-Q1-K1-E8
Method
                   BLASTX
                   q4455169
NCBI GI
BLAST score
                   391
                   4.0e-38
E value
Match length
                   109
% identity
                   (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   213063
Seq. ID
                   LIB3146-010-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g133872
BLAST score
                   490
E value
                   9.0e-50
Match length
                   104
% identity
                   95
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                   >gi 282838 pir S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404 pir_ A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060 emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
Seq. No.
                   213064
Seq. ID
                   LIB3146-010-Q1-K1-F10
Method
                   BLASTX
                   g2894592
NCBI GI
BLAST score
                   468
E value
                   4.0e-47
Match length
                   108
% identity
                   81
                   (AL021889) predicted protein [Arabidopsis thaliana]
NCBI Description
                   213065
Seq. No.
Seq. ID
                   LIB3146-010-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   q485514
BLAST score
                   390
E value
                   6.0e-38
Match length
                   79
% identity
                   91
                   ADR11-2 protein - soybean (fragment)
NCBI Description
                   >gi 296443 emb CAA49341 (X69640) auxin down regulated
```

[Glycine max]

213066 Seq. No.

Seq. ID LIB3146-010-Q1-K1-F6

Method BLASTX

BLAST score

157



```
NCBI GI
                  q2244996
BLAST score
                  416
E value
                  5.0e-41
                  111
Match length
                  24
% identity
                  (Z97341) similarity to a membrane-associated salt-inducible
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  213067
Seq. ID
                  LIB3146-010-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2344901
BLAST score
                  521
E value
                  2.0e-53
Match length
                  108
                  90
% identity
                  (AC002388) serine/threonine protein kinase isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  213068
                  LIB3146-010-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1469930
BLAST score
                  328
E value
                  1.0e-30
Match length
                  100
% identity
                  71
                  (U48777) fiber-specific acyl carrier protein [Gossypium
NCBI Description
                  hirsutum]
                  213069
Seq. No.
                  LIB3146-010-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129942
BLAST score
                  374
E value
                  4.0e-36
Match length
                  88
                  76
% identity
                  cathepsin B-like cysteine proteinase (EC 3.4.22.-) - Aztec
NCBI Description
                  tobacco
                  213070
Seq. No.
Seq. ID
                  LIB3146-010-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2581785
BLAST score
                  360
E value
                  2.0e-34
Match length
                  90
% identity
                  79
NCBI Description
                   (U94999) class 2 non-symbiotic hemoglobin [Arabidopsis
                  thaliana]
                  213071
Seq. No.
Seq. ID
                  LIB3146-010-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g21699
```



```
E value
                    1.0e-10
Match length
 % identity
                    68
NCBI Description
                   (X66013) cathepsin B [Triticum aestivum]
Seq. No.
                    213072
Seq. ID
                    LIB3146-010-Q1-K1-G3
Method
                    BLASTX
NCBI GI
                    q4100060
BLAST score
                    173
E value
                    2.0e-12
Match length
                    72
% identity
                    53
                   (U93161) receptor lectin kinase 3 [Arabidopsis thaliana]
NCBI Description
                    213073
Seq. No.
                    LIB3146-010-Q1-K1-G4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4538948
BLAST score
                    160
                    5.0e-11
E value
                    67
Match length
 % identity
                    46
                   (AL049483) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    213074
                    LIB3146-010-Q1-K1-G8
 Seq. ID
Method
                    BLASTX
NCBI GI
                    q1628471
BLAST score
                    274
                    2.0e-24
E value
Match length
                    83
                    58
 % identity
NCBI Description
                   (Y08780) Men-8 [Silene latifolia]
 Seq. No.
                    213075
 Seq. ID
                    LIB3146-010-Q1-K1-H10
Method
                    BLASTX
NCBI GI
                    q2499931
BLAST score
                    146
                    2.0e-09
 E value
Match length
                    32
 % identity
NCBI Description
                    ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
                    >gi_2129534_pir__S71272 adenine phosphoribosyltransferase
                    (EC 2.4.2.7) - Arabidopsis thaliana
                    >gi_1321681_emb_CAA65609_ (X96866) adenine
phosphoribosyltransferase [Arabidopsis thaliana]
 Seq. No.
                    213076
 Seq. ID
                    LIB3146-010-Q1-K1-H5
```

Method BLASTX
NCBI GI g2464855
BLAST score 465
E value 9.0e-47
Match length 111
% identity 81





```
(Z99707) myb-related protein [Arabidopsis thaliana]
NCBI Description
                  213077
Seq. No.
                  LIB3146-010-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g1769891
NCBI GI
BLAST score
                  228
                  5.0e-19
E value
Match length
                  110
% identity
                   50
                  (X99747) bZIP transcription factor [Arabidopsis thaliana]
NCBI Description
                  >gi 1865679 emb CAB04795 (Z82043) ATB2 [Arabidopsis
                  thaliana]
Seq. No.
                   213078
                  LIB3146-010-Q1-K1-H8
Seq. ID
                  BLASTX
Method
                   q1350956
NCBI GI
BLAST score
                   393
                   2.0e-38
E value
Match length
                   83
                   92
% identity
                  40S RIBOSOMAL PROTEIN S20 (S22)
NCBI Description
                   213079
Seq. No.
                   LIB3146-011-Q1-K1-A11
Seq. ID
                   BLASTX
Method
                   g629561
NCBI GI
BLAST score
                   187
                   3.0e-14
E value
                   94
Match length
                   44
% identity
                   SRG1 protein - Arabidopsis thaliana
NCBI Description
                   >gi 479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                   thaliana]
                   213080
Seq. No.
                   LIB3146-011-Q1-K1-A12
Seq. ID
Method
                   BLASTX
                   g1652856
NCBI GI
BLAST score
                   156
E value
                   2.0e-10
Match length
                   116
                   36
% identity
                  (D90909) hypothetical protein [Synechocystis sp.]
NCBI Description
                   213081
Seq. No.
                   LIB3146-011-Q1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3461845
BLAST score
                   238
E value
                   4.0e-20
Match length
                   90
                   54
% identity
```

Seq. No. 213082

NCBI Description

29627

(AC005315) hypothetical protein [Arabidopsis thaliana]

```
Seq. ID
                  LIB3146-011-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q4512676
BLAST score
                  281
E value
                  3.0e-25
Match length
                  98
% identity
                  55
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213083
Seq. ID
                  LIB3146-011-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3080425
                  229
BLAST score
E value
                  2.0e-19
Match length
                  82
                  67
% identity
NCBI Description
                  (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  213084
                  LIB3146-011-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123264
BLAST score
                  248
                  2.0e-21
E value
Match length
                  61
                  77
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
                  213085
Seq. No.
Seq. ID
                  LIB3146-011-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4206122
BLAST score
                  415
E value
                  9.0e-41
Match length
                  107
                  74
% identity
NCBI Description
                  (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                  crystallinum]
Seq. No.
                  213086
Seq. ID
                  LIB3146-011-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  561
E value
                  6.0e-58
```

Match length 121 % identity

(X98063) polyubiquitin [Pinus sylvestris] NCBI Description

Seq. No. 213087

Seq. ID LIB3146-011-Q1-K1-B8

Method BLASTX NCBI GI g4574139 BLAST score 419 2.0e-41 E value



Match length 94 % identity 89 NCBI Description (AF073697) cysteine synthase [Oryza sativa]

 Seq. No.
 213088

 Seq. ID
 LIB3146-011-Q1-K1-B9

 Method
 BLASTX

 NCBI GI
 g2388891

 BLAST score
 150

BLAST score 150 E value 6.0e-10 Match length 46 % identity 72

NCBI Description (Y14765) calmodulin [Lycopersicon esculentum]

Seq. No. 213089

Seq. ID LIB3146-011-Q1-K1-C1

Method BLASTX
NCBI GI g3776005
BLAST score 152
E value 4.0e-10
Match length 42
% identity 71

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 213090

Seq. ID LIB3146-011-Q1-K1-C12

Method BLASTX
NCBI GI g2827659
BLAST score 200
E value 1.0e-15
Match length 66
% identity 58

NCBI Description (AL021637) putative protein [Arabidopsis thaliana]

Seq. No. 213091

Seq. ID LIB3146-011-Q1-K1-C2

Method BLASTX
NCBI GI g1362086
BLAST score 586
E value 8.0e-61
Match length 128
% identity 87

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_2129919\_pir\_\_\$65957

5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 213092

Seq. ID LIB3146-011-Q1-K1-C4

Method BLASTX
NCBI GI 94490323
BLAST score 240
E value 4.0e-29
Match length 112



```
% identity
                  (AJ131464) nitrate transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213093
Seq. ID
                  LIB3146-011-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q1841464
BLAST score
                  270
E value
                  5.0e-24
Match length
                  56
% identity
                  44
NCBI Description
                 (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
                  213094
Seq. No.
                  LIB3146-011-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  g4091117
NCBI GI
BLAST score
                  376
                  3.0e-36
E value
                  126
Match length
% identity
                  59
                  (AF047428) nucleic acid binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  213095
                  LIB3146-011-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415933
BLAST score
                  324
E value
                  2.0e-30
                  90
Match length
% identity
                  68
NCBI Description
                  (AC006418) putative cellular apoptosis susceptibility
                  protein [Arabidopsis thaliana]
                  >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative
                  cellular apoptosis susceptibility protein [Arabidopsis
                  thaliana]
                  213096
Seq. No.
Seq. ID
                  LIB3146-011-01-K1-D1
Method
                  BLASTX
NCBI GI
                  q729737
BLAST score
                  205
E value
                  3.0e-16
Match length
                  71
% identity
                  61
NCBI Description
                  HMG1/2-LIKE PROTEIN >gi_541981_pir__S39556 HMG protein -
                  fava bean
Seq. No.
                  213097
Seq. ID
                  LIB3146-011-Q1-K1-D10
Method
                  BLASTX
                  q4468999
NCBI GI
```

NCBI Description (Z97342) unnamed protein product [Arabidopsis thaliana]

141 1.0e-08

99 9

BLAST score

% identity

E value Match length

Seq. No.

Seq. ID

Method

213103

BLASTX

LIB3146-011-Q1-K1-E10



```
213098
Seq. No.
                  LIB3146-011-Q1-K1-D11
Seq. ID
                  BLASTX
Method
                  g4454464
NCBI GI
BLAST score
                  228
                  5.0e-19
E value
                  70
Match length
% identity
                  67
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  213099
Seq. No.
                  LIB3146-011-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171577
BLAST score
                  379
                  9.0e-37
E value
                  98
Match length
                  70
% identity
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
                  213100
Seq. No.
                  LIB3146-011-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122673
BLAST score
                  477
                  4.0e-48
E value
Match length
                  117
                  77
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027_emb_CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  213101
Seq. No.
                  LIB3146-011-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g2795805
NCBI GI
                  274
BLAST score
                  2.0e-24
E value
Match length
                  76
% identity
                   67
                   (AC003674) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3355493 (AC004218) putative protein kinase [Arabidopsis
                  thaliana]
                  213102
Seq. No.
                  LIB3146-011-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2982297
BLAST score
                  206
E value
                  2.0e-16
Match length
                  91
% identity
                   52
                  (AF051233) KIAA0107-like protein [Picea mariana]
NCBI Description
```



q417103 NCBI GI BLAST score 198 5.0e-29 E value 80 Match length % identity

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa]  $>gi_488569$  ( $\overline{U}09461$ ) histone H3.2 [Medicago sativa]  $>gi_488575$  (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi 4038469 gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 213104

LIB3146-011-Q1-K1-E2 Seq. ID

Method BLASTX q3355311 NCBI GI BLAST score 278 7.0e-25 E value 60 Match length % identity

(AJ009737) eukaryotic translation initiation factor 6 [Beta NCBI Description

vulgaris]

Seq. No. 213105

LIB3146-011-Q1-K1-E5 Seq. ID

Method BLASTX NCBI GI q1749596 BLAST score 117 4.0e-11 E value Match length 116 37 % identity

NCBI Description (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT

Accession Number P16638 [Schizosaccharomyces pombe]

Seq. No. 213106

Seq. ID LIB3146-011-Q1-K1-E6

Method BLASTX NCBI GI q1707018 BLAST score 151 E value 4.0e-10 75 Match length % identity 48

(U78721) CutA isolog [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  213107
Seq. ID
                  LIB3146-011-Q1-K1-E8
Method
                  BLASTX
                  g3600033
NCBI GI
BLAST score
                  287
                  6.0e-26
E value
                  83
Match length
                  67
% identity
NCBI Description
                  (AF080119) contains similarity to the N terminal domain of
                  the E1 protein (Pfam: E1 N.hmm, score: 12.36) [Arabidopsis
                  thaliana]
                  213108
Seq. No.
Seq. ID
                  LIB3146-011-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g3776566
                  257
BLAST score
E value
                  2.0e-22
                  75
Match length
% identity
                  71
                  (AC005388) Strong similarity to histone H2A gb AJ006768
NCBI Description
                  from Cicer arietinum. [Arabidopsis thaliana]
                  213109
Seq. No.
                  LIB3146-011-Q1-K1-F12
Seq. ID
Method
                  BLASTX
                  g1706377
NCBI GI
BLAST score
                  353
E value
                  7.0e - 34
Match length
                  82
                  79
% identity
                  DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
NCBI Description
                  4-REDUCTASE) >gi_499018_emb_CAA53578 (X75964)
                  dihydroflavonol reductase [Vitis vinifera]
Seq. No.
                  213110
                  LIB3146-011-Q1-K1-F3
Seq. ID
Method
                  BLASTX
                  g1171579
NCBI GI
                  140
BLAST score
E value
                  1.0e-08
Match length
                  95
% identity
                  34
NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]
Seq. No.
                  213111
                  LIB3146-011-Q1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g746510
BLAST score
                  325
                  2.0e-30
```

E value Match length 90 % identity 62

(U23517) similar to ubiquitin conjugating enzyme NCBI Description

[Caenorhabditis elegans]

Seq. No. 213112



```
LIB3146-011-01-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  a1326163
BLAST score
                  285
                  1.0e-25
E value
Match length
                  83
% identity
                  61
                  (U54704) stress related protein PvSRP [Phaseolus vulgaris]
NCBI Description
Seq. No.
                  213113
Seq. ID
                  LIB3146-011-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3935164
BLAST score
                  204
E value
                  1.0e-16
Match length
                  71
% identity
                  54
NCBI Description
                  (AC004557) F17L21.7 [Arabidopsis thaliana]
Seq. No.
                  213114
                  LIB3146-011-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1742951
BLAST score
                  497
E value
                  2.0e-50
Match length
                  112
                  87
% identity
NCBI Description
                  (Y09817) Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.
                  213115
Seq. ID
                  LIB3146-011-Q1-K1-H11
Method
                  BLASTX
                  g585960
NCBI GI
BLAST score
                  159
                  8.0e-11
E value
Match length
                  40
% identity
                  80
                  PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
NCBI Description
                  >gi 433665_emb_CAA81412_ (Z26753) Sec61 beta-subunit
                  homolog [Arabidopsis thaliana]
Seq. No.
                  213116
Seq. ID
                  LIB3146-011-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  534
E value
                  8.0e-55
Match length
                  101
% identity
                  95
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
```

213117

Seq. No. Seq. ID

LIB3146-011-Q1-K1-H4 Method BLASTX

NCBI GI g4210334 BLAST score 254



E value 5.0e-22 Match length 60 % identity 82

NCBI Description (AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit

[Arabidopsis thaliana]

Seq. No. 213118

Seq. ID LIB3146-011-Q1-K1-H5

Method BLASTX
NCBI GI 94056420
BLAST score 309
E value 2.0e-28
Match length 83
% identity 71

NCBI Description (AC005322) ESTs qb T144077 and qb T43352 come from this

gene. [Arabidopsis thaliana]

Seq. No. 213119

Seq. ID LIB3146-011-Q1-K1-H7

Method BLASTX
NCBI GI g1708975
BLAST score 174
E value 1.0e-12
Match length 81
% identity 46

NCBI Description METHIONINE GAMMA-LYASE (L-METHIONINASE)

>gi\_1084040\_pir\_\_JC4174 methionine gamma-lyase (EC
4.4.1.11) - Pseudomonas putida >gi\_902932\_dbj\_BAA13642\_
(D88554) L-methionine gamma-lyase [Pseudomonas putida]
>gi\_2217945\_dbj\_BAA20553\_ (D89015) L-methionine gamma-lyase

[Pseudomonas putida] >gi 1096717 prf 2112270A Met

gamma-lyase [Pseudomonas putida]

Seq. No. 213120

Seq. ID LIB3146-011-Q1-K1-H8

Method BLASTX
NCBI GI g1763277
BLAST score 503
E value 4.0e-51
Match length 121
% identity 73

NCBI Description (U73656) tryptophan decarboxylase [Camptotheca acuminata]

Seq. No. 213121

Seq. ID LIB3146-012-Q1-K1-A1

Method BLASTX
NCBI GI g2497753
BLAST score 140
E value 2.0e-13
Match length 108
% identity 44

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)

>gi 1321915 emb CAA65477 (X96716) lipid transfer protein

[Prunus dulcis]

Seq. No. 213122

Seq. ID LIB3146-012-Q1-K1-A4



```
Method
NCBI GI
                  q2384671
BLAST score
                   445
                   3.0e-44
E value
                  129
Match length
% identity
                   69
NCBI Description
                   (AF012657) putative potassium transporter AtKT2p
                   [Arabidopsis thaliana]
Seq. No.
                   213123
Seq. ID
                  LIB3146-012-Q1-K1-A8
Method
                  BLASTX
                  g2335097
NCBI GI
BLAST score
                   482
E value
                  1.0e-48
Match length
                   128
                   70
% identity
```

NCBI Description (AC002339) putative receptor-like protein kinase

[Arabidopsis thaliana]

 Seq. No.
 213124

 Seq. ID
 LIB3146-012-Q1-K1-A9

 Method
 BLASTX

 NCBI GI
 g4263711

BLAST score 422 E value 8.0e-42 Match length 96 % identity 79

NCBI Description (AC006223) putative CCR4-associated transcription factor

[Arabidopsis thaliana]

Seq. No. 213125

Seq. ID LIB3146-012-Q1-K1-B1

Method BLASTX
NCBI GI 94388829
BLAST score 325
E value 3.0e-30
Match length 133
% identity 49

NCBI Description (AC006528) putative pol polyprotein with a Zn-finger CCHC

type domain (prosite:QDOC50158) and a DDE integrase

signature motif [Arabidopsis thaliana]

Seq. No. 213126

Seq. ID LIB3146-012-Q1-K1-B2

Method BLASTX
NCBI GI g3552003
BLAST score 611
E value 9.0e-64
Match length 137
% identity 86

NCBI Description (AF085083) alcohol dehydrogenase A [Gossypium hirsutum]

>gi\_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140632 (AF090165) alcohol

dehydrogenase A [Gossypium hirsutum] >gi\_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140636



(AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140638 (AF090168) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No. 213127 LIB3146-012-Q1-K1-B7 Seq. ID Method BLASTX NCBI GI q629733 BLAST score 313 9.0e-29 E value 63 Match length 90 % identity sulfate adenylyltransferase (EC 2.7.7.4) met3-2 - potato NCBI Description >gi 2130000 pir S67498 sulfate adenylyltransferase (EC 2.7.7.4) (clone StMet3-2) - potato >gi\_479090\_emb\_CAA55655\_ (X79053) sulfate adenylyltransferase [Solanum tuberosum] Seq. No. 213128 LIB3146-012-Q1-K1-B8 Seq. ID Method BLASTX NCBI GI g1737169 350 BLAST score 4.0e-33 E value 79 Match length % identity 81 (U70034) homologue to SKP1 [Arabidopsis thaliana] NCBI Description Seq. No. 213129 Seq. ID LIB3146-012-Q1-K1-C1 Method BLASTX NCBI GI q2583130 BLAST score 95 1.0e-09 E value Match length 96 39 % identity (AC002387) putative reverse transcriptase [Arabidopsis NCBI Description thaliana] 213130 Seq. No. LIB3146-012-Q1-K1-C3 Seq. ID Method BLASTX NCBI GI q1840425 BLAST score 161 E value 5.0e-11 Match length 43 % identity 67 (U36586) alcohol dehydrogenase [Vitis vinifera] NCBI Description 213131 Seq. No. LIB3146-012-Q1-K1-C4 Seq. ID

Method BLASTX
NCBI GI g2342735
BLAST score 417
E value 6.0e-41

Match length 106 % identity 79

NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  213132
                  LIB3146-012-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2499115
BLAST score
                  458
E value
                  7.0e-46
Match length
                  122
% identity
                  71
                  VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1835788
NCBI Description
                   (U86662) VPS41 [Lycopersicon esculentum]
Seq. No.
                  213133
Seq. ID
                  LIB3146-012-Q1-K1-C8
Method
                  BLASTN
                  g4567237
NCBI GI
BLAST score
                  42
E value
                  3.0e-14
Match length
                  86
                  87
% identity
                  Arabidopsis thaliana chromosome II BAC T22F11 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  213134
Seq. ID
                  LIB3146-012-Q1-K1-C9
Method
                  BLASTX
                  g2384669
NCBI GI
BLAST score
                  153
                  5.0e-10
E value
Match length
                   45
                   64
% identity
NCBI Description
                   (AF012656) putative potassium transporter AtKT1p
                   [Arabidopsis thaliana]
Seq. No.
                   213135
Seq. ID
                  LIB3146-012-Q1-K1-D1
Method
                  BLASTX
                  g3378104
NCBI GI
BLAST score
                   336
E value
                  1.0e-31
Match length
                  102
                   59
% identity
NCBI Description
                  (AF047473) testis mitotic checkpoint BUB3 [Homo sapiens]
Seq. No.
                   213136
Seq. ID
                  LIB3146-012-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                   q4406780
BLAST score
                   238
E value
                   2.0e-20
Match length
                   66
                   73
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 213137

Seq. ID LIB3146-012-Q1-K1-D2



Method BLASTX
NCBI GI g464985
BLAST score 480
E value 2.0e-48
Match length 98
% identity 93

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN

LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)

>gi 398699 emb CAA78713 (Z14989) ubiquitin conjugating

enzyme homolog [Arabidopsis thaliana]

Seq. No. 213138

Seq. ID LIB3146-012-Q1-K1-D4

Method BLASTN
NCBI GI g18483
BLAST score 66
E value 9.0e-29
Match length 66
% identity 100

NCBI Description Cotton mRNA for cottonseed catalase subunit 1 (EC 1.11.1.6)

Seq. No. 213139

Seq. ID LIB3146-012-Q1-K1-D5

Method BLASTX
NCBI GI g3142300
BLAST score 207
E value 2.0e-16
Match length 109
% identity 42

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb\_L29224 from S. cerevisiae. ESTs gb\_R64908

and gb\_T88158, gb\_N38703 and gb\_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 213140

Seq. ID LIB3146-012-Q1-K1-D6

Method BLASTX
NCBI GI g2642648
BLAST score 525
E value 1.0e-53
Match length 134
% identity 81

NCBI Description (AF033852) cytosolic heat shock 70 protein; HSC70-3

[Spinacia oleracea] >gi\_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi\_2660770 (AF034617)

cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 213141

Seq. ID LIB3146-012-Q1-K1-D7

Method BLASTX
NCBI GI g3914015
BLAST score 151
E value 7.0e-10
Match length 43
% identity 67

NCBI Description TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)

>gi\_1001661\_dbj\_BAA10395\_ (D64002) transcription-repair



## coupling factor [Synechocystis sp.]

```
213142
Seq. No.
Seq. ID
                  LIB3146-012-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2129709
BLAST score
                  199
                  1.0e-15
E value
                  87
Match length
                  46
% identity
NCBI Description
                  reverse transcriptase - Arabidopsis thaliana
                  retrotransposon Tall-1 >gi_976278 (L47193) reverse
                  transcriptase [Arabidopsis thaliana]
Seq. No.
                  213143
                  LIB3146-012-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3980393
BLAST score
                  377
E value
                  3.0e-36
Match length
                  122
                  59
% identity
NCBI Description
                  (AC004561) putative glutathione S-transferase [Arabidopsis
                  thaliana]
Seq. No.
                  213144
                  LIB3146-012-Q1-K1-E2
Seq. ID
Method
                  BLASTX
                  g1769887
NCBI GI
BLAST score
                  284
                  2.0e-25
E value
Match length
                  61
% identity
                  82
NCBI Description
                  (X95736) amino acid permease 6 [Arabidopsis thaliana]
Seq. No.
                  213145
Seq. ID
                  LIB3146-012-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  q2956717
BLAST score
                  482
E value
                  1.0e-48
Match length
                  102
% identity
                  85
NCBI Description
                  (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
Seq. No.
                  213146
Seq. ID
                  LIB3146-012-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2739168
BLAST score
                  186
E value
                  6.0e-14
Match length
                  109
% identity
                  (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
```

29640

tabacum]

213147

Seq. No.



```
LIB3146-012-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885328
                  198
BLAST score
                  3.0e-15
E value
Match length
                  63
                  54
% identity
                  (AC005623) putative serine/threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  213148
Seq. No.
                  LIB3146-012-Q1-K1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3158473
BLAST score
                  43
                  6.0e-15
E value
Match length
                  83
                  88
% identity
                  Samanea saman aquaporin 1 (Aqp1) mRNA, complete cds
NCBI Description
Seq. No.
                  213149
                  LIB3146-012-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129753
BLAST score
                  630
E value
                  6.0e-66
                                            34
                  135
Match length
% identity
                  89
NCBI Description
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
                  thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                   [Arabidopsis thaliana]
                  213150
Seq. No.
                  LIB3146-012-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245120
BLAST score
                  141
E value
                  5.0e-09
Match length
                  43
% identity
                  60
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
                  213151
Seq. No.
                  LIB3146-012-Q1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2275090
BLAST score
                  173
E value
                  1.0e-92
Match length
                  193
% identity
                  97
NCBI Description Swietenia humilis DNA for simple tandem repeat (341bp)
```

Seq. No. 213152

Seq. ID LIB3146-012-Q1-K1-F6

Method BLASTX NCBI GI g464444 BLAST score 630



E value 6.0e-66
Match length 139
% identity 85

NCBI Description PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX 30 KD SUBUNIT) >gi\_541889\_pir\_\_S39900 proteasome -

Arabidopsis thaliana >gi\_166830 (M98495) proteasome

[Arabidopsis thaliana]

Seq. No. 213153

Seq. ID LIB3146-012-Q1-K1-G1

Method BLASTX
NCBI GI g729974
BLAST score 517
E value 9.0e-53
Match length 117
% identity 84

NCBI Description FLORAL HOMEOTIC PROTEIN PMADS1 (GREEN PETAL HOMEOTIC

PROTEIN) >gi\_322773\_pir\_S31693 transcription factor gp - garden petunia >gi\_22665\_emb\_CAA49567\_ (X69946) GP (green

petal) [Petunia x hybrida]

Seq. No. 213154

Seq. ID LIB3146-012-Q1-K1-G5

Method BLASTX
NCBI GI g3095111
BLAST score 144
E value 5.0e-09
Match length 99
% identity 36

NCBI Description (AF051894) 15 kDa selenoprotein [Homo sapiens]

Seq. No. 213155

Seq. ID LIB3146-012-Q1-K1-G6

Method BLASTX
NCBI GI g3252807
BLAST score 178
E value 5.0e-13
Match length 94
% identity 48

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213156

Seq. ID LIB3146-012-Q1-K1-G9

Method BLASTX
NCBI GI g2246452
BLAST score 301
E value 2.0e-40
Match length 111
% identity 74

NCBI Description (U71107) S-adenosyl-methionine-sterol-C-methyltransferase

homolog [Nicotiana tabacum]

Seq. No. 213157

Seq. ID LIB3146-012-Q1-K1-H1

Method BLASTX NCBI GI g2266947 BLAST score 261

E value

Match length

% identity

4.0e-25

106

56



```
E value
                  3.0e-23
Match length
                  54
                  98
% identity
NCBI Description
                  (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium
                  hirsutum]
Seq. No.
                  213158
                  LIB3146-012-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407800
BLAST score
                  146
                  2.0e-09
E value
Match length
                  46
% identity
                  65
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
Seq. No.
                  213159
                  LIB3146-012-Q1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832616
BLAST score
                  130
E value
                  2.0e-09
Match length
                  77
% identity
                  53
                  (AL021711) heat shock transcription factor - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  213160
Seq. ID
                  LIB3146-013-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2493318
BLAST score
                  180
                  2.0e-13
E value
                  57
Match length
% identity
                  56
NCBI Description
                  BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
                   (Z25471) blue copper protein [Pisum sativum]
                  >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]
Seq. No.
                  213161
Seq. ID
                  LIB3146-013-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2347199
BLAST score
                  208
                  9.0e-17
E value
Match length
                  74
                  59
% identity
NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]
Seq. No.
                  213162
Seq. ID
                  LIB3146-013-Q1-K1-B1
Method
                  BLASTX
                  g1173638
NCBI GI
BLAST score
                  280
```



NCBI Description (U35779) 1-aminocyclopropane-1-carboxylate synthase [Triticum aestivum]

Seq. No. 213163

Seq. ID LIB3146-013-Q1-K1-B3

Method BLASTX
NCBI GI g1711507
BLAST score 219
E value 4.0e-18
Match length 85
% identity 51

NCBI Description SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19)

>gi 624221 (U19030) signal recognition particle 19 kDa

protein subunit SRP19 [Oryza sativa]

Seq. No. 213164

Seq. ID LIB3146-013-Q1-K1-B9

Method BLASTX
NCBI GI g3395432
BLAST score 463
E value 2.0e-46
Match length 117
% identity 74

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 213165

Seq. ID LIB3146-013-Q1-K1-C10

Method BLASTX
NCBI GI g2982259
BLAST score 244
E value 4.0e-21
Match length 72
% identity 62

NCBI Description (AF051212) probable 60s ribosomal protein L13a [Picea

mariana]

Seq. No. 213166

Seq. ID LIB3146-013-Q1-K1-C12

Method BLASTX
NCBI GI g2982251
BLAST score 218
E value 9.0e-18
Match length 90
% identity 54

NCBI Description (AF051208) putative RNA-binding protein [Picea mariana]

Seq. No. 213167

Seq. ID LIB3146-013-Q1-K1-C4

Method BLASTX
NCBI GI g818849
BLAST score 139
E value 6.0e-09
Match length 49
% identity 51

NCBI Description (U25430) nucleotide pyrophosphatase precursor [Oryza

sativa]



```
Seq. No.
                  213168
Seq. ID
                  LIB3146-013-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q399046
                  309
BLAST score
E value
                  1.0e-28
Match length
                  92
% identity
                  68
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
NCBI Description
                  >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC
                  2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
                  (X58640) adenine phosphoribosyltransferase [Arabidopsis
                  thaliana] >gi_433050 (L19637) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
                  >gi 3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
                  213169
Seq. No.
Seq. ID
                  LIB3146-013-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q3913004
BLAST score
                  499
E value
                  1.0e-50
Match length
                  118
% identity
                  84
NCBI Description AGAMOUS PROTEIN (TAG1) >gi 457382 (L26295) TAG1
                  [Lycopersicon esculentum]
Seq. No.
                  213170
                  LIB3146-013-Q1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760166
                  35
BLAST score
E value
                  3.0e-10
Match length
                  91
% identity
                  28
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213171
Seq. ID
                  LIB3146-013-Q1-K1-D5
Method
                  BLASTX
                  q3298540
NCBI GI
BLAST score
                  402
E value
                  2.0e-39
Match length
                  99
% identity
                  79
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                  213172
Seq. ID
                  LIB3146-013-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q4432854
BLAST score
                  144
```

E value 4.0e-09 57 Match length % identity 49

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

% identity

81



```
213173
   Seq. No.
                     LIB3146-013-Q1-K1-E7
   Seq. ID
   Method
                     BLASTX
                     q1730512
   NCBI GI
  BLAST score
                     442
                     4.0e-44
  E value
  Match length
                     98
   % identity
                     93
                     PHOSPHOGLYCERATE KINASE, CHLOROPLAST
  NCBI Description
                     >gi_2129669_pir__S71368 phosphoglycerate kinase -
                     Arabidopsis thaliana (fragment) >gi 1022805 (U37701)
                     phosphoglycerate kinase [Arabidopsis thaliana]
   Seq. No.
                     213174
                     LIB3146-013-Q1-K1-E9
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     q2695931
  BLAST score
                     231
  E value
                     3.0e-27
  Match length
                     115
% identity
                     61
                     (AJ222779) hypothetical protein [Hordeum vulgare]
  NCBI Description
   Seq. No.
                     213175
                     LIB3146-013-Q1-K1-F11
   Seq. ID
  Method
                     BLASTX
   NCBI GI
                     q3236261
   BLAST score
                     469
   E value
                     4.0e-47
  Match length
                     123
   % identity
                     67
   NCBI Description
                     (AC004684) putative zinc finger protein [Arabidopsis
                     thaliana]
   Seq. No.
                     213176
                     LIB3146-013-Q1-K1-F9
   Seq. ID
   Method
                     BLASTX
                     g3925277
   NCBI GI
   BLAST score
                     189
   E value
                     2.0e-14
  Match length
                     97
                     45
   % identity
   NCBI Description
                     (AL032643) similar to Uncharacterized protein family
                     UPF0034, Double-stranded RNA binding motif; cDNA EST
                     yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes
                     from this gene [Caenorhabditis elegans]
   Seq. No.
                     213177
   Seq. ID
                     LIB3146-013-Q1-K1-G11
   Method
                     BLASTX
   NCBI GI
                     g2492772
   BLAST score
                     150
   E value
                     9.0e-10
   Match length
                     32
```

29646

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)



(FALDH) (GSH-FDH) >gi\_1498024 (U63931) glutathione-dependent formaldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No. 213178 Seq. ID LIB3146-013-Q1-K1-H2

Method BLASTX
NCBI GI g3702608
BLAST score 251

E value 4.0e-22 Match length 51 % identity 90

NCBI Description (AJ224165) shaggy kinase 7 [Petunia x hybrida]

Seq. No. 213179

Seq. ID LIB3146-013-Q1-K1-H7

Method BLASTX
NCBI GI g3702608
BLAST score 386
E value 1.0e-37
Match length 79
% identity 90

NCBI Description (AJ224165) shaggy kinase 7 [Petunia x hybrida]

Seq. No. 213180

Seq. ID LIB3146-013-Q1-K1-H8

Method BLASTX
NCBI GI g4490752
BLAST score 253
E value 3.0e-22
Match length 60
% identity 80

NCBI Description (AL035708) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 213181

Seq. ID LIB3146-014-Q1-K1-A3

Method BLASTX
NCBI GI g3176669
BLAST score 506
E value 1.0e-51
Match length 101
% identity 84

NCBI Description (AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No. 213182

Seq. ID LIB3146-014-Q1-K1-A4

Method BLASTX
NCBI GI g2618731
BLAST score 377
E value 3.0e-36
Match length 102
% identity 70

NCBI Description (U49077) IAA21 [Arabidopsis thaliana]

Seq. No. 213183

Seq. ID LIB3146-014-Q1-K1-A5

E value

Match length

% identity

8.0e-52

117

79



```
Method
                  BLASTX
                  g3643608
NCBI GI
BLAST score
                  239
E value
                  3.0e-22
Match length
                  118
                  56
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                  213184
Seq. No.
                  LIB3146-014-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3881976
BLAST score
                  287
E value
                  3.0e-26
                  90
Match length
                  60
% identity
NCBI Description
                  (AJ012409) hypothetical protein [Homo sapiens]
Seq. No.
                  213185
Seq. ID
                  LIB3146-014-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g3641837
BLAST score
                  204
E value
                  4.0e-16
Match length
                  51
                  78
% identity
                  (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  213186
Seq. ID
                  LIB3146-014-Q1-K1-B11
Method
                  BLASTX
                  g2832677
NCBI GI
BLAST score
                  146
                  2.0e-09
E value
Match length
                  49
% identity
                  59
NCBI Description
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  213187
                  LIB3146-014-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097585
BLAST score
                  231
E value
                  4.0e-19
Match length
                  70
                  73
% identity
NCBI Description
                  (U64925) NTGP4 [Nicotiana tabacum]
Seq. No.
                  213188
Seq. ID
                  LIB3146-014-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q2673917
BLAST score
                  509
```



NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No. 213189

Seq. ID LIB3146-014-Q1-K1-B7

Method BLASTX
NCBI GI g4099914
BLAST score 263
E value 4.0e-23
Match length 91
% identity 56

NCBI Description (U91857) ethylene-responsive element binding protein

homolog [Stylosanthes hamata]

Seq. No. 213190

Seq. ID LIB3146-014-Q1-K1-C1

Method BLASTX
NCBI GI g3953471
BLAST score 570
E value 6.0e-59
Match length 125
% identity 82

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 213191

Seq. ID LIB3146-014-Q1-K1-C10

Method BLASTX
NCBI GI g3264778
BLAST score 233
E value 2.0e-19
Match length 89
% identity 58

NCBI Description (AF072536) H-protein promoter binding factor-1 [Arabidopsis

thaliana]

Seq. No. 213192

Seq. ID LIB3146-014-Q1-K1-C11

Method BLASTX
NCBI GI g3024127
BLAST score 676
E value 2.0e-71
Match length 133
% identity 94

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi\_1655578\_emb\_CAA95857\_ (Z71272) S-adenosyl-L-methionine

synthetase 2 [Catharanthus roseus]

Seq. No. 213193

Seq. ID LIB3146-014-Q1-K1-C7

Method BLASTX
NCBI GI g4455235
BLAST score 255
E value 4.0e-22
Match length 68
% identity 75

NCBI Description (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA

Seq. No.

213199



## SUBUNIT-like [Arabidopsis thaliana]

```
213194
Seq. No.
                  LIB3146-014-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2558962
BLAST score
                  202
                  7.0e-16
E value
Match length
                  40
                  100
% identity
NCBI Description
                  (AF025667) histone H2B1 [Gossypium hirsutum]
                  213195
Seq. No.
                  LIB3146-014-Q1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464840
BLAST score
                  577
E value
                  8.0e-60
Match length
                  109
% identity
                  98
NCBI Description
                  TUBULIN ALPHA-1 CHAIN >qi 421781 pir S32666 tubulin
                  alpha-1 chain - fern (Anemia phyllitidis)
                  >gi 296494 emb CAA48927 (X69183) alpha tubulin [Anemia
                  phyllitidis]
Seq. No.
                  213196
                  LIB3146-014-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1082766
BLAST score
                  217
E value
                  1.0e-17
Match length
                  52
% identity
                  75
                  ribosomal protein L29 - human >gi 793843 emb CAA89008
NCBI Description
                  (Z49148) ribosomal protein L29 [Homo sapiens]
Seq. No.
                  213197
                  LIB3146-014-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911072
BLAST score
                  339
E value
                  4.0e-38
Match length
                  139
% identity
                  64
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                  213198
Seq. No.
                  LIB3146-014-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567316
BLAST score
                  132
                  5.0e-12
E value
Match length
                  101
% identity
                  54
NCBI Description
                  (AC005956) hypothetical protein [Arabidopsis thaliana]
```

```
LIB3146-014-Q1-K1-D5
Seq. ID ~
                  BLASTX
Method
NCBI GI
                  q4567202
BLAST score
                  637
E value
                  9.0e-67
                  135
Match length
% identity
                  90
                  (AC007168) putative myo-inositol 1-phosphate synthase
NCBI Description
                  [Arabidopsis thaliana]
                  213200
Seq. No.
                  LIB3146-014-Q1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
E value
                  1.0e-11
Match length
                  49
% identity
                  67
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  213201
                  LIB3146-014-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224927
BLAST score
                  493
E value
                  2.0e-54
Match length
                  111
% identity
                  78
                  (AF004213) ethylene-insensitive3-like1 [Arabidopsis
NCBI Description
                  thaliana]
                  213202
Seq. No.
                  LIB3146-014-Q1-K1-E11
Seq. ID
Method
                  BLASTX
                  g320585
NCBI GI
BLAST score
                  549
                  2.0e-56
E value
                  118
Match length
% identity
                  84
                  polygalacturonase (EC 3.2.1.15) 1 beta chain precursor -
NCBI Description
                  tomato >gi_170480 (M98466) polygalacturonase isoenzyme 1
                  beta subunit [Lycopersicon esculentum] >gi_1762586 (U63374)
                  polygalacturonase isoenzyme 1 beta subunit [Lycopersicon
                  esculentum]
                  213203
Seq. No.
                  LIB3146-014-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g1008904
NCBI GI
BLAST score
                   639
E value
                   4.0e-67
Match length
                  122
                   89
% identity
                  (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
NCBI Description
```

Seq. No. 213204

Seq. ID LIB3146-014-Q1-K1-E3



```
Method
                  BLASTX
NCBI GI
                  q1903364
BLAST score
                  255
                  4.0e-22
E value
Match length
                  101
                  51
% identity
                  (ACO00104) EST gb T45093 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  213205
Seq. No.
                  LIB3146-014-Q1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2853219
BLAST score
                  527
                  5.0e-54
E value
                  118
Match length
% identity
                  80
                  (AJ000923) glutathione transferase [Carica papaya]
NCBI Description
Seq. No.
                  213206
                  LIB3146-014-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  g1399380
NCBI GI
BLAST score
                  597
E value
                   4.0e-62
Match length
                  139
% identity
                   81
                  (U43683) S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                  methyltransferase [Glycine max]
Seq. No.
                   213207
                  LIB3146-014-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4432855
BLAST score
                   471
E value
                   3.0e-47
Match length
                   136
% identity
                   69
                  (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213208
Seq. ID
                   LIB3146-014-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g3212865
BLAST score
                   192
E value
                   1.0e-14
Match length
                   82
% identity
                   55
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   213209
                   LIB3146-014-Q1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1546700
BLAST score
                   275
```

29652

3.0e-24

118

E value Match length

NCBI Description



```
% identity
NCBI Description
                  (X98804) peroxidase ATP18a [Arabidopsis thaliana]
Seq. No.
                  213210
                  LIB3146-014-Q1-K1-F7
Seq. ID
Method
                  BLASTX
                  q4415992
NCBI GI
BLAST score
                  667
                  2.0e-70
E value
Match length
                  126
                  100
% identity
                  (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
                  213211
Seq. No.
                  LIB3146-014-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2582645
BLAST score
                  139
                  6.0e-09
E value
                  51
Match length
% identity
                  55
                  (AJ002378) RSZp22 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213212
                  LIB3146-014-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  g1076511
NCBI GI
BLAST score
                  411
E value
                  2.0e-40
                  124
Match length
                  65
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                  >qi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase
                   [Phaseolus vulgaris]
Seq. No.
                  213213
                  LIB3146-014-Q1-K1-G12
Seq. ID
Method
                  BLASTX
                  g1172003
NCBI GI
BLAST score
                  276
E value
                  2.0e-24
                  125
Match length
                  46
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi 484062 (M91192)
NCBI Description
                  phenylalanine ammonia-lyase [Trifolium subterraneum]
                  213214
Seq. No.
                  LIB3146-014-Q1-K1-G2
Seq. ID
Method
                  BLASTX
                  g1345642
NCBI GI
BLAST score
                   399
E value
                   4.0e-39
Match length
                  105
                  72
% identity
```

29653

3',5'-hydroxylase Hf1 - garden petunia

FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450

75A1) (CYPLXXVA1) >gi\_629710\_pir\_\_S38985 flavonoid



>gi\_311656\_emb\_CAA80266\_ (Z22545) flavonoid
3',5'-hydroxylase [Petunia x hybrida]
>gi\_1853972\_dbj\_BAA03438\_ (D14588)

flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi\_3426337 (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi\_738772 prf\_2001426B flavonoid 3',5'-hydroxylase [Petunia x hybrida]

[reculta x hybr

Seq. No. 213215

Seq. ID LIB3146-014-Q1-K1-G4

Method BLASTX
NCBI GI g169989
BLAST score 684
E value 3.0e-72
Match length 134
% identity 96

NCBI Description (L12157) NADPH-specific isocitrate dehydrogenase [Glycine

max]

Seq. No. 213216

Seq. ID LIB3146-014-Q1-K1-G7

Method BLASTX
NCBI GI g3264767
BLAST score 397
E value 1.0e-38
Match length 134
% identity 56

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 213217

Seq. ID LIB3146-014-Q1-K1-H1

Method BLASTX
NCBI GI g417103
BLAST score 473
E value 6.0e-55
Match length 118
% identity 98

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_ S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911\_emb\_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum]

>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa]
>gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755 emb\_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]



```
Seq. No. 213218
```

Seq. ID LIB3146-014-Q1-K1-H5

Method BLASTX
NCBI GI g461530
BLAST score 338
E value 1.0e-31
Match length 129
% identity 53

NCBI Description N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG

>gi\_159365 (L11348) ARD1 protein homologue [Leishmania

donovani]

Seq. No. 213219

Seq. ID LIB3146-014-Q1-K1-H6

Method BLASTX
NCBI GI g3915847
BLAST score 161
E value 2.0e-16
Match length 60
% identity 78

NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative

40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 213220

Seq. ID LIB3146-014-Q1-K1-H8

Method BLASTX
NCBI GI g294668
BLAST score 312
E value 8.0e-29
Match length 84
% identity 73

NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No. 213221

Seq. ID LIB3146-014-Q1-K1-H9

Method BLASTX
NCBI GI g3522950
BLAST score 150
E value 6.0e-10
Match length 88
% identity 40

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213222

Seq. ID LIB3146-015-Q1-K1-A1

Method BLASTX
NCBI GI g2505870
BLAST score 120
E value 1.0e-09
Match length 60
% identity 48

NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213223

Seq. ID LIB3146-015-Q1-K1-A11

Method BLASTX NCBI GI g100332



```
BLAST score
E value
                  3.0e-56
Match length
                  119
                  86
% identity
                  glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) -
NCBI Description
                  common tobacco >gi_19875_emb_CAA46787_ (X65974)
                  glutamate-1-semialdehyde 2,1-aminomutase [Nicotiana
                  tabacum]
                  213224
Seq. No.
                  LIB3146-015-Q1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1848212
BLAST score
                  579
                  5.0e-60
E value
Match length
                  117
                  53
% identity
                  (Y11209) protein disulfide-isomerase precursor [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  213225
                  LIB3146-015-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  g1684857
NCBI GI
BLAST score
                  566
                  2.0e-58
E value
Match length
                  112
% identity
                  35
                  (U77940) polyubiquitin [Phaseolus vulgaris]
NCBI Description
                  213226
Seq. No.
                  LIB3146-015-Q1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980779
BLAST score
                  281
E value
                  3.0e-25
Match length
                  89
% identity
                  63
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213227
                  LIB3146-015-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4127456
BLAST score
                  342
E value
                  3.0e-32
Match length
                  128
                  58
% identity
NCBI Description
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                  213228
Seq. ID
                  LIB3146-015-Q1-K1-B11
```

注 -

Method BLASTX NCBI GI g3355480 BLAST score 217 E value 1.0e-17 Match length 76



% identity 58
NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No. 213229

Seq. ID LIB3146-015-Q1-K1-B3

Method BLASTX
NCBI GI g267072
BLAST score 784
E value 6.0e-84
Match length 150
% identity 97

NCBI Description TUBULIN BETA-1 CHAIN >gi\_100072\_pir\_\_S20868 tubulin beta-1

chain - garden pea >gi 20758 emb\_CAA38613\_ (X54844)

beta-tubulin 1 [Pisum sativum]

Seq. No. 213230

Seq. ID LIB3146-015-Q1-K1-B4

Method BLASTX
NCBI GI g3043428
BLAST score 356
E value 5.0e-34
Match length 80
% identity 84

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 213231

Seq. ID LIB3146-015-Q1-K1-B7

Method BLASTX
NCBI GI g3033400
BLAST score 375
E value 3.0e-36
Match length 108
% identity 68

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 213232

Seq. ID LIB3146-015-Q1-K1-C1

Method BLASTX
NCBI GI g4115377
BLAST score 431
E value 1.0e-42
Match length 136
% identity 54

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 213233

Seq. ID LIB3146-015-Q1-K1-C12

Method BLASTX
NCBI GI g1170567
BLAST score 600
E value 1.0e-62
Match length 128
% identity 91

NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi 1085960 pir S52648 INO1 protein - Citrus paradisi



>gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]

213234 Seq. No.

LIB3146-015-Q1-K1-C8 Seq. ID

Method BLASTX NCBI GI g1296816 BLAST score 555 3.0e-57 E value Match length 116 92 % identity

(X94995) naringenin-chalcone synthase [Juglans sp.] NCBI Description

213235 Seq. No.

LIB3146-015-Q1-K1-C9 Seq. ID

Method BLASTX NCBI GI q974782 BLAST score 515 E value 2.0e-52 Match length 104 98 % identity

(Z49150) cobalamine-independent methionine synthase NCBI Description

[Solenostemon scutellarioides]

213236 Seq. No.

LIB3146-015-Q1-K1-D1 Seq. ID

Method BLASTX g2388689 NCBI GI BLAST score 336 2.0e-31 E value Match length 75

% identity 81

(AF016633) GH1 protein [Glycine max] NCBI Description

213237 Seq. No.

LIB3146-015-Q1-K1-D11 Seq. ID

Method BLASTX g3193314 NCBI GI BLAST score 139 E value 1.0e-10 Match length 95 % identity 40

NCBI Description (AF069299) contains similarity to Arabidopsis scarecrow

(GB:U62798) [Arabidopsis thaliana]

Seq. No. 213238

Seq. ID LIB3146-015-Q1-K1-D2

Method BLASTX NCBI GI g2894607 BLAST score 444 4.0e-44 E value Match length 132 % identity 63

(ALO21889) NAM (no apical meristem) - like protein NCBI Description

[Arabidopsis thaliana]

213239 Seq. No.

Seq. ID LIB3146-015-Q1-K1-D4



```
BLASTX
Method
NCBI GI
                  g2497753
BLAST score
                  356
E value
                  8.0e-34
Match length
                  118
                  53
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi 1321915 emb CAA65477 (X96716) lipid transfer protein
                  [Prunus dulcis]
Seq. No.
                  213240
                  LIB3146-015-Q1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914435
BLAST score
                  464
                  1.0e-46
E value
Match length
                  105
% identity
                  89
                  PROFILIN 1 >gi 3021375 emb CAA11756 (AJ223982) profilin
NCBI Description
                  [Glycine max]
Seq. No.
                  213241
                  LIB3146-015-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  g2213871
NCBI GI
BLAST score
                  305
                  5.0e-28
E value
Match length
                  68
% identity
                  91
                  (AF003126) poly(A)-binding protein [Mesembryanthemum
NCBI Description
                  crystallinum]
                  213242
Seq. No.
                  LIB3146-015-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1263291
BLAST score
                  500
E value
                  9.0e-51
Match length
                  115
% identity
                  81
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
Seq. No.
                  213243
                  LIB3146-015-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2495365
BLAST score
                  437
E value
                  3.0e-43
Match length
                  120
% identity
                  72
NCBI Description
                  HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
```

213244 Seq. No.

Seq. ID LIB3146-015-Q1-K1-E3

Method BLASTX

NCBI GI g1769887



BLAST score 589 E value 4.0e-61 Match length 142 % identity 80

NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No. 213245

Seq. ID LIB3146-015-Q1-K1-E5

Method BLASTX
NCBI GI g4006914
BLAST score 308
E value 3.0e-28
Match length 121
% identity 55

NCBI Description (299708) serine C-palmitoyltransferase like protein

[Arabidopsis thaliana]

Seq. No. 213246

Seq. ID LIB3146-015-Q1-K1-E7

Method BLASTX
NCBI GI g3335378
BLAST score 431
E value 1.0e-42
Match length 138
% identity 66

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 213247

Seq. ID LIB3146-015-Q1-K1-E8

Method BLASTX
NCBI GI g728882
BLAST score 187
E value 5.0e-14
Match length 40
% identity 80

NCBI Description ADP-RIBOSYLATION FACTOR 3 >gi 541846 pir S41938

ADP-ribosylation factor 3 - Arabidopsis thaliana

>gi\_453191\_emb\_CAA54564\_ (X77385) ADP-ribosylation factor 3

[Arabidopsis thaliana]

Seq. No. 213248

Seq. ID LIB3146-015-Q1-K1-F1

Method BLASTX
NCBI GI g485514
BLAST score 293
E value 2.0e-26
Match length 105
% identity 53

NCBI Description ADR11-2 protein - soybean (fragment)

>gi\_296443 emb\_CAA49341 (X69640) auxin down regulated

[Glycine max]

Seq. No. 213249

Seq. ID LIB3146-015-Q1-K1-F11

Method BLASTX NCBI GI g2982262

```
BLAST score
E value
                  5.0e-20
Match length
                  112
% identity
                  49
NCBI Description
                  (AF051214) probable glutathione S-transferase [Picea
                  mariana]
                  213250
Seq. No.
Seq. ID
                  LIB3146-015-Q1-K1-F12
Method
                  BLASTX
                  g4467157
NCBI GI
BLAST score
                  349
                  5.0e-33
E value
Match length
                  136
% identity
                  52
NCBI Description
                  (AL035540) disease resistance response like protein
                  [Arabidopsis thaliana]
                  213251
Seq. No.
                  LIB3146-015-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2811025
BLAST score
                  537
E value
                  4.0e-55
Match length
                  132
% identity
                  72
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                  213252
Seq. ID
                  LIB3146-015-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g485514
BLAST score
                  229
```

E value 5.0e-19 Match length 66 76 % identity

NCBI Description ADR11-2 protein - soybean (fragment)

>gi\_296443\_emb\_CAA49341\_ (X69640) auxin down regulated

[Glycine max]

213253 Seq. No.

Seq. ID LIB3146-015-Q1-K1-G1

Method BLASTX NCBI GI g4206122 540 BLAST score E value 2.0e-55 Match length 121 % identity 83

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 213254

Seq. ID LIB3146-015-Q1-K1-G2

Method BLASTX NCBI GI g4455207 BLAST score 427



```
4.0e-42
E value
Match length
                  91
% identity
                  90
                  (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
                  213255
Seq. No.
                  LIB3146-015-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245109
BLAST score
                  282
E value
                  3.0e-25
Match length
                  70
% identity
                  76
                  (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  213256
Seq. ID
                  LIB3146-015-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4049399
BLAST score
                  152
E value
                  6.0e-10
Match length
                  97
% identity
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]
Seq. No.
                  213257
Seq. ID
                  LIB3146-015-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  q2252841
BLAST score
                  287
E value
                  8.0e-26
Match length
                  113
% identity
                  49
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                  213258
                  LIB3146-015-Q1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827300
BLAST score
                  164
                  6.0e-12
E value
Match length
                  60
                  55
% identity
                  (AF042068) MADS-box protein NMH 7 [Medicago sativa]
NCBI Description
Seq. No.
                  213259
                  LIB3146-015-Q1-K1-H10
Seq. ID
Method
                  BLASTX
                  g4210948
NCBI GI
BLAST score
                  196
E value
                  7.0e-27
Match length
                  89
                  74
% identity
```

Seq. No. 213260

29662

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]



```
LIB3146-015-Q1-K1-H12
Seq. ID
Method
                  BLASTX
                  g2809246
NCBI GI
BLAST score
                  375
                  4.0e-36
E value
                  123
Match length
% identity
                  61
                  (ACO02560) F2401.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213261
                  LIB3146-015-Q1-K1-H3
Seq. ID
Method
                  BLASTX
                  g4006921
NCBI GI
BLAST score
                  550
E value
                  1.0e-56
Match length
                  142
% identity
                  75
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213262
Seq. ID
                  LIB3146-015-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g2129675
BLAST score
                  257
E value
                  1.0e-22
Match length
                  83
% identity
                  55
                  probable chlorophyll synthetase G4 - Arabidopsis thaliana
NCBI Description
                  >qi 972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >qi 3068709 (AF049236) putative
                  chlorophyll synthetase [Arabidopsis thaliana]
Seq. No.
                  213263
                  LIB3146-015-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160172
BLAST score
                   326
E value
                  1.0e-30
Match length
                  93
% identity
                   66
NCBI Description
                  (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  213264
                  LIB3146-015-Q1-K1-H8
Seq. ID
Method
                  BLASTX
                  g3785977
NCBI GI
BLAST score
                  572
                  3.0e-59
E value
Match length
                  131
% identity
                  83
                   (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 213265

Seq. ID LIB3146-016-Q1-K1-A12

Method BLASTX NCBI GI g3250679

% identity

NCBI Description

62



```
BLAST score
                  7.0e-21
E value
Match length
                  87
% identity
                  54
                  (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
                  213266
Seq. No.
Seq. ID
                  LIB3146-016-Q1-K1-A2
Method
                  BLASTX'
                   g3184285
NCBI GI
BLAST score
                   214
                  2.0e-17
E value
                  50
Match length
                  76
% identity
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   213267
Seq. No.
                  LIB3146-016-Q1-K1-A4
Seq. ID
Method
                  BLASTX
                   g3264805
NCBI GI
BLAST score
                   205
                   3.0e-16
E value
Match length
                   45
                   93
% identity
                   (AF071788) phosphoenolpyruvate carboxylase [Arabidopsis
NCBI Description
                   thaliana] >gi 4079630 emb CAA10486 (AJ131710) phospho
                   enole pyruvate carboxylase [Arabidopsis thaliana]
Seq. No.
                   213268
                   LIB3146-016-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   q2765837
NCBI GI
BLAST score
                   236
                   5.0e-20
E value
                   77
Match length
                   70
% identity
                  (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213269
                   LIB3146-016-Q1-K1-B9
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   33
E value
                   5.0e-09
                                           , The .
Match length
                   57
% identity
                   44
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   213270
                   LIB3146-016-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2460200
BLAST score
                   322
                   7.0e-30
E value
Match length
                   102
```

29664

(AF020833) eukaryotic translation initiation factor 3

Seq. ID

Method



## subunit [Homo sapiens]

```
Seq. No.
                  213271
Seq. ID
                  LIB3146-016-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4490732
BLAST score
                  167
E value
                  8.0e-20
                  59
Match length
                  88
% identity
                  (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  213272
                  LIB3146-016-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3776031
BLAST score
                  457
E value
                  9.0e-46
Match length
                  111
% identity
                  82
                  (AJ010477) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213273
                  LIB3146-016-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2792297
BLAST score
                  226
E value
                  1.0e-18
Match length
                  70
% identity
                  56
NCBI Description
                  (AF039183) GAST-like gene product [Fragaria x ananassa]
Seq. No.
                  213274
Seq. ID
                  LIB3146-016-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g4107276
BLAST score
                  356
E value
                  5.0e-34
Match length
                  97
% identity
                  73
NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum]
Seq. No.
                  213275
Seq. ID
                  LIB3146-016-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4490705
BLAST score
                  555
E value
                  3.0e-57
Match length
                  130
% identity
                  86
NCBI Description
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  213276
```

29665

LIB3146-016-Q1-K1-E6

BLASTX



NCBI GI g3873707 BLAST score 231 E value 3.0e-19 Match length 99 % identity 48

NCBI Description (Z73102) Similarity to B. subtilis DNAJ protein

(SW:DNAJ\_BACSU); cDNA EST yk437a1.5 comes from this gene

[Caenorhabditis elegans]

Seq. No. 213277

Seq. ID LIB3146-016-Q1-K1-F11

Method BLASTX
NCBI GI g417103
BLAST score 573
E value 2.0e-59
Match length 114
% identity 100

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153 (X79714) histone

H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa]
>gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 213278

Seq. ID LIB3146-016-Q1-K1-F12

Method BLASTX
NCBI GI g1345698
BLAST score 530
E value 3.0e-54
Match length 99
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

a/b-binding protein - upland cotton

>gi\_452314\_emb\_CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 213279

Seq. ID LIB3146-016-Q1-K1-F4

Method BLASTX
NCBI GI g2569938
BLAST score 366
E value 2.0e-35

Seq. ID



```
Match length
% identity
                  80
NCBI Description
                  (Y15193) GAI [Arabidopsis thaliana]
Seq. No.
                  213280
                  LIB3146-016-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2789660
BLAST score
                  515
                  2.0e-52
E value
Match length
                  127
% identity
                  76
NCBI Description (AF040102) p105 [Arabidopsis thaliana]
Seq. No.
                  213281
                  LIB3146-016-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1255852
BLAST score
                  186
E value
                  7.0e-14
Match length
                  110
                  32
% identity
                  (U53339) simmilar to enoyl-CoA hydratases [Caenorhabditis
NCBI Description
                  elegans]
Seq. No.
                  213282
Seq. ID
                  LIB3146-016-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2789660
BLAST score
                  322
                  4.0e-30
E value
Match length
                  93
                  69
% identity
NCBI Description (AF040102) p105 [Arabidopsis thaliana]
Seq. No.
                  213283
Seq. ID
                  LIB3146-016-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4580463
BLAST score
                  173
E value
                  2.0e-12
Match length
                  43
% identity
                  81
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.
                  213284
                  LIB3146-016-Q1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2582639
BLAST score
                  408
E value
                  6.0e - 40
Match length
                  115
% identity
NCBI Description
                  (AJ002414) hnRNP-like protein [Arabidopsis thaliana]
Seq. No.
                  213285
```

29667

LIB3146-016-Q1-K1-G4

ST. 20 .

```
Method -
                  BLASTN
NCBI GI
                  q2582638
BLAST score
                  41
                  2.0e-14
E value
                  69
Match length
                  90
% identity
NCBI Description Arabidosis thaliana mRNA for a hnRNP-like protein
Seq. No.
                  213286
                  LIB3146-016-Q1-K1-G5
Seq. ID
Method
                  BLASTX
                  g606648
NCBI GI
BLAST score
                  315
E value
                  3.0e-29
Match length
                  78
% identity
                  78
                  (U09612) alpha tubulin [Leishmania donovani]
NCBI Description
                  213287
Seq. No.
                  LIB3146-016-Q1-K1-G8
Seq. ID
Method
                  BLASTX
                  g3600039
NCBI GI
                  399
BLAST score
                  3.0e-39
E value
                  89
Match length
% identity
                  81
                  (AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                  protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                  213288
                  LIB3146-016-Q1-K1-H1
Seq. ID
Method
                  BLASTX
                  q1346802
NCBI GI
BLAST score
                  187
E value
                  4.0e-14
Match length
                  37
                  92
% identity
                  PROFILIN 1 >gi_1076516_pir__S49351 profilin - kidney bean
NCBI Description
                  >gi_556836_emb_CAA57508_ (X81982) profilin [Phaseolus
                  vulgaris]
                  213289
Seq. No.
                  LIB3146-016-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g4191782
NCBI GI
BLAST score
                  636
                  1.0e-66
E value
                  140
Match length
% identity
                  84
NCBI Description
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
```

Seq. No. 213290

Seq. ID LIB3146-016-Q1-K1-H8

Method BLASTX
NCBI GI g2267139
BLAST score 142
E value 4.0e-09



```
Match length
% identity
                   87
```

NCBI Description (AF008910) ubiquitin-conjugating enzyme [Prunus armeniaca]

Seq. No.

213291

Seq. ID

LIB3146-017-Q1-K1-A1

Method NCBI GI BLASTX q1946355

BLAST score E value

403 2.0e-39

Match length % identity

131 55

NCBI Description

(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi 2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.

213292

Seq. ID

LIB3146-017-Q1-K1-A12

Method NCBI GI BLAST score BLASTX g1743354 583

E value Match length

2.0e-60 133 83

% identity NCBI Description

(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.

213293

BLASTX

419

q3047123

Seq. ID

LIB3146-017-Q1-K1-A4

Method NCBI GI BLAST score E value

4.0e-60 Match length 137 % identity 78

NCBI Description

(AF058919) similar to the family of glycosyl hydrolases

[Arabidopsis thaliana]

Seq. No.

213294

Seq. ID

LIB3146-017-Q1-K1-A5

Method BLASTN NCBI GI q167346 BLAST score 35 E value 4.0e-10 Match length 75 % identity 87

NCBI Description

Gossypium hirsutum Lea5-A late embryogenesis-abundant

protein (Lea5-A) gene, complete cds

Seq. No.

213295

75

Seq. ID

LIB3146-017-Q1-K1-A6

Method BLASTX NCBI GI g1170368 BLAST score 199 E value 2.0e-15 Match length 52

% identity

NCBI Description MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR



>gi\_2129884\_pir\_\_S59528 heat shock protein 22 precursor garden pea >gi\_773581\_emb\_CAA60120\_ (X86222) heat shock
protein [Pisum sativum]

Seq. No. 213296

Seq. ID LIB3146-017-Q1-K1-B11

Method BLASTX
NCBI GI g2583130
BLAST score 152
E value 7.0e-10
Match length 109
% identity 38

NCBI Description (AC002387) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 213297

Seq. ID LIB3146-017-Q1-K1-B12

Method BLASTX
NCBI GI g2213590
BLAST score 363
E value 1.0e-34
Match length 137
% identity 55

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 213298

Seq. ID LIB3146-017-Q1-K1-B2

Method BLASTX
NCBI GI g2583123
BLAST score 272
E value 3.0e-24
Match length 101
% identity 57

NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis

thaliana]

Seq. No. 213299

Seq. ID LIB3146-017-Q1-K1-C1

Method BLASTX
NCBI GI g2501498
BLAST score 295
E value 1.0e-26
Match length 128
% identity 44

NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID

3-O-GLUCOSYLTRANSFERASE) >gi\_1076656\_pir\_\_S51767 glycosyl transferase - eggplant >gi 607192 emb CAA54558 (X77369)

glycosyl transferase [Solanum melongena]

Seq. No. 213300

Seq. ID LIB3146-017-Q1-K1-C10

Method BLASTX
NCBI GI g1174718
BLAST score 563
E value 4.0e-58
Match length 141
% identity 76



NCBI Description

PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR

>gi\_322579\_pir\_\_JQ1674 receptor protein kinase TMK1 (EC
2.7.1.-) precursor - Arabidopsis thaliana >gi\_166888
(L00670) protein kinase [Arabidopsis thaliana]

Seq. No.
213301

Seq. ID
LIB3146-017-Q1-K1-C2
Method
BLASTX

NCBI GI g224293
BLAST score 331
E value 5.0e-31
Match length 68
% identity 97

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 213302

Seq. ID LIB3146-017-Q1-K1-C6

Method BLASTX
NCBI GI g4138265
BLAST score 158
E value 6.0e-11
Match length 42
% identity 62

NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana

tabacum]

Seq. No. 213303

Seq. ID LIB3146-017-Q1-K1-C7

Method BLASTX
NCBI GI g1172556
BLAST score 498
E value 2.0e-50
Match length 137
% identity 73

NCBI Description 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi\_629729\_pir\_\_S46925 porin II, 36K - potato >gi\_1076681\_pir\_\_B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi\_515360\_emb\_CAA56600\_ (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 213304

Seq. ID LIB3146-017-Q1-K1-C8

Method BLASTX
NCBI GI g2981131
BLAST score 181
E value 4.0e-15
Match length 67
% identity 73

NCBI Description (AF052570) AGAMOUS homolog [Populus balsamifera subsp.

trichocarpa]

Seq. No. 213305

Seq. ID LIB3146-017-Q1-K1-C9

Method BLASTX
NCBI GI g3128228
BLAST score 581



E value 4.0e-60 Match length 134 % identity 81

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis

thaliana] >gi\_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 213306

Seq. ID LIB3146-017-Q1-K1-D12

Method BLASTX
NCBI GI g1708971
BLAST score 174
È value 2.0e-12
Match length 71
% identity 42

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR

(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)

>gi\_421871\_pir\_\_S32156 mandelonitrile lyase (EC 4.1.2.10) -

black cherry >gi\_288116\_emb\_CAA51194\_ (X72617)

mandelonitrile lyase [Prunus serotina] >gi\_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi 1090776 prf 2019441A mandelonitrile lyase

[Prunus serotina]

Seq. No. 213307

Seq. ID LIB3146-017-Q1-K1-D2

Method BLASTX
NCBI GI g3334138
BLAST score 276
E value 9.0e-25
Match length 93
% identity 61

NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin

[Glycine max]

Seq. No. 213308

Seq. ID LIB3146-017-Q1-K1-D3

Method BLASTX
NCBI GI g2465923
BLAST score 165
E value 2.0e-11
Match length 138
% identity 33

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 213309

Seq. ID LIB3146-017-Q1-K1-D7

Method BLASTN
NCBI GI g2264317
BLAST score 45
E value 4.0e-16
Match length 124
% identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUG13, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  213310
Seq. ID
                  LIB3146-017-Q1-K1-D8
Method
                  BLASTN
NCBI GI
                  q1066312
BLAST score
                  64
E value
                  1.0e-27
Match length
                  168
% identity
                  85
                  Cloning vector TLF97-3, phage lambda lacZ translational
NCBI Description
                  fusion vector, complete sequence
Seq. No.
                  213311
                  LIB3146-017-Q1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583130
BLAST score
                  144
E value
                  6.0e-09
                  106
Match length
% identity
                  34
NCBI Description
                  (AC002387) putative reverse transcriptase [Arabidopsis
                  thaliana]
                  213312
Seq. No.
                  LIB3146-017-Q1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869075
BLAST score
                  47
                  2.0e-17
E value
Match length
                  155
% identity
                  83
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213313
                  LIB3146-017-Q1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2281093
BLAST score
                  276
                  3.0e-48
E value
Match length
                  134
% identity
                  78
NCBI Description
                  (AC002333) beta transducin isolog [Arabidopsis thaliana]
                  213314
Seq. No.
Seq. ID
                  LIB3146-017-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3935168
BLAST score
                  306
E value
                  6.0e-28
Match length
                  78
% identity
                  69
```

NCBI Description

Seq. No.

Seq. ID LIB3146-017-Q1-K1-F3

213315

Method BLASTX NCBI GI g3047080

29673

(AC004557) F17L21.11 [Arabidopsis thaliana]



BLAST score 285 E value 2.0e-25 Match length 110 % identity 55

NCBI Description (AF058914) contains similarity to Arabidopsis thaliana DNA-damage-repair/tolerance resistance protein DRT111

(SW:P42698) [Arabidopsis thaliana]

Seq. No. 213316

...

Seq. ID LIB3146-017-Q1-K1-F4

Method BLASTX
NCBI GI 94455293
BLAST score 135
E value 4.0e-11
Match length 93
% identity 52

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 213317

Seq. ID LIB3146-017-Q1-K1-G2

Method BLASTX
NCBI GI g2500345
BLAST score 450
E value 7.0e-45
Match length 128
% identity 71

NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)

>gi\_2618578\_dbj\_BAA23363\_ (D50420) OTK27 [Homo sapiens]

>gi 3859990 (AF091076) OTK27 [Homo sapiens]

>gi 1589072 prf 2210268A nuclear protein-NHP2-like protein

[Homo sapiens]

Seq. No. 213318

Seq. ID LIB3146-017-Q1-K1-G4

Method BLASTX
NCBI GI 9400650
BLAST score 170
E value 5.0e-12
Match length 96
% identity 36

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX

I-13KD-B) (CI-13KD-B) (B13) >gi\_346535\_pir\_S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 - bovine >gi\_238\_emb\_CAA44903\_ (X63218) NADH dehydrogenase

[Bos taurus]

Seq. No. 213319

Seq. ID LIB3146-017-Q1-K1-G7

Method BLASTX
NCBI GI g2558962
BLAST score 406
E value 1.0e-39
Match length 97
% identity 89

NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]



```
Seq. No.
                  213320
Seq. ID
                  LIB3146-017-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2244807
BLAST score
                  197
E value
                  3.0e-15
Match length
                  118
% identity
                  44
NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  213321
                  LIB3146-017-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  567
                  1.0e-58
E value
Match length
                  117
                  96
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  213322
                  LIB3146-018-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1813329
BLAST score
                  193
                  7.0e-15
E value
Match length
                  58
% identity
                  67
NCBI Description (AB000637) HMG-1 [Canavalia gladiata]
Seq. No.
                  213323
Seq. ID
                  LIB3146-018-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4063748
BLAST score
                  136
E value
                  1.0e-08
Match length
                  44
% identity
                  64
NCBI Description (AC005851) unknown protein [Arabidopsis thaliana]
Seq. No.
                  213324
Seq. ID
                  LIB3146-018-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4539350
BLAST score
                  263
E value
                  7.0e-23
Match length
                  69
% identity
                  67
NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]
Seq. No.
                  213325
Seq. ID
                  LIB3146-018-Q1-K1-A4
```

Method BLASTX NCBI GI g3643609 BLAST score 339 E value 6.0e-32



Match length % identity 79 NCBI Description (AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana] Seq. No. 213326 LIB3146-018-Q1-K1-A5 Seq. ID Method BLASTX g3135693

NCBI GI BLAST score 436 E value 3.0e-43Match length 128 % identity 62

NCBI Description (AF064201) glutathione S-transferase [Gossypium hirsutum]

Seq. No. 213327

Seq. ID LIB3146-018-Q1-K1-A6

Method BLASTX NCBI GI g2129742 BLAST score 275 E value 2.0e-24 Match length 75 % identity 65

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

thaliana >gi\_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi\_2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

213328 Seq. No.

Seq. ID LIB3146-018-Q1-K1-B10

Method BLASTX NCBI GI g3212610 BLAST score 188 E value 3.0e-14 Match length 101 % identity 42

NCBI Description Chain A, Sulfite Oxidase From Chicken Liver

>gi\_3212611\_pdb\_1SOX\_B Chain B, Sulfite Oxidase From

Chicken Liver

Seq. No. 213329

Seq. ID LIB3146-018-Q1-K1-B11

Method BLASTX NCBI GI g4510364 BLAST score 198 E value 2.0e-15 Match length 94 % identity 49

NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213330

Seq. ID LIB3146-018-Q1-K1-B12

Method BLASTX NCBI GI g4510364 BLAST score 154



```
E value
                  2.0e-10
Match length
                  80
% identity
                  46
NCBI Description
                  (AC007017) hypothetical protein [Arabidopsis thaliana]
                  213331
Seq. No.
                  LIB3146-018-Q1-K1-B3
Seq. ID
Method
                  BLASTN
                  g4406805
NCBI GI
BLAST score
                  35
                  3.0e-10
E value
Match length
                  107
% identity
                  83
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213332
                  LIB3146-018-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281090
BLAST score
                  290
                  3.0e-26
E value
Match length
                  95
% identity
                  63
NCBI Description
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
                  213333
Seq. No.
                  LIB3146-018-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4103324
BLAST score
                  496
E value
                  3.0e-50
Match length
                  145
% identity
                  68
NCBI Description
                  (AF022716) GDP-mannose pyrophosphorylase [Solanum
                  tuberosum]
Seq. No.
                  213334
Seq. ID
                  LIB3146-018-Q1-K1-B9
Method
                  BLASTX
                  g3036808
NCBI GI
BLAST score
                  161
E value
                  4.0e-11
Match length
                  77
                  48
% identity
NCBI Description
                  (AL022373) DnaJ-like protein [Arabidopsis thaliana]
Seq. No.
                  213335
Seq. ID
                  LIB3146-018-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3551838
```

Method BLASTX
NCBI GI g3551838
BLAST score 234
E value 1.0e-19
Match length 52

87

% identity

NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]



```
213336
Seq. No.
                  LIB3146-018-Q1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4210948
BLAST score
                  244
                  1.0e-41
E value
                  100
Match length
                  78
% identity
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
Seq. No.
                  213337
                  LIB3146-018-Q1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206206
BLAST score
                  275
E value
                   3.0e-24
Match length
                  140
% identity
                   43
                   (AF071527) putative M-type thioredoxin [Arabidopsis
NCBI Description
                  thaliana] >qi 4263039 gb AAD15308 (AC005142) putative
                  M-type thioredoxin [Arabidopsis thaliana]
Seq. No.
                  213338
Seq. ID
                  LIB3146-018-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                   g3122060
BLAST score
                   199
E value
                   8.0e-16
Match length
                   51
% identity
                   75
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >qi 2598657 emb CAA10847 (AJ222579) elongation factor
                   1-alpha (EF1-a) [Vicia faba]
Seq. No.
                   213339
                   LIB3146-018-Q1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3036812
BLAST score
                   289
E value
                   6.0e-26
Match length
                   103
% identity
                   53
                  (AL022373) ATM-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213340
                   LIB3146-018-Q1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539345
BLAST score
                   447
                   2.0e-44
E value
                   129
Match length
% identity
                   70
```

(AL035539) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. Seq. ID

213341 LIB3146-018-Q1-K1-D11

Method BLASTX



```
q1168555
NCBI GI
BLAST score
                   334
E value
                   1.0e-31
Match length
                   90
                   77
% identity
```

ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (PKIWI505) NCBI Description

>gi 1085656 pir S48039 H+-transporting ATP synthase (EC 3.6.1.34) beta chain - kiwi fruit (fragment) >gi 450243 (L27812) 'beta subunit of ATP synthase' [Actinidīa

deliciosa]

```
213342
Seq. No.
                  LIB3146-018-Q1-K1-D5
Seq. ID
Method
                  BLASTX
                   g3328221
NCBI GI
                   580
BLAST score
                   5.0e-60
```

E value 143 Match length % identity 76

(AF076920) thioredoxin peroxidase [Secale cereale] NCBI Description

```
213343
Seq. No.
```

LIB3146-018-Q1-K1-E11 Seq. ID

Method BLASTX NCBI GI g1702983 BLAST score 261 E value 8.0e-23 Match length 108 % identity 50

AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850 NCBI Description

hypothetical protein - garden strawberry >gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 213344

Seq. ID LIB3146-018-Q1-K1-E12

Method BLASTN NCBI GI q3821780 BLAST score 37 2.0e-11 E value Match length 37 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 213345

LIB3146-018-Q1-K1-E2 Seq. ID

Method BLASTX NCBI GI q481828 BLAST score 292 E value 3.0e-26 Match length 64 % identity

NCBI Description 5B protein - tomato >gi 415833 emb CAA80273 (Z22553) 5B

protein [Lycopersicon esculentum]

Seq. No. 213346



```
Seq. ID
                  LIB3146-018-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1458245
BLAST score
                  287
E value
                  1.0e-25
Match length
                  140
% identity
                  46
NCBI Description
                  (U64834) coded for by C. elegans cDNA cm17a1; coded for by
                  C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                  CEMSE26F; similar to methyltransferases [Caenorhabditis
                  elegans]
Seq. No.
                  213347
Seq. ID
                  LIB3146-018-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g3776005
BLAST score
                  595
E value
                  7.0e-62
Match length
                  127
% identity
                  88
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  213348
                  LIB3146-018-Q1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
E value
                  2.0e-11
Match length
                  37
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213349
                  LIB3146-018-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585241
BLAST score
                  207
E value
                  2.0e-16
Match length
                  79
                  59
% identity
                  HISTONE H1 >gi_629668_pir__S45662 histone H1 - tomato
NCBI Description
                  >gi 424100 (U03391) histone H1 [Lycopersicon esculentum]
Seq. No.
                  213350
Seq. ID
                  LIB3146-018-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3377820
BLAST score
                  172
E value
                  3.0e-12
Match length
                  60
% identity
                  60
NCBI Description
                  (AF076275) contains similarity to coatomer zeta chains
                  [Arabidopsis thaliana]
```

Seq. No. 213351

Seq. ID LIB3146-018-Q1-K1-F10

Method BLASTX



q4580456

NCBI GI

```
BLAST score
                  331
                  7.0e-31
E value
                  143
Match length
% identity
                  55
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213352
                  LIB3146-018-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911054
BLAST score
                  165
E value
                  2.0e-11
Match length
                  113
% identity
                  35
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  213353
Seq. No.
                  LIB3146-018-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1653513
BLAST score
                  278
                  1.0e-24
E value
Match length
                  103
% identity
                  51
NCBI Description
                  (D90914) hypothetical protein [Synechocystis sp.]
                  213354
Seq. No.
                  LIB3146-018-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g3128177
NCBI GI
BLAST score
                  308
E value
                  2.0e-28
Match length
                  73
% identity
                  81
NCBI Description
                  (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  213355
Seq. ID
                  LIB3146-018-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  q2970051
                  243
BLAST score
                  2.0e-20
E value
                  69
Match length
% identity
                  68
NCBI Description
                  (AB012110) ARG10 [Vigna radiata]
Seq. No.
                  213356
                  LIB3146-018-Q1-K1-G10
Seq. ID
Method
                  BLASTX
                  g4049346
NCBI GI
BLAST score
                  311
                  2.0e-28
E value
Match length
                  123
                  50
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
```



```
Seq. No.
                  213357
                  LIB3146-018-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g1350720
NCBI GI
BLAST score
                  384
E value
                  3.0e-37
                  98
Match length
% identity
                  73
NCBI Description 60S RIBOSOMAL PROTEIN L32
                  213358
Seq. No.
                  LIB3146-018-Q1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076668
BLAST score
                  663
                  8.0e-70
E value
Match length
                  138
% identity
                  88
NCBI Description
                  NADH dehydrogenase (EC 1.6.99.3) - potato
                  >gi 639834 emb CAA58823 (X83999) NADH dehydrogenase
                  [Solanum tuberosum]
Seq. No.
                  213359
Seq. ID
                  LIB3146-018-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3913192
BLAST score
                  233
E value
                  2.0e-19
                  99
Match length
                  47
% identity
NCBI Description
                  CYTOCHROME P450 93A1 >gi 2129824 pir S62899 cytochrome
                  P450 (CYP93 A1) - soybean >gi 1232111 dbj BAA12159
                  (D83968) Cytochrome P-450 (CYP93A1) [Glycine max]
                  >gi 1588679 prf 2209281A cytochrome P450 [Glycine max]
Seq. No.
                  213360
Seq. ID
                  LIB3146-018-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3123745
BLAST score
                  184
E value
                  6.0e-14
Match length
                  73
% identity
                  53
NCBI Description
                  (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  213361
                  LIB3146-018-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2257598
BLAST score
                  116
E value
                  6.0e-14
Match length
                  85
% identity
                  61
NCBI Description
                  (AB005551) phosphoglycerate kinase [Robinia pseudoacacia]
```

Seq. No. 213362

Seq. ID LIB3146-018-Q1-K1-H2

NCBI Description



```
Method
NCBI GI
                   q2264304
BLAST score
                   36
E value
                   9.0e-11
Match length
                   88
                   85
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBG8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   213363
                   LIB3146-018-Q1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115923
BLAST score
                   276
                   1.0e-24
E value
Match length
                   90
% identity
                   58
NCBI Description
                   (AF118222) contains similarity to ubiquitin
                   carboxyl-terminal hydrolase family 2 (Pfam: PF00443,
                   score=40.0, E=5.2e-08, N=1) and (Pfam:PF00442, Score=37.9
                   E=5.3e-10, N=1) [Arabidopsis thaliana]
Seq. No.
                   213364
Seq. ID
                   LIB3146-019-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q2842480
BLAST score
                   577
E value
                   1.0e-59
Match length
                   137
% identity
                   55
NCBI Description
                   (AL021749) ADP, ATP carrier-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   213365
Seq. ID
                   LIB3146-019-Q1-K1-A2
Method
                   BLASTX
                   g267131
NCBI GI
BLAST score
                   219
E value
                   6.0e-18
Match length
                   85
% identity
                   48
NCBI Description
                  NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)
                  >gi_423120_pir__A46174 RNA-binding protein TIAR - human
                  >gi_189310 (M96954) nucleolysin TIAR [Homo sapiens]
                  >gi_4507499_ref_NP_003243.1 pTIAL1 TIA1 cytotoxic
                   granule-associated RNA-binding protein-like
Seq. No.
                   213366
Seq. ID
                  LIB3146-019-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3702321
BLAST score
                  277
E value
                  2.0e-24
Match length
                  88
% identity
                   40
```

29683

[Arabidopsis thaliana]

(AC005397) putative TGF-beta receptor interacting protein



Seq. No. 213367

Seq. ID LIB3146-019-Q1-K1-B1

Method BLASTX
NCBI GI g1065484
BLAST score 203
E value 5.0e-16
Match length 117
% identity 32

NCBI Description (U40415) similar to S. cerevisiae LAG1 (SP:P38703)

[Caenorhabditis elegans]

Seq. No. 213368

Seq. ID LIB3146-019-Q1-K1-B4

Method BLASTX
NCBI GI g417103
BLAST score 410
E value 2.0e-40
Match length 83
% identity 98

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi 488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]
>gi\_12558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana
tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa]
>gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia
coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 213369

Seq. ID LIB3146-019-Q1-K1-B6

Method BLASTX
NCBI GI g100796
BLAST score 629
E value 7.0e-66
Match length 128
% identity 91

NCBI Description phosphoribulokinase (EC 2.7.1.19) - wheat

Seq. No. 213370

Seq. ID LIB3146-019-Q1-K1-B9

Method BLASTX
NCBI GI g3559816
BLAST score 196
E value 4.0e-15
Match length 51



```
% identit*
NCBI Description (Y15782) transketolase 2 [Capsicum annuum]
                  213371
Seq. No.
                  LIB3146-019-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  539
E value
                  3.0e-55
Match length
                  111
                  96
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
                  213372
Seq. No.
                  LIB3146-019-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1149569
BLAST score
                  230
                  3.0e-21
E value
Match length
                  81
                  62
% identity
                  (Z50851) HD-zip [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213373
                  LIB3146-019-Q1-K1-C2
Seq. ID
Method
                  BLASTX
                  g4490737
NCBI GI
BLAST score
                  449
E value
                  8.0e-45
                  119
Match length
                  58
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                  213374
Seq. ID
                  LIB3146-019-Q1-K1-C4
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  9.0e-11
E value
                  37
Match length
% identity
                  61
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213375
Seq. ID
                  LIB3146-019-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  q2281115
BLAST score
                  625
E value
                  2.0e-65
Match length
                  136
% identity
                  86
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                  thaliana]
```

29685

213376

LIB3146-019-Q1-K1-D1

Seq. No.

Seq. ID

```
Method
NCBI GI
                  q629864
BLAST score
                  211
E value
                  6.0e-17
Match length
                  43
                  100
% identity
NCBI Description
                  histone H2B - garden asparagus >gi_563329_emb_CAA57778_
                  (X82362) histone 2B [Asparagus officinalis]
Seq. No.
                  213377
                  LIB3146-019-Q1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213378
                  LIB3146-019-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860797
BLAST score
                  216
                  2.0e-17
E value
Match length
                  93
                  54
% identity
                  (AJ235271) 30S RIBOSOMAL PROTEIN S9 (rpsI) [Rickettsia
NCBI Description
                  prowazekii]
                  213379
Seq. No.
                  LIB3146-019-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047124
BLAST score
                  338
E value
                  8.0e-32
Match length
                  118
                  57
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  213380
Seq. No.
Seq. ID
                  LIB3146-019-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q1362093
BLAST score
                  195
E value
                  1.0e-15
Match length
                  64
                  58
% identity
NCBI Description
                  hypothetical protein (clone TPP15) - tomato (fragment)
                  >gi 924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.
                  213381
Seq. ID
                  LIB3146-019-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4469025
```

29686

199

9.0e-16

BLAST score E value

NCBI Description



```
Match length
% identity
                   44
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
                   213382
Seq. No.
Seq. ID
                   LIB3146-019-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   q4262162
BLAST score
                   252
                   1.0e-21
E value
Match length
                   109
% identity
                   48
NCBI Description
                   (AC005275) putative glycosylation enzyme [Arabidopsis
                   thaliana]
                   213383
Seq. No.
Seq. ID
                   LIB3146-019-01-K1-E1
Method
                   BLASTX
NCBI GI
                   g1362093
BLAST score
                   527
E value
                   6.0e-54
Match length
                   125
% identity
                   76
NCBI Description
                  hypothetical protein (clone TPP15) - tomato (fragment)
                   >gi_924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.
                   213384
                   LIB3146-019-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1171577
BLAST score
                   199
E value
                   5.0e-16
Match length
                   52
% identity
                   77
NCBI Description
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.
                   213385
Seq. ID
                   LIB3146-019-Q1-K1-E12
Method
                   BLASTX
NCBI GI
                   q4008159
BLAST score
                   114
E value
                   2.0e-13
Match length
                   77
% identity
                   58
NCBI Description
                   (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                   213386
Seq. ID
                   LIB3146-019-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g2252866
BLAST score
                   151
E value
                   7.0e-10
Match length
                   41
                   71
% identity
```

[Arabidopsis thaliana]

(AF013294) contains region of similarity to SYT

% identity

61

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
Seq. No.
                  213387
                  LIB3146-019-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g4218115
NCBI GI
BLAST score
                  254
                  8.0e-22
E value
Match length
                  119
                  50
% identity
                  (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213388
                  LIB3146-019-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730645
BLAST score
                  542
                  1.0e-55
E value
Match length
                  119
% identity
                  90
NCBI Description
                  40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal
                  protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679
                  (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                  >gi 313188 emb CAA80681 (Z23162) ribosomal protein S15
                  [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                  Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                  gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                  thaliana]
                  213389
Seq. No.
                  LIB3146-019-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1236961
BLAST score
                  198
                  2.0e-15
E value
Match length
                  109
% identity
                  41
NCBI Description
                  (U50201) prunasin hydrolase precursor [Prunus serotina]
Seq. No.
                  213390
                  LIB3146-019-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  g3319355
NCBI GI
BLAST score
                  234
E value
                  2.0e-19
Match length
                  66
% identity
                  73
                  (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
                  gamma chain [Arabidopsis thaliana]
Seq. No.
                  213391
                  LIB3146-019-Q1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  37
```

```
Seq. No.
                    213392
 Seq. ID
                    LIB3146-019-Q1-K1-F4
 Method
                    BLASTX
 NCBI GI
                    q4512699
 BLAST score
                    189
 E value
                    1.0e-14
 Match length
                    77
 % identity
                    53
 NCBI Description
                    (AC006569) putative NADH-ubiquinone oxireductase
                    [Arabidopsis thaliana]
 Seq. No. Seq. ID
                    213393
                    LIB3146-019-Q1-K1-F9
 Method
                    BLASTX
 NCBI GI
                    g1236961
 BLAST score
                    407
 E value
                    9.0e-40
 Match length
                    132
 % identity
                    56
 NCBI Description (U50201) prunasin hydrolase precursor [Prunus serotina]
 Seq. No.
                    213394
 Seq. ID
                    LIB3146-019-Q1-K1-G2
 Method
                    BLASTX
                    g289920
 NCBI GI
 BLAST score
                    709
 E value
                    2.0e-75
 Match length
                    141
 % identity
                    97
                    (L07119) chlorophyll A/B binding protein [Gossypium
 NCBI Description
                    hirsutum]
 Seq. No.
                    213395
 Seq. ID
                    LIB3146-019-Q1-K1-G4
 Method
                    BLASTX
 NCBI GI
                    g1483228
 BLAST score
                    451
 E value
                    5.0e-45
 Match length
                    122
 % identity
                    75
 NCBI Description (X99653) MADS3 protein [Betula pendula]
 Seq. No.
                    213396
 Seq. ID
                    LIB3146-019-Q1-K1-H10
 Method
                    BLASTX
 NCBI GI
                    g732893
 BLAST score
                    435
 E value
                    4.0e-43
 Match length
                    83
 % identity
                    88
 NCBI Description (X85382) tobacco calretulin [Nicotiana tabacum]
 Seq. No.
                    213397
```

Seq. ID LIB3146-019-Q1-K1-H4

Method BLASTX NCBI GI g417073



BLAST score 255 E value 2.0e-22 Match length 86 % identity 57

NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)

>gi\_484529\_pir\_\_JQ1977 glutamate synthase (NADH) (EC
1.4.1.14) - alfalfa >gi\_166412 (L01660) NADH-glutamate

synthase [Medicago sativa]

Seq. No. 213398

Seq. ID LIB3146-019-Q1-K1-H9

Method BLASTX
NCBI GI g872116
BLAST score 621
E value 2.0e-65
Match length 145
% identity 35

NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 213399

Seq. ID LIB3146-020-Q1-K1-A11

Method BLASTX
NCBI GI g2499535
BLAST score 500
E value 1.0e-50
Match length 141
% identity 71

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >qi 595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 213400

Seq. ID LIB3146-020-Q1-K1-A2

Method BLASTX
NCBI GI g3023751
BLAST score 457
E value 7.0e-46
Match length 112
% identity 79

NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS

ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi\_1076772\_pir\_\_\$55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

>gi\_854626\_emb\_CAA60505 (X86903) peptidylprolyl isomerase

[Triticum aestīvum]

Seq. No. 213401

Seq. ID LIB3146-020-Q1-K1-A5

Method BLASTX
NCBI GI g2191165
BLAST score 161
E value 6.0e-11
Match length 60
% identity 50

NCBI Description (AF007270) A IG002P16.14 gene product [Arabidopsis

thaliana]

Seq. No. 213402



```
LIB3146-020-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3219271
BLAST score
                  434
                  3.0e-43
E value
Match length
                  103
% identity
                  83
                  (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213403
                  LIB3146-020-Q1-K1-B4
Seq. ID
Method
                  BLASTX
                  g125887
NCBI GI
BLAST score
                  215
E value
                  3.0e-17
Match length
                  117
                  43
% identity
NCBI Description
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                  >gi 82092 pir S04765 LAT52 protein precursor - tomato
                  >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
                  esculentum]
Seq. No.
                  213404
Seq. ID
                  LIB3146-020-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g4510346
BLAST score
                  369
E value
                  2.0e-35
Match length
                  99
                  74
% identity
NCBI Description
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  213405
                  LIB3146-020-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024386
BLAST score
                  530
E value
                  3.0e-54
Match length
                  139
% identity
                  65
NCBI Description
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
                  >gi 2129500 pir S52006 polygalacturonase - upland cotton
                  >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  213406
                  LIB3146-020-Q1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642153
BLAST score
                  381
                  9.0e-37
E value
Match length
                  96
                  77
% identity
```

(AC003000) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 2795810 (AC003674) unknown protein [Arabidopsis

thaliana]

Seq. No. 213407



```
LIB3146-020-Q1-K1-C12
Seq. ID
                   BLASTN
Method
                   q642263
NCBI GI
BLAST score
                   102
E value
                   3.0e-50
Match length
                   258
% identity
                   85
NCBI Description R.enysii ITS2 and 28S rRNA gene (partial)
Seq. No.
                   213408
                   LIB3146-020-Q1-K1-C2
Seq. ID
Method
                   BLASTX
                   g729442
NCBI GI
BLAST score
                   479
E value
                   3.0e-48
Match length
                   125
 % identity
                   75
                   PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR
NCBI Description
                   >qi 166380 (M80235) qlucose-regulated endoplasmic reticular
                   protein precursor [Medicago sativa]
Seq. No.
                   213409
Seq. ID
                   LIB3146-020-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   q4249382
BLAST score
                   602
 E value
                   1.0e-62
Match length
                   129
                   87
 % identity
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
 NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
 Seq. No.
                   213410
                   LIB3146-020-Q1-K1-C4
 Seq. ID
 Method
                   BLASTX
                   q1708292
 NCBI GI
 BLAST score
                   192
                   1.0e-14
 E value
 Match length
                   74
 % identity
                   46
                   HEAT-RESPONSIVE PROTEIN 12 >gi 1255116 (U50631)
 NCBI Description
                   heat-responsive protein [Mus musculus]
                   213411
 Seq. No.
                   LIB3146-020-Q1-K1-C7
 Seq. ID
 Method
                   BLASTX
                   g3386604
 NCBI GI
 BLAST score
                   605
 E value
                   5.0e-63
 Match length
                   144
 % identity
                   75
```

NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No. 213412

Seq. ID LIB3146-020-Q1-K1-C8

Method BLASTX

% identity

4

```
q2943792
NCBI GI
     BLAST score
                        673
     E value
                        5.0e-71
     Match length
                        139
     % identity
                        85
                        (AB006809) PV72 [Cucurbita sp.]
     NCBI Description
                        213413
     Seq. No.
                        LIB3146-020-Q1-K1-C9
     Seq. ID
     Method
                        BLASTX
     NCBI GI
                        g4091804
     BLAST score
                        268
     E value
                        2.0e-23
     Match length
                        130
      % identity
                        (AF052584) CONSTANS-like protein 1 [Malus domestica]
     NCBI Description
     Seq. No.
                        213414
     Seq. ID
                        LIB3146-020-Q1-K1-D1
     Method
                        BLASTX
     NCBI GI
                        g2961300
     BLAST score
                        606
     E value
                        4.0e-63
     Match length
                        126
                        93
      % identity
                        (AJ225027) ribosomal protein L24 [Cicer arietinum]
     NCBI Description
                        213415
      Seq. No.
      Seq. ID
                        LIB3146-020-Q1-K1-D10
     Method
                        BLASTX
                        g4001803
      NCBI GI
      BLAST score
                        202
                        8.0e-16
      E value
                        58
      Match length
                        62
      % identity
                        (AF041474) BAF53a [Homo sapiens] >gi_4218064_dbj_BAA74577_
      NCBI Description
                         (AB015907) actin-related protein [Homo sapiens]
                        213416
      Seq. No.
                        LIB3146-020-Q1-K1-D2
      Seq. ID
                        BLASTX
      Method
                        g3738332
      NCBI GI
      BLAST score
                        480
                        2.0e-48
      E value
                        141
      Match length
                        61
      % identity
                        (AC005170) putative eukaryotic initiation factor
      NCBI Description
                         [Arabidopsis thaliana]
                        213417
      Seq. No.
                        LIB3146-020-Q1-K1-D3
      Seq. ID
      Method
                        BLASTX
      NCBI GI
                        g4220445
                        208
      BLAST score
                        2.0e-16
      E value
      Match length
                        134
```



(AC006216) Similar to gi 3004555 F19F24.14 salt inducible NCBI Description protein homolog from Arabidopsis thaliana BAC gb\_AC003673. [Arabidopsis thaliana]

Seq. No. 213418

Seq. ID LIB3146-020-Q1-K1-D4

BLASTX Method q289920 NCBI GI 719 BLAST score 2.0e-76 E value Match length 133 100 % identity

(L07119) chlorophyll A/B binding protein [Gossypium NCBI Description

hirsutum]

Seq. No. 213419

LIB3146-020-Q1-K1-D5 Seq. ID

Method BLASTX NCBI GI q122085 BLAST score 546 4.0e-56 E value Match length 127 % identity

HISTONE H3 >qi 81641 pir S06250 histone H3 - Arabidopsis NCBI Description thaliana >gi 82482 pir S04099 histone H3 (variant H3R-21)

> - rice >gi 1362194 pir S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253\_emb\_CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa]  $>gi_168493$  (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays]

>qi 168497 (M13379) histone H3 [Zea mays] >gi\_168506

(M35388) histone H3 [Zea mays] >gi 169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi 169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi 886738 emb CAA59111 (X84377) histone 3 [Zea mays] >gi  $1\overline{0}40764$  (M35 $\overline{3}87$ ) histone H3

homolog [Brassica napus]  $\overline{gi}_1531754$  emb\_CAA57811 (X82414) Histone H3 [Asparagus officinalis]  $> \overline{gi}_1 \overline{1667592}$  (U $\overline{7}7296$ ) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to

[Arabidopsis thaliana] >qi\_1314779 (U54827) histone H3

histone H3 gene gb\_M17131 and gb\_M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb\_N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana] >gi 225459 prf 1303352A histone H3 [Helicoverpa zea]

>gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 213420

LIB3146-020-Q1-K1-D6 Seq. ID

Method BLASTX g4106696 NCBI GI BLAST score 270 9.0e-24 E value 67 Match length 79 % identity

NCBI Description (AB021872) ribosome-sedimenting protein [Pisum sativum]



```
3 , ,
                  213421
Seq. No.
                  LIB3146-020-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1200205
BLAST score
                  353
                  2.0e-33
E value
Match length
                  122
% identity
                  55
NCBI Description
                  (X95753) DAG [Antirrhinum majus]
Seq. No.
                  213422
Seq. ID
                  LIB3146-020-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2244993
                  358
BLAST score
                  5.0e-34
E value
                  135
Match length
                  55
% identity
                  (Z97341) similarity to AMP-activated protein kinase beta
NCBI Description
                  [Arabidopsis thaliana]
                  213423
Seq. No.
Seq. ID
                  LIB3146-020-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  235
                  1.0e-19
E value
Match length
                  48
% identity
                  88
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  213424
                  LIB3146-020-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459429
BLAST score
                  363
                  1.0e-34
E value
Match length
                  105
% identity
                  62
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                  213425
Seq. No.
Seq. ID
                  LIB3146-020-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q3618320
BLAST score
                  244
E value
                  1.0e-20
Match length
                  109
% identity
                  50
                  (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
Seq. No.
                  213426
```

Seq. ID

LIB3146-020-Q1-K1-E8

Method BLASTX NCBI GI g2760839

Seq. ID

Method



```
BLAST score
E value
                  7.0e-33
Match length
                  130
% identity
                  55
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213427
Seq. ID
                  LIB3146-020-Q1-K1-E9
Method
                  BLASTN
NCBI GI
                  g642263
BLAST score
                  55
E value
                  4.0e-22
Match length
                  67
% identity
                  97
NCBI Description R.enysii ITS2 and 28S rRNA gene (partial)
Seq. No.
                  213428
                  LIB3146-020-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82512
BLAST score
                  615
E value
                  4.0e-64
Match length
                  122
% identity
                  43
NCBI Description
                  ubiquitin precursor - rice (fragment)
                  >gi_218189_dbj_BAA02241 (D12776) poly-ubiquitin [Oryza
                  sativa]
Seq. No.
                  213429
Seq. ID
                  LIB3146-020-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q541979
BLAST score
                  162
E value
                  4.0e-11
Match length
                  46
% identity
                  72
NCBI Description
                  guanine nucleotide regulatory protein - fava bean
                  >gi_303744_dbj_BAA02113_ (D12545) GTP-binding protein
                  [Pisum sativum] >gi_452361 emb CAA82709 (Z29592) guanine
                  nucleotide regulatory protein [Vicia faba]
                  >gi 738937_prf__2001457E GTP-binding protein [Pisum
                  sativum] >gi 1098295_prf 2115367C small GTP-binding
                  protein [Vicia faba]
Seq. No.
                  213430
Seq. ID
                  LIB3146-020-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4490297
BLAST score
                  301
E value
                  2.0e-27
Match length
                  138
% identity
                  45
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  213431
```

29696

LIB3146-020-Q1-K1-F6

BLASTN

```
NCBI GI
                  q433664
BLAST score
                  42
E value
                  3.0e-14
Match length
                  136
                  87
% identity
NCBI Description A.thaliana for Sec61 beta-subunit homolog
Seq. No.
                  213432
Seq. ID
                  LIB3146-020-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  q1171579
BLAST score
                  569
E value
                  9.0e-59
Match length
                  135
% identity
                  79
NCBI Description
                  (X95342) cytochrome P450 [Nicotiana tabacum]
Seq. No.
                  213433
Seq. ID
                  LIB3146-020-Q1-K1-F8
Method
                  BLASTX
                  g4336692
NCBI GI
BLAST score
                  164
E value
                  3.0e-11
Match length
                  123
% identity
                  31
NCBI Description
                  (AF101361) Abnormal X segregation [Drosophila melanogaster]
Seq. No.
                  213434
Seq. ID
                  LIB3146-020-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1171579
BLAST score
                  376
                  2.0e-36
E value
Match length
                  89
% identity
                  76
NCBI Description
                  (X95342) cytochrome P450 [Nicotiana tabacum]
Seq. No.
                  213435
Seq. ID
                  LIB3146-020-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q123178
BLAST score
                  249
E value
                  3.0e-21
Match length
                  84
% identity
                  63
NCBI Description
                  HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH)
                  >gi_99844_pir__A39358 histidinol dehydrogenase (EC
                  1.1.1.23) precursor, chloroplast - cabbage >gi 167142
                  (M60466) histidinol dehydrogenase [Brassica oleracea]
Seq. No.
                  213436
```

Seq. ID LIB3146-020-Q1-K1-G5

Method BLASTX
NCBI GI g1171579
BLAST score 483
E value 9.0e-49
Match length 124



% identity 75

NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 213437

Seq. ID LIB3146-020-Q1-K1-G6

Method BLASTN
NCBI GI 9755147
BLAST score 263
E value 1.0e-146
Match length 316
% identity 97

NCBI Description Gossypium hirsutum vacuolar H+-ATPase proteolipid (16 kDa)

subunit (cva16-2) mRNA, complete cds

Seq. No. 213438

Seq. ID LIB3146-020-Q1-K1-G7

Method BLASTX
NCBI GI g2191165
BLAST score 246
E value 5.0e-21
Match length 78
% identity 67

NCBI Description (AF007270) A IG002P16.14 gene product [Arabidopsis

thaliana]

Seq. No. 213439

Seq. ID LIB3146-020-Q1-K1-G8

Method BLASTX
NCBI GI g3334138
BLAST score 192
E value 1.0e-14
Match length 75
% identity 53

NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin

[Glycine max]

Seq. No. 213440

Seq. ID LIB3146-020-Q1-K1-H1

Method BLASTX
NCBI GI 94204575
BLAST score 373
E value 8.0e-36
Match length 115
% identity 64

NCBI Description (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]

Seq. No. 213441

Seq. ID LIB3146-020-Q1-K1-H2

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 49
% identity 51

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 213442

Seq. ID

Method

NCBI GI

BLAST score

```
Seq. ID
                    LIB3146-020-Q1-K1-H3
  Method
                     BLASTX
  NCBI GI
                     q1345642
  BLAST score
                     321
  E value
                     8.0e-30
  Match length
                     127
                     49
  % identity
  NCBI Description
                     FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450
                     75A1) (CYPLXXVA1) >gi_629710_pir__S38985 flavonoid
                     3',5'-hydroxylase Hf1 - garden petunia
                     >gi 311656 emb CAA80266 (Z22545) flavonoid
                     3',5'-hydroxylase [Petunia x hybrida]
                     >gi 1853972 dbj BAA03438 (D14588)
                     flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi_3426337
                     (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida]
                     >gi 738772 prf 2001426B flavonoid 3',5'-hydroxylase
                     [Petunia x hybrida]
  Seq. No.
                     213443
  Seq. ID
                    LIB3146-020-Q1-K1-H4
  Method
                     BLASTX
  NCBI GI
                     g3746069
  BLAST score
                     147
                     2.0e-09
  E value
  Match length
                     97
  % identity
                     33
                     (AC005311) putative reverse transcriptase [Arabidopsis
  NCBI Description
                     thaliana]
  Seq. No.
                     213444
  Seq. ID
                     LIB3146-020-Q1-K1-H5
  Method
                     BLASTX
  NCBI GI
                     q3876642
                     256
  BLAST score
                     4.0e-22
  E value
  Match length
                     127
  % identity
                     (Z81526) predicted using Genefinder; cDNA EST EMBL:C09939
  NCBI Description
                     comes from this gene; cDNA EST EMBL:C12888 comes from this
                     gene; cDNA EST yk265g7.5 comes from this gene; cDNA EST
                     yk412g10.5 comes from this gene; cDNA EST yk224f7.5 co
  Seq. No.
                     213445
  Seq. ID
                     LIB3146-020-Q1-K1-H9
  Method
                     BLASTX
  NCBI GI
                     q99600
  BLAST score
                     440
  E value
                     9.0e-44
  Match length
                     87
                     95
  % identity
  NCBI Description chlorophyll a/b-binding protein - upland cotton
  Seq. No.
                     213446
```

29699

LIB3146-021-Q1-K1-A12

BLASTX

209

q1911765

```
E value
                     .0e-16
Match length
                   123
% identity
                   36
                   (S83359) iEP4=42.6-kda elicitor-induced glycoprotein/EP4
NCBI Description
                   homolog/ENOD8 homolog [carrots, Peptide, 391 aa] [Daucus
                   carota] >gi_4204870 (U56392) iEP4 [Daucus carota]
Seq. No.
                   213447
Seq. ID
                   LIB3146-021-Q1-K1-A3
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   6.0e-11
Match length
                   36
                   100
% identity
NCBI Description
                   Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   213448
                   LIB3146-021-Q1-K1-A7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   8.0e-11
Match length
                   36
% identity
                   100
NCBI Description
                   Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   213449
Seq. ID
                   LIB3146-021-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   q3056595
BLAST score
                   244
E value
                   5.0e-21
Match length
                   91
% identity
                   35
                   (AC004255) T1F9.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213450
Seq. ID
                   LIB3146-021-Q1-K1-B1
Method
                   BLASTN
NCBI GI
                   g2267138
BLAST score
                   45
E value
                   3.0e-16
Match length
                   97
% identity
                   87
NCBI Description
                   Prunus armeniaca ubiquitin-conjugating enzyme mRNA, partial
                   cds
Seq. No.
                   213451
```

Seq. ID LIB3146-021-Q1-K1-B10

Method BLASTX NCBI GI g3549667 BLAST score 204 E value 2.0e-16 Match length 58 % identity 72

NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2



## [Arabidopsis thaliana]

```
Seq. No.
                  213452
                  LIB3146-021-Q1-K1-B6
Seq. ID
Method
                  BLASTX
                  g2244904
NCBI GI
BLAST score
                  159
E value
                  4.0e-11
Match length
                  51
                  69
% identity
NCBI Description (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
                  [Arabidopsis thaliana]
Seq. No.
                  213453
Seq. ID
                  LIB3146-021-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3688123
BLAST score
                  430
E value
                  1.0e-42
Match length
                  102
% identity
                  79
                  (AJ006293) granule-bound starch synthase [Antirrhinum
NCBI Description
                  majus]
Seq. No.
                  213454
                  LIB3146-021-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1780757
BLAST score
                  286
                  1.0e-25
E value
Match length
                  69
% identity
                  74
NCBI Description (Y10291) highly expressed in proliferating cells
                  [Arabidopsis thaliana]
Seq. No.
                  213455
                  LIB3146-021-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100481
BLAST score
                  139
E value
                  9.0e-09
Match length
                  46
                  59
% identity
NCBI Description fill protein - garden snapdragon
Seq. No.
                  213456
                  LIB3146-021-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263779
BLAST score
                  389
E value
                  1.0e-37
Match length
                  131
% identity
NCBI Description
                  (AC006068) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  213457
                  LIB3146-021-Q1-K1-C6
Seq. ID
```



Method BLASTX
NCBI GI g3056595
BLAST score 376
E value 3.0e-36
Match length 131
% identity 30

NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No. 213458

Seq. ID LIB3146-021-Q1-K1-C7

Method BLASTX
NCBI GI g1771780
BLAST score 444
E value 4.0e-44
Match length 111
% identity 77

NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 213459

Seq. ID LIB3146-021-Q1-K1-C9

Method BLASTX
NCBI GI g116054
BLAST score 455
E value 1.0e-45
Match length 99
% identity 42

NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)

>gi\_280393\_pir\_\_A43713 calcium-dependent protein kinase (EC
2.7.1.-) - soybean >gi 169931 (M64987) Glycine max calcium

dependent protein kinase mRNA. [Glycine max]

Seq. No. 213460

Seq. ID LIB3146-021-Q1-K1-D4

Method BLASTX
NCBI GI g3924613
BLAST score 242
E value 1.0e-20
Match length 97
% identity 52

NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]

>gi 4263512 gb AAD15338 (AC004044) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 213461

Seq. ID LIB3146-021-Q1-K1-D5

Method BLASTX
NCBI GI g3334157
BLAST score 444
E value 3.0e-44
Match length 90
% identity 94

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi\_1220142\_emb\_CAA59468\_ (X85185) cyclophilin

[Catharanthus roseus]

Seq. No. 213462

NCBI Description



```
LIB3146-021-Q1-K1-D8
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g4432861
 BLAST score
                   167
 E value
                    9.0e-12
                   58
 Match length
 % identity
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   213463
                   LIB3146-021-Q1-K1-D9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g728744
 BLAST score
                    418
 E value
                    4.0e-41
 Match length
                    129
 % identity
                    65
                   AUXIN-INDUCED PROTEIN PCNT115 >gi 100305_pir__S16390
 NCBI Description
                    auxin-induced protein - common tobacco
                    >gi 19799 emb CAA39708 (X56267) auxin-induced protein
                    [Nicotiana tabacum]
 Seq. No.
                    213464
                    LIB3146-021-Q1-K1-E10
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2695860
 BLAST score
                    55
                    5.0e-22
 E value
 Match length
                    167
                    84
 % identity
 NCBI Description
                   Pisum sativum mRNA for
                    3-deoxy-D-manno-2-octulosonate-8-phosphate synthase, clone
                    pPS40
                    213465
 Seq. No.
                    LIB3146-021-Q1-K1-E11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3688174
 BLAST score
                    258
                    1.0e-28
 E value
 Match length
                    94
 % identity
                    66
                   (AL031804) putative protein [Arabidopsis thaliana]
 NCBI Description
                    213466
 Seq. No.
                    LIB3146-021-Q1-K1-E12
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1170747
 BLAST score
                    427
                    3.0e-42
 E value
Match length
                    95
 % identity
                    86
```

embryogenesis-abundant protein [Gossypium hirsutum]

hirsutum] >gi 167347 (M37697) Lea5-A late

LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345

(M88324) late embryogenesis-abundant protein [Gossypium



```
213467
Seq. No.
                  LIB3146-021-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q729668
BLAST score
                  338
                  8.0e-32
E value
                  103
Match length
% identity
                  71
                  HISTONE H1 >gi 2147479 pir_S65059 histone H1,
NCBI Description
                   drought-inducible - Lycopersicon pennellii >gi_436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                   213468
                   LIB3146-021-Q1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4322948
BLAST score
                   216
E value
                   1.0e-17
Match length
                   47
                   83
% identity
                  (AF097180) cystathionine gamma-synthase precursor
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   213469
                   LIB3146-021-Q1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3789911
BLAST score
                   262
E value
                   5.0e-23
Match length
                   102
                   47
% identity
                   (AF081802) developmental protein DG1118 [Dictyostelium
NCBI Description
                   discoideum]
                   213470
Seq. No.
                   LIB3146-021-Q1-K1-F2
Seq. ID
Method
                   BLASTN
                   g2062705
NCBI GI
BLAST score
                   37
                   2.0e-11
E value
Match length
                   50
                   40
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   213471
Seq. No.
                   LIB3146-021-Q1-K1-F9
Seq. ID
Method
                   BLASTX
                   g4309969
NCBI GI
BLAST score
                   540
                   2.0e-55
E value
                   130
Match length
% identity
                   73
                   (AC002983) putative phosphoglyceride transfer protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID LIB3146-021-Q1-K1-G1

29704

```
BLASTX
   Method
NCBI GI
                      g1703375
   BLAST score
                      482
                      1.0e-48
   E value
                      96
   Match length
                      98
    % identity
   NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483 dbj_BAA08259 (D45420)
                      DcARF1 [Daucus carota]
                      213473
    Seq. No.
                      LIB3146-021-Q1-K1-G10
    Seq. ID
    Method
                      BLASTX
                      g3800878
    NCBI GI
    BLAST score
                      455
                      2.0e-45
    E value
    Match length
                      113
    % identity
                      45
                      (AF096281) threonine dehydratase/deaminase [Arabidopsis
    NCBI Description
                      thaliana]
                      213474
    Seq. No.
                      LIB3146-021-Q1-K1-G12
    Seq. ID
                      BLASTX
    Method
                      g3122673
    NCBI GI
    BLAST score
                      336
                      1.0e-31
    E value
                      99
    Match length
                      69
    % identity
                      60S RIBOSOMAL PROTEIN L15 >gi 2245027_emb_CAB10447_
    NCBI Description
                      (Z97341) ribosomal protein [Arabidopsis thaliana]
    Seq. No.
                      213475
                      LIB3146-021-Q1-K1-G3
    Seq. ID
    Method
                      BLASTX
                      g3182981
    NCBI GI
    BLAST score
                      275
                      2.0e-24
    E value
    Match length
                      58
                      90
    % identity
                      CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj_BAA13096_
    NCBI Description
                      (D86494) diminuto [Pisum sativum]
                      213476
    Seq. No.
                      LIB3146-021-Q1-K1-G4
    Seq. ID
    Method
                      BLASTX
                      q1352821
    NCBI GI
                      546
    BLAST score
                      4.0e-56
    E value
    Match length
                      106
                      98
    % identity
    NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
```

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU

ribulose-bisphosphate carboxylase  $\overline{\text{(EC 4.1.1.39)}}$  small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026\_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 213477

29705



```
LIB3146-021-Q1-K1-G5
Seq. ID
                  BLASTX
Method
                  g4337175
NCBI GI
BLAST score
                  390
E value
                  5.0e-38
                  106
Match length
% identity
                  70
                   (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                   gb T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   213478
                  LIB3146-021-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3980393
BLAST score
                   356
E value
                   5.0e - 34
Match length
                   98
                   67
% identity
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thalianal
                   213479
Seq. No.
                   LIB3146-021-Q1-K1-G9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   9.0e-11
Match length
                   36
                   100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   213480
Seq. No.
                   LIB3146-021-Q1-K1-H10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2618599
                   39
BLAST score
                   1.0e-12
E value
Match length
                   59
% identity
                   92
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBD2, complete sequence [Arabidopsis thaliana]
                   213481
Seq. No.
                   LIB3146-021-Q1-K1-H11
Seq. ID
                   BLASTX
Method
                   g488571
NCBI GI
BLAST score
                   219
                   7.0e-18
E value
Match length
                   44
                   100
% identity
                  (U09462) histone H3.2 [Medicago sativa]
NCBI Description
```

Seq. ID LIB3146-021-Q1-K1-H2

Method BLASTX



```
a118490
NCBI GI-
                   455
BLAST score
                   2.0e-45
E value
                   123
Match length
% identity
                   68
                  BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
NCBI Description
                   >gi_99517_pir__S19135 betaine-aldehyde dehydrogenase (EC
                   1.2.1.8) precursor - beet >gi_17934_emb_CAA41377_ (X58463)
                  betaine aldehyd dehydrogenase [Beta vulgaris]
                   213483
Seq. No.
                  LIB3146-021-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   g556612
NCBI GI
BLAST score
                   161
                   3.0e-11
E value
                   37
Match length
                   86
% identity
                  (U14735) histone H3 [Plasmodium falciparum]
NCBI Description
Seq. No.
                   213484
                   LIB3146-021-Q1-K1-H7
Seq. ID
                   BLASTX
Method
                   g2660670
NCBI GI
                   559
BLAST score
                   1.0e-57
E value
                   125
Match length
% identity
                   88
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   213485
Seq. No.
                   LIB3146-022-Q1-K1-A1
Seq. ID
                   BLASTX
Method
                   g3281851
NCBI GI
                   178
BLAST score
                   1.0e-21
E value
                   81
Match length
% identity
                   67
                   (AL031004) RNA lariat debranching enzyme - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   213486
Seq. No.
                   LIB3146-022-Q1-K1-A11
Seq. ID
```

BLASTX Method NCBI GI g1906830 595 BLAST score 2.0e-62 E value 139 Match length 89 % identity

(Y11829) heat shock protein [Arabidopsis thaliana] NCBI Description

213487 Seq. No.

LIB3146-022-Q1-K1-A4 Seq. ID

Method BLASTX NCBI GI g2997591 158 BLAST score

```
1.0e-10
E value
Match length
% identity
                  (AF020814) glucose-6-phosphate/phosphate-translocator
NCBI Description
                  precursor [Pisum sativum]
                  213488
Seq. No.
                  LIB3146-022-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  g3334244
NCBI GI
BLAST score
                  627
                  1.0e-65
E value
Match length
                  143
% identity
                  81
                  LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
NCBI Description
                   (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                  >gi 2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica
                  juncea]
                  213489
Seq. No.
                  LIB3146-022-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g225267
BLAST score
                   173
                   8.0e-13
E value
                   90
Match length
                   43
% identity
NCBI Description ORF 1244 [Nicotiana tabacum]
                   213490
Seq. No.
                   LIB3146-022-Q1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3935167
BLAST score
                  513
E value
                   3.0e-52
Match length
                   119
                   86
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
                   213491
Seq. No.
                   LIB3146-022-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3421384
BLAST score
                   332
                   6.0e-40
E value
                   129
Match length
                   65
% identity
                   (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID LIB3146-022-Q1-K1-B10

Method BLASTX
NCBI GI g4512705
BLAST score 397
E value 7.0e-39



```
Match length
% identity
                   76
                   (AC006569) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  213493
Seq. No.
                  LIB3146-022-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  g303736
NCBI GI
BLAST score
                  303
                  1.0e-27
E value
                  100
Match length
                   63
% identity
                  (D12541) GTP-binding protein [Pisum sativum]
NCBI Description
                   >gi_738934_prf__2001457B GTP-binding protein [Pisum
                   sativum]
                   213494
Seq. No.
                  LIB3146-022-Q1-K1-B5
Seq. ID
                  BLASTN
Method
                  g12292
NCBI GI
                   239
BLAST score ·
                   1.0e-132
E value
                   395
Match length
% identity
                   90
                  Spinach chloroplast DNA homologous to ARS and ARC elements
NCBI Description
                   upstream of rDNA operon
                   213495
Seq. No.
                   LIB3146-022-Q1-K1-B6
Seq. ID
                   BLASTN
Method
                   g2326340
NCBI GI
BLAST score
                   34
E value
                   2.0e-09
                   74
Match length
                   86
% identity
NCBI Description A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
                   213496
Seq. No.
                   LIB3146-022-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2739168
BLAST score
                   302
E value
                   2.0e-27
Match length
                   115
% identity
                   (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   213497
                   LIB3146-022-Q1-K1-B9
Seq. ID
```

Method BLASTX
NCBI GI 9437327
BLAST score 613
E value 6.0e-64
Match length 138
% identity 79

29709

```
NCBI Description (L04497) MYB A; putative [Gossypium hirsutum]
                  213498
Seq. No.
                  LIB3146-022-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g3264769
NCBI GI
                  546
BLAST score
                  3.0e-56
E value
                  126
Match length
                  56
% identity
                  (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                  armeniaca]
```

Seq. ID LIB3146-022-Q1-K1-C11

Method BLASTX
NCBI GI g1184075
BLAST score 278
E value 1.0e-24
Match length 139
% identity 2

NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon

esculentum]

Seq. No. 213500

Seq. ID LIB3146-022-Q1-K1-C2

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 37
% identity 61

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 213501

Seq. ID LIB3146-022-Q1-K1-C4

Method BLASTX
NCBI GI g289920
BLAST score 525
E value 9.0e-54
Match length 100
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 213502

Seq. ID LIB3146-022-Q1-K1-C7

Method BLASTX
NCBI GI g2160160
BLAST score 215
E value 4.0e-22
Match length 87
% identity 59

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 213503

29710

% identity

NCBI Description

94

[Arabidopsis thaliana]

```
LIB3146-022-Q1-K1-C8
Seq. ID
Method
                  BLASTX
                  q2462671
NCBI GI
                  202
BLAST score
                  1.0e-15
E value
                  132
Match length
% identity
                  (Z98529) putative RNA-binding protein [Schizosaccharomyces
NCBI Description
                  pombe]
                  213504
Seq. No.
Seq. ID
                  LIB3146-022-Q1-K1-C9
Method
                  BLASTX
                  g1362093
NCBI GI
                  493
BLAST score
                  6.0e-50
E value
Match length
                  132
% identity
NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)
                  >gi 924632 (U20595) unknown [Solanum lycopersicum]
                  213505
Seq. No.
                  LIB3146-022-Q1-K1-D1
Seq. ID
Method
                  BLASTX
                  g1361979
NCBI GI
BLAST score
                  686
                  2.0e-72
E value
Match length
                  142
% identity
                  serine O-acetyltransferase (EC 2.3.1.30) - watermelon
NCBI Description
                  >gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase
                   [Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535)
                   serine acetyltransferase. [Citrullus lanatus]
                   >gi 2337772 dbj_BAA21827_ (AB006530) serine
                   acetyltransferase [Citrullus lanatus]
Seq. No.
                   213506
                   LIB3146-022-Q1-K1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1469929
BLAST score
                   139
                   2.0e-72
E value
                   159
Match length
                   97
% identity
                  Gossypium hirsutum fiber-specific acyl carrier protein
NCBI Description
                   (ACP1) mRNA, complete cds
Seq. No.
                   213507
                   LIB3146-022-Q1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567202
BLAST score
                   370
                   7.0e-36
E value
                   78
Match length
```

29711

(AC007168) putative myo-inositol 1-phosphate synthase

Seq. ID Method



```
213508
Seq. No.
                  LIB3146-022-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  q3023847
NCBI GI
                  146
BLAST score
                  6.0e-21
E value
Match length
                  67
                  84
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 2385376 emb_CAA69934_ (Y08678) G protein beta
                  subunit-like [Medicago sativa]
                  213509
Seq. No.
Seq. ID
                  LIB3146-022-Q1-K1-E11
Method
                  BLASTX
                  g3643607
NCBI GI
BLAST score
                  306
                  6.0e-28
E value
Match length
                  87
% identity
                  39
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                  213510
Seq. No.
                  LIB3146-022-Q1-K1-E12
Seq. ID
Method
                  BLASTN
                   g3821780
NCBI GI
BLAST score
                   37
                   1.0e-11
E value
                  48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   213511
Seq. No.
                   LIB3146-022-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g1663722
NCBI GI
                   449
BLAST score
                   1.0e-44
E value
                   141
Match length
                   59
% identity
                  (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
NCBI Description
                   213512
Seq. No.
                   LIB3146-022-Q1-K1-E5
Seq. ID
Method
                   BLASTX
                   g4185740
NCBI GI
                   494
BLAST score
                   5.0e-50
E value
Match length
                   138
% identity
                   (AF079999) putative glutamate receptor [Arabidopsis
NCBI Description
                   thaliana]
                   213513
 Seq. No.
```

29712

LIB3146-022-Q1-K1-E9

BLASTX

```
q4559330
NCBI GI
BLAST score
                  425
                  7.0e-42
E value
                  93
Match length
                  85
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
                  213514
Seq. No.
                  LIB3146-022-Q1-K1-F1
Seq. ID
Method
                  BLASTX
                  g282950
NCBI GI
                  238
BLAST score
E value
                  5.0e-20
Match length
                  66
                  59
% identity
                  protein 108 precursor - tomato >gi 19152 emb CAA78466_
NCBI Description
                   (Z14088) 108 protein [Lycopersicon esculentum]
Seq. No.
                  213515
                  LIB3146-022-Q1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4103635
BLAST score
                  175°
E value
                  1.0e-12
Match length
                  120
                   31
% identity
NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]
                   213516
Seq. No.
                  LIB3146-022-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g1353709
NCBI GI
                   259
BLAST score
E value
                   4.0e-23
                   69
Match length
% identity
                   71
                  (U42385) FIN16 gene product [Mus musculus]
NCBI Description
Seq. No.
                   213517
                   LIB3146-022-Q1-K1-F5
Seq. ID
Method
                   BLASTX
                   g3776005
NCBI GI
BLAST score
                   401
E value
                   4.0e-39
Match length
                   88
                   92
% identity
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
                   213518
Seq. No.
                   LIB3146-022-Q1-K1-F6
Seq. ID
                   BLASTX
Method
                   q2832677
NCBI GI
BLAST score
                   183
E value
                   1.0e-24
                   117
Match length
                   52
% identity
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]
```



```
213519
Seq. No.
Seq. ID
                  LIB3146-022-Q1-K1-F9
                  BLASTX
Method
NCBI GI
                  g2982322
                  535
BLAST score
                  8.0e-55
E value
                  120
Match length
% identity
                  82
NCBI Description (AF051246) probable proteasome subunit [Picea mariana]
Seq. No.
                  213520
                  LIB3146-022-Q1-K1-G1
Seq. ID
                  BLASTX
Method
                  q2665890
NCBI GI
                  185
BLAST score
                  2.0e-14
E value
Match length
                  47
                  72
% identity
                  (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                  ananassa]
Seq. No.
                  213521
                  LIB3146-022-Q1-K1-G11
Seq. ID
Method
                  BLASTX
                  q3860250
NCBI GI
BLAST score
                  596
E value
                  6.0e-62
Match length
                  131
% identity
                  89
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                  213522
Seq. No.
                  LIB3146-022-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  q3176677
NCBI GI
BLAST score
                   320
                   6.0e-30
E value
                   90
Match length
                   73
% identity
                   (AC003671) Similar to S. cerevisiae SIK1P protein,
NCBI Description
                  A TM021B04.13 from A. thaliana BAC gb_AF007271.
                   [Arabidopsis thaliana]
                   213523
Seq. No.
Seq. ID
                   LIB3146-022-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                   g629844
                   435
BLAST-score
                   3.0e-43
E value
                   101
Match length
                   84
% identity
                  heat shock protein hsp70-5 - maize (fragment)
NCBI Description
```

[Zea mays]

>gi\_498775\_emb\_CAA55184\_ (X78415) heat shock protein 70 kDa

Method NCBI GI



```
Seq. No.
                  213524
                  LIB3146-022-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g480672
                  284
BLAST score
E value
                   5.0e-26
                   67
Match length
                  79
% identity
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - spring
NCBI Description
                   vetch >gi 400532 emb CAA81211 (Z26252)
                  NADPH-ferrihemoprotein reductase [Vicia sativa]
Seq. No.
                   LIB3146-022-Q1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2662415
BLAST score
                   168
E value
                   9.0e-12
                   56
Match length
                   54
% identity
                  (U97494) metallothionein-like protein [Prunus armeniaca]
NCBI Description
Seq. No.
                   213526
Seq. ID
                   LIB3146-022-Q1-K1-H5
Method
                   BLASTX
                   q3659907
NCBI GI
                   403
BLAST score
                   3.0e-39
E value
Match length
                   111
                   76
% identity
                   (AF091857) protein translation factor SUI1 homolog
NCBI Description
                   [Pimpinella brachycarpa]
                   213527
Seq. No.
Seq. ID
                   LIB3146-022-Q1-K1-H7
Method
                   BLASTN
NCBI GI
                   q12216
BLAST score
                   88
E value
                   9.0e-42
Match length
                   146
                   93
% identity
                   Sinapis alba chloroplast rps16 gene
NCBI Description
Seq. No.
                   213528
                   LIB3146-022-Q1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2801536
BLAST score
                   419
                   4.0e-41
E value
                   125
Match length
% identity
                   63
                   (AF039531) lysophospholipase homolog [Oryza sativa]
NCBI Description
                   213529
Seq. No.
Seq. ID
                   LIB3146-023-Q1-K1-A10
                   BLASTX
```

g2144271

```
BLAST score
                  9.0e-22
E value
Match length
                  85
                  60
% identity
                  trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus
NCBI Description
                  kitakamiensis (fragment) >qi 1777372 dbj BAA11578 (D82814)
                  cinnamic acid 4-hydroxylase [Populus kitakamiensis]
                  213530
Seq. No.
                  LIB3146-023-Q1-K1-A11
Seq. ID
                  BLASTN
Method
                  g1217627
NCBI GI
                  305
BLAST score
                  1.0e-171
E value
                  374
Match length
                  94
% identity
                  G.hinsutum mRNA for stearoyl-acyl-carrier protein
NCBI Description
                  desaturase
                  213531
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-A2
Method
                  BLASTX
                  g2641242
NCBI GI
                  171
BLAST score
                  2.0e-12
E value
                  89
Match length
                   44
% identity
                   (AF031709) cystathionine gamma-lyase-like protein
NCBI Description
                   [Stenotrophomonas maltophilia]
                  213532
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-A3
                  BLASTX
Method
NCBI GI
                  g1171577
                  259
BLAST score
                  2.0e-22
E value
                  126
Match length
                   39
% identity
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]
                  213533
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-A4
                  BLASTX
Method
NCBI GI
                  g4580384
                  177
BLAST score
                   5.0e-13
E value
                   37
Match length
                   95
% identity
                  (AC007184) putative histone H2B [Arabidopsis thaliana]
NCBI Description
                   213534
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-A6
                   BLASTN
Method
                   g4376087
NCBI GI
BLAST score
                   33
E value
                   6.0e-09
```

93

Match length



% identity 84

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No. 213535

Seq. ID LIB3146-023-Q1-K1-A7

Method BLASTX
NCBI GI g3355473
BLAST score 319
E value 1.0e-29
Match length 102

% identity 66

NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213536

Seq. ID LIB3146-023-Q1-K1-A8

Method BLASTX
NCBI GI g2218152
BLAST score 591
E value 2.0e-61
Match length 115
% identity 90

NCBI Description (AF005279) type IIIa membrane protein cp-wap13 [Vigna

unguiculata]

Seq. No. 213537

Seq. ID LIB3146-023-Q1-K1-B11

Method BLASTX
NCBI GI g2558962
BLAST score 259
E value 2.0e-22
Match length 52
% identity 100

NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 213538

Seq. ID LIB3146-023-Q1-K1-B3

Method BLASTX
NCBI GI g3413170
BLAST score 228
E value 8.0e-19
Match length 82
% identity 60

NCBI Description (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]

Seq. No. 213539

Seq. ID LIB3146-023-Q1-K1-B4

Method BLASTN
NCBI GI 94539353
BLAST score 34
E value 2.0e-09
Match length 62
% identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F25I24

(ESSA project)

Seq. No. 213540

```
LIB3146-023-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g2218152
NCBI GI
                   630
BLAST score
                   6.0e-66
E value
Match length
                   141
                   81
% identity
                   (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                  unguiculata]
                   213541
Seq. No.
                  LIB3146-023-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                   q2129721
NCBI GI
BLAST score
                   181
                   3.0e-13
E value
Match length
                   109
% identity
                   44
                  ribosomal protein S15 - Arabidopsis thaliana
NCBI Description
                   >gi 1107485 emb CAA63028 (X91962) 40S ribosomal protein
                   S15 [Arabidopsis thaliana]
Seq. No.
                   213542
                   LIB3146-023-Q1-K1-C10
Seq. ID
Method
                   BLASTX
                   g3953471
NCBI GI
                   528
BLAST score
E value
                   5.0e-54
                   142
Match length
                   65
% identity
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213543
                   LIB3146-023-Q1-K1-C11
Seq. ID
Method
                   BLASTX
                   g1173043
NCBI GI
BLAST score
                   251
                   2.0e-21
E value
                   69
Match length
                   75
% identity
                   60S RIBOSOMAL PROTEIN L38 >gi_479441_pir__S33899 ribosomal
NCBI Description
                   protein L38 - tomato (cv. Moneymaker)
                   >gi 313027 emb CAA49599 (X69979) ribosomal protein L38
                   [Lycopersicon esculentum]
                   213544
Seq. No.
                   LIB3146-023-Q1-K1-C6
Seq. ID
                   BLASTX
Method
                   q1483563
NCBI GI
                   362
BLAST score
                   2.0e-34
E value
                   106
Match length
                   63
% identity
                   (X99825) leucine aminopeptidase [Petroselinum crispum]
NCBI Description
                   213545
Seq. No.
                   LIB3146-023-Q1-K1-C8
Seq. ID
```



```
BLASTX
Method
                  g2244914
NCBI GI
BLAST score
                  208
                  1.0e-16
E value
                  102
Match length
                  53
% identity
                  (Z97339) similarity to probable splicing factor Ceprp21
NCBI Description
                  [Arabidopsis thaliana]
                  213546
Seq. No.
                  LIB3146-023-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g2244749
NCBI GI
                  208
BLAST score
                  2.0e-16
E value
                  51
Match length
                  75
% identity
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                  213547
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-D12
Method
                  BLASTX
                  g3851001
NCBI GI
                  620
BLAST score
                  9.0e-65
E value
                  135
Match length
                  91
% identity
                   (AF069909) pyruvate dehydrogenase El beta subunit isoform 2
NCBI Description
                   [Zea mays]
                  213548
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-D2
Method
                  BLASTX
                  g1172811
NCBI GI
                   659
BLAST score
                   2.0e-69
E value
Match length
                  126
                   96
% identity
                  60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                   >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
                   - rice >gi 575355 emb CAA57339 (X81691) putative tumor
                   suppresser [Oryza sativa]
Seq. No.
                   213549
Seq. ID
                   LIB3146-023-Q1-K1-D3
                   BLASTX
Method
NCBI GI
                   g2065531
BLAST score
                   436
                   2.0e-43
E value
```

112 Match length % identity 71

(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] NCBI Description

Seq. No. 213550

Seq. ID LIB3146-023-Q1-K1-D7

Method BLASTX NCBI GI q1086147



```
BLAST score
                  7.0e-39
E value
Match length
                  111
                  63
% identity
                  protein S2 - Phalaris coerulescens >gi_556833_emb_CAA57520_
NCBI Description
                   (X81992) S2 [Phalaris coerulescens]
Seq. No.
                  213551
                  LIB3146-023-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g416650
BLAST score
                  425
                   6.0e-42
E value
                   134
Match length
                   60
% identity
                   PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
NCBI Description
                   PGNT35/PCNT111) >gi_100304_pir__S16268 auxin-induced
                   protein (clone pGNT35) - common tobacco
                   >gi 19797 emb CAA39706 (X56265) auxin-induced protein
                   [Nicotiana tabacum] >gi_19801_emb_CAA39710_ (X56269)
                   auxin-induced protein [Nicotiana Tabacum]
Seq. No.
                   213552
                   LIB3146-023-Q1-K1-E11
Seq. ID
                   BLASTX
Method
                   q3482918
NCBI GI
                   616
BLAST score
                   3.0e-64
E value
Match length
                   141
                   83
% identity
                   (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   213553
Seq. No.
                   LIB3146-023-Q1-K1-E12
Seq. ID
                   BLASTX
Method
                   q584794
NCBI GI
                   538
BLAST score
                   3.0e-55
E value
                   135
Match length
                   78
% identity
                   PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                   >gi 282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35)
                   - curled-leaved tobacco >gi 170289 (M80489) plasma membrane
                   H+ ATPase [Nicotiana plumbaginifolia]
Seq. No.
                   213554
                   LIB3146-023-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   q3947719
NCBI GI
BLAST score
                   249
```

Method BLASIX
NCBI GI g3947719
BLAST score 249
E value 3.0e-21
Match length 53
% identity 92

NCBI Description (AJ012653) ribosomal protein S28 [Prunus persica]

>gi\_3947721\_emb\_CAA10102 (AJ012654) ribosomal protein S28

[Prunus persica] >gi\_3947723\_emb\_CAA10103\_ (AJ012655)





## ribosomal protein S28 [Prunus persica]

```
213555
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g131770
BLAST score
                  395
                  2.0e-38
E value
                  108
Match length
                  67
% identity
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                  (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >qi 7353 emb CAA29844 (X06636) rp1024 protein
                   [Dictyostelium discoideum]
                  213556
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-F1
                  BLASTX
Method
                  g2911073
NCBI GI
                  158
BLAST score
                  3.0e-11
E value
Match length
                  49
% identity
                   65
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                  213557
Seq. No.
                   LIB3146-023-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2970051
BLAST score
                   434
                   6.0e-43
E value
Match length
                   114
% identity
                   73
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                   213558
                   LIB3146-023-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   g4204265
NCBI GI
                   190
BLAST score
                   2.0e-14
E value
                   57
Match length
% identity
                   63
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
                   213559
Seq. No.
                   LIB3146-023-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g3413511
NCBI GI
                   520
BLAST score
                   3.0e-53
E value
Match length
                   104
                   92
% identity
                  (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
```

oleracea]



```
Seq. No.
                  213560
                  LIB3146-023-Q1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4406805
BLAST score
                  41
                  1.0e-13
E value
Match length
                  93
                  86
% identity
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213561
                  LIB3146-023-Q1-K1-F8
Seq. ID
                  BLASTX
Method
                  q100481
NCBI GI
                  227
BLAST score
                  1.0e-18
E value
Match length
                  69
% identity
                  61
NCBI Description fill protein - garden snapdragon
                  213562
Seq. No.
Seq. ID
                  LIB3146-023-Q1-K1-G12
Method
                  BLASTX
                   q2500378
NCBI GI
                   348
BLAST score
                   7.0e-33
E value
                   90
Match length
                   76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
                   213563
Seq. No.
                   LIB3146-023-Q1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2507281
BLAST score
                   510
E value
                   6.0e-52
Match length
                   101
                   94
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
NCBI Description
                   (X97380) atran2 [Arabidopsis thaliana]
                   213564
Seq. No.
Seq. ID
                   LIB3146-023-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   g2281115
BLAST score
                   271
                   5.0e-24
E value
                   95
Match length
                   75
% identity
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
```

thaliana]

213565 Seq. No.

Seq. ID LIB3146-023-Q1-K1-H1

BLASTX Method g2507281 NCBI GI

29722



```
BLAST score
                  2.0e-24
E value
                  54
Match length
                  96
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706 emb_CAA66048_
NCBI Description
                  (X97380) atran2 [Arabidopsis thaliana]
                  213566
Seq. No.
                  LIB3146-023-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q445613
BLAST score
                  154
                  2.0e-10
E value
                  55
Match length
                  62
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
                  213567
Seq. No.
                  LIB3146-023-Q1-K1-H2
Seq. ID
                  BLASTX
Method
                  g2281115
NCBI GI
                  145
BLAST score
E value
                  1.0e-09
Match length
                  38
% identity
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                  thaliana]
                  213568
Seq. No.
                  LIB3146-023-Q1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2981131
BLAST score
                   535
                   8.0e-55
E value
                   125
Match length
% identity
                   85
                   (AF052570) AGAMOUS homolog [Populus balsamifera subsp.
NCBI Description
                   trichocarpa]
                   213569
Seq. No.
                   LIB3146-023-Q1-K1-H5
Seq. ID
Method
                   BLASTX
                   g629735
NCBI GI
                   236
BLAST score
                   9.0e-20
E value
                   71
Match length
% identity
                   63
                  fill protein - garden snapdragon >gi_406309_emb_CAA40553_
NCBI Description
                   (X57296) FIL1 [Antirrhinum majus]
                   213570
Seq. No.
                   LIB3146-023-Q1-K1-H8
Seq. ID
```

29723

BLASTX

191

54

g1710008

7.0e-15

Method

NCBI GI

E value

BLAST score

Match length



```
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN1B >gi_1370205 emb_CAA98188
NCBI Description
                   (Z73960) RAN1B [Lotus japonicus]
                   213571
Seq. No.
                  LIB3146-023-Q1-K1-H9
Seq. ID
Method
                  BLASTX
                   q1431629
NCBI GI
                   475
BLAST score
E value
                   9.0e-48
Match length
                   138
                   63
% identity
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                   213572
Seq. No.
                   LIB3146-024-Q1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2565305
                   717
BLAST score
E value
                   4.0e-76
                   144
Match length
                   93
% identity
                  (AF024589) glycine decarboxylase P subunit [Hordeum sp. x
NCBI Description
                   Triticum sp.]
                   213573
Seq. No.
                   LIB3146-024-Q1-K1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3608485
                   623
BLAST score
                   3.0e-69
E value
                   138
Match length
% identity
                  (AF088915) proteasome beta subunit [Petunia x hybrida]
NCBI Description
Seq. No.
                   213574
                   LIB3146-024-Q1-K1-A3
Seq. ID
Method
                   BLASTX
                   g4138265
NCBI GI
BLAST score
                   192
                   6.0e-15
E value
Match length
                   42
                   71
 % identity
                   (AJ006228) Avr9 elicitor response protein [Nicotiana
NCBI Description
                   tabacum]
                   213575
 Seq. No.
                   LIB3146-024-Q1-K1-A4
 Seq. ID
                   BLASTX
 Method
                   q139780
 NCBI GI
                   158
 BLAST score
                   1.0e-10
 E value
                   53
Match length
                   66
 % identity
 NCBI Description WOUND-INDUCED PROTEIN 1 >gi_82293_pir__JQ0398 wun1 protein
```

- potato



Seq. ID LIB3146-024-Q1-K1-A5

Method BLASTX
NCBI GI g2108252
BLAST score 272
E value 6.0e-24
Match length 140
% identity 25

NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]

>gi\_2108254\_emb\_CAA71276\_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi\_4538925\_emb\_CAB39661.1\_

(ALO49483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 213577

Seq. ID LIB3146-024-Q1-K1-A7

Method BLASTX
NCBI GI g464707
BLAST score 616
E value 3.0e-64
Match length 125
% identity 95

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi\_480908\_pir\_\_S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910 emb\_CAB39647.1\_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 213578

Seq. ID LIB3146-024-Q1-K1-A8

Method BLASTX
NCBI GI g2244778
BLAST score 227
E value 1.0e-18
Match length 74
% identity 69

NCBI Description (297335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213579

Seq. ID LIB3146-024-Q1-K1-A9

Method BLASTX
NCBI GI g543565
BLAST score 288
E value 7.0e-26
Match length 90
% identity 58

NCBI Description hypothetical 10.0K protein - Zinnia elegans

>gi\_493721\_dbj\_BAA06462\_ (D30802) TED4 [Zinnia elegans]



89

thaliana]

% identity

NCBI Description



>gi\_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

213580 Seq. No. LIB3146-024-Q1-K1-B11 Seq. ID Method BLASTX NCBI GI g3024020 BLAST score 650 3.0e-68 E value Match length 128 % identity 95 INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) NCBI Description >gi\_2225881\_dbj\_BAA20877\_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum] Seq. No. 213581 Seq. ID LIB3146-024-Q1-K1-B2 Method BLASTX NCBI GI g1653655 BLAST score 296 8.0e-27 E value 132 Match length % identity (D90915) ATP-dependent Clp protease proteolytic subunit NCBI Description [Synechocystis sp.] 213582 Seq. No. Seq. ID LIB3146-024-Q1-K1-B3 Method BLASTX NCBI GI g2464852 BLAST score 228 8.0e-19 E value Match length 140 % identity 43 NCBI Description (Z99707) putative protein [Arabidopsis thaliana] 213583 Seq. No. LIB3146-024-Q1-K1-B4 Seq. ID Method BLASTX g2924792 NCBI GI BLAST score 570 7.0e-59 E value Match length 129 % identity 84 (AC002334) similar to synaptobrevin [Arabidopsis thaliana] NCBI Description Seq. No. 213584 Seq. ID LIB3146-024-Q1-K1-B8 Method BLASTX g2392895 NCBI GI BLAST score 607 3.0e-63 E value 130 Match length

(AF017056) brassinosteroid insensitive 1 [Arabidopsis

```
Seq. No.
                  LIB3146-024-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  q2213608
NCBI GI
                  196
BLAST score
                  5.0e-15
E value
                  129
Match length
                  46
% identity
NCBI Description (AC000103) F21J9.2 [Arabidopsis thaliana]
                  213586
Seq. No.
                  LIB3146-024-Q1-K1-C10
Seq. ID
                  BLASTX
Method
                  g2673917
NCBI GI
BLAST score
                  603
                  9.0e-63
E value
                  144
Match length
                  42
% identity
                  (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
                  213587
Seq. No.
                  LIB3146-024-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                  g1168728
NCBI GI
                  312
BLAST score
                  1.0e-28
E value
                   65
Match length
                   92
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)
NCBI Description
                  cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
                   213588
Seq. No.
                   LIB3146-024-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2911076
BLAST score
                   216
E value
                   2.0e-17
                   99
Match length
                   44
% identity
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
                   213589
Seq. No.
                   LIB3146-024-Q1-K1-C4
Seq. ID
Method
                   BLASTX
                   q586339
NCBI GI
BLAST score
                   157
                   2.0e-10
E value
Match length
                   65
```

40 % identity

PEROXISOMAL-COENZYME A SYNTHETASE >gi\_626794\_pir\_\_S46098 NCBI Description

probable AMP-binding protein - yeast (Saccharomyces

cerevisiae) >gi\_536615\_emb\_CAA85185\_ (Z36091) ORF YBR222c

[Saccharomyces cerevisiae]

213590 Seq. No.

LIB3146-024-Q1-K1-C5 Seq. ID



```
Method
NCBI GI
                    q549063
                    418
BLAST score
E value
                    4.0e-41
Match length
                    91
                    85
% identity
                    TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                    >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                    factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
                    213591
Seq. No.
Seq. ID
                    LIB3146-024-Q1-K1-C6
Method
                    BLASTX
                    g122007
NCBI GI
                    287
BLAST score
                    9.0e-26
E value
Match length
                    79
% identity
                    73
                    <code>HISTONE H2A >gi_100161_pir__S11498</code> histone <code>H2A - parsley >gi_20448_emb_CAA37828_</code> (X53831) <code>H2A</code> histone protein (AA 1
NCBI Description
                    - 149) [Petroselinum crispum]
Seq. No.
                    213592
                    LIB3146-024-Q1-K1-C8
Seq. ID
Method
                    BLASTX
                    g4572674
NCBI GI
BLAST score
                    422
                    2.0e-43
E value
Match length
                    146
                    66
% identity
NCBI Description
                    (AC006954) unknown protein [Arabidopsis thaliana]
                    213593
Seq. No.
                    LIB3146-024-Q1-K1-C9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4572674
                     359
BLAST score
                     3.0e-34
E value
Match length
                     123
% identity
                    (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                    213594
Seq. No.
Seq. ID
                    LIB3146-024-Q1-K1-D1
Method
                    BLASTX
                     g3021485
NCBI GI
BLAST score
                     292
E value
                     2.0e-26
Match length
                     60
% identity
                     100
                    (AJ224932) histone H2B-3 [Lycopersicon esculentum]
NCBI Description
```

Seq. ID LIB3146-024-Q1-K1-D11

Method BLASTX NCBI GI g3482924



BLAST score 357
E value 6.0e-34
Match length 128
% identity 60

NCBI Description (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi\_1143445 [Arabidopsis thaliana]

Seq. No. 213596

Seq. ID LIB3146-024-Q1-K1-D2

Method BLASTX
NCBI GI g3292830
BLAST score 372
E value 1.0e-35
Match length 99
% identity 73

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 213597

Seq. ID LIB3146-024-Q1-K1-D3

Method BLASTX
NCBI GI g1168607
BLAST score 384
E value 5.0e-40
Match length 106
% identity 77

NCBI Description AUXIN-INDUCED PROTEIN AUX2-11 >gi\_16197\_emb\_CAA37526

(X53435) Aux2-11 protein [Arabidopsis thaliana] >gi\_454285 (L15450) auxin-responsive protein [Arabidopsis thaliana]

Seq. No. 213598

Seq. ID LIB3146-024-Q1-K1-D4

Method BLASTX
NCBI GI g2190550
BLAST score 457
E value 2.0e-51
Match length 146
% identity 73

NCBI Description (AC001229) ESTs gb\_T45673,gb\_N37512 come from this gene.

[Arabidopsis thaliana]

Seq. No. 213599

Seq. ID LIB3146-024-Q1-K1-D9

Method BLASTX
NCBI GI g1777312
BLAST score 274
E value 3.0e-24
Match length 114
% identity 52

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 213600

Seq. ID LIB3146-024-Q1-K1-E1

Method BLASTX
NCBI GI g3281846
BLAST score 188
E value 2.0e-14



Match length % identity 48

(AJ006404) late elongated hypocotyl [Arabidopsis thaliana] NCBI Description

213601 Seq. No.

LIB3146-024-Q1-K1-E11 Seq. ID

BLASTX Method NCBI GI g1001263 BLAST score 349 3.0e-36 E value 128 Match length % identity 62

NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

213602 Seq. No.

Seq. ID LIB3146-024-Q1-K1-E12

Method BLASTX g4406821 NCBI GI BLAST score 305 7.0e-28 E value 73 Match length % identity 79

(AC006201) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 213603

LIB3146-024-Q1-K1-E2 Seq. ID

Method BLASTX NCBI GI g122085 BLAST score 390 3.0e-46 E value Match length 119 % identity 82

NCBI Description HISTONE H3 >gi 81641 pir S06250 histone H3 - Arabidopsis thaliana >gi 82482 pir S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays] >qi 168497 (M13379) histone H3 [Zea mays] >qi 168506 (M35388) histone H3 [Zea mays] >gi 169655 (M77493) histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3 [Petroselinum crispum] >gi 169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi 387567 (M17131) histone H3 [Arabidopsis thaliana] >gi 886738 emb CAA59111 (X84377) histone 3 [Zea mays] >gi  $1\overline{0}40764$  (M35 $\overline{3}87$ ) histone H3 [Arabidopsis thaliana]  $>\overline{g}i_1314779$  (U54827) histone H3 homolog [Brassica napus] >gi 1531754 emb CAA57811 (X82414) Histone H3 [Asparagus officinalis] >gi\_1667592 (U77296) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb\_N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi 225459 prf 1303352A histone H3 [Helicoverpa zea] >gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]



```
213604
Seq. No.
                  LIB3146-024-Q1-K1-E3
Seq. ID
Method
                  BLASTX
                  g4104242
NCBI GI
BLAST score
                  220
                  7.0e-18
E value
                  67
Match length
                  72
% identity
                   (AF034266) palmitoyl-acyl carrier protein thioesterase
NCBI Description
                   [Gossypium hirsutum]
Seq. No.
                  213605
                  LIB3146-024-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706369
                  156
BLAST score
E value
                  2.0e-10
Match length
                  117
                  31
% identity
                  DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
NCBI Description
                   4-REDUCTASE) >gi 1066451_emb_CAA91922_ (Z67981)
                  dihydroflavonol 4-reductase [Callistephus chinensis]
Seq. No.
                   213606
                  LIB3146-024-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g950299
BLAST score
                   539
E value
                   2.0e-55
Match length
                   113
                   88
% identity
                   (L46792) xyloglucan endotransglycosylase precursor
NCBI Description
                   [Actinidia deliciosa]
Seq. No.
                   213607
                   LIB3146-024-Q1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2367392
                   228
BLAST score
                   8.0e-19
E value
                   89
Match length
                   51
% identity
                   (U82513) random slug cDNA25 protein [Dictyostelium
NCBI Description
                   discoideum]
                   213608
Seq. No.
Seq. ID
                   LIB3146-024-Q1-K1-F10
                   BLASTX
Method
                   g3080393
NCBI GI
                   139
BLAST score
                   1.0e-08
E value
```

44 Match length % identity

(AL022603) NADH dehydrogenase like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 213609

```
LIB3146-024-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g584706
NCBI GI
                   654
BLAST score
                   9.0e-69
E value
                   138
Match length
% identity
                   ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                   >gi_2130066_pir__JC5124 aspartate transaminase (EC
                   2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
                   (D14673) aspartate aminotransferase [Oryza sativa]
Seq. No.
                   213610
                   LIB3146-024-Q1-K1-F2
Seq. ID
Method
                   BLASTX
                   g1346156
NCBI GI
BLAST score
                   564
E value
                   3.0e-58
                   125
Match length
                   83
% identity
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 2 PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481943 pir_S40213 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                   >gi_437997_emb_CAA81079_ (Z25860) glycine
hydroxymethyltransferase [Flaveria pringlei]
                   213611
Seq. No.
                   LIB3146-024-Q1-K1-F9
Seq. ID
Method
                   BLASTX
                   g4371285
NCBI GI
                   589
BLAST score
                   4.0e-61
E value
Match length
                   141
                   77
% identity
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   213612
Seq. No.
                   LIB3146-024-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   g4567250
NCBI GI
                    262
BLAST score
                   8.0e-23
E value
                   88
Match length
                    53
 % identity
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
                    213613
 Seq. No.
```

Seq. ID LIB3146-024-Q1-K1-G10

Method BLASTX
NCBI GI 94580384
BLAST score 124
E value 2.0e-14
Match length 61
% identity 70

NCBI Description (AC007184) putative histone H2B [Arabidopsis thaliana]

E value

2.0e-14



```
Seq. No.
                   213614
                  LIB3146-024-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g2642158
NCBI GI
                   259
BLAST score
E value
                   2.0e-22
Match length
                  72
                   68
% identity
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213615
                   LIB3146-024-Q1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3269284
BLAST score
                   423
E value
                   1.0e-41
Match length
                   124
% identity
                   70
                  (AL030978) histone H2A- like protein [Arabidopsis thaliana]
NCBI Description
                   213616
Seq. No.
Seq. ID
                   LIB3146-024-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4580394
BLAST score
                   468
E value
                   6.0e-47
Match length
                   145
                   61
% identity
                   (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                   thaliana]
                   213617
Seq. No.
                   LIB3146-024-Q1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4580384
                   364
BLAST score
                   9.0e-35
E value
Match length
                   75
                   97
% identity
                   (AC007184) putative histone H2B [Arabidopsis thaliana]
NCBI Description
                   213618
Seq. No.
Seq. ID
                   LIB3146-024-Q1-K1-H2
                   BLASTX
Method
                   g3063396
NCBI GI
                   451
BLAST score
                   3.0e-50
E value
Match length
                   118
                   82
% identity
                  (AB012947) vcCyP [Vicia faba]
NCBI Description
                   213619
Seq. No.
Seq. ID
                   LIB3146-024-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   g470340
BLAST score
                   190
```



Match length 127 % identity 38

NCBI Description (U00043) similar to beta-mannosyltransferase

[Caenorhabditis elegans]

Seq. No. 213620

Seq. ID LIB3146-024-Q1-K1-H6

Method BLASTX
NCBI GI g729671
BLAST score 171
E value 9.0e-26
Match length 106
% identity 69

NCBI Description HISTONE H2A >gi\_473603 (U08225) histone H2A [Zea mays]

Seq. No. 213621

Seq. ID LIB3146-024-Q1-K1-H7

Method BLASTX
NCBI GI g3434975
BLAST score 441
E value 9.0e-44
Match length 119
% identity 76

NCBI Description (AB008107) ethylene responsive element binding factor 5

[Arabidopsis thaliana]

Seq. No. 213622

Seq. ID LIB3146-024-Q1-K1-H8

Method BLASTX
NCBI GI g3860247
BLAST score 430
E value 2.0e-42
Match length 90
% identity 89

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 213623

Seq. ID LIB3146-024-Q1-K1-H9

Method BLASTX
NCBI GI g3204101
BLAST score 144
E value 6.0e-09
Match length 108
% identity 31

NCBI Description (AJ006760) hypothetical protein [Cicer arietinum]

Seq. No. 213624

Seq. ID LIB3146-025-Q1-K1-A1

Method BLASTX
NCBI GI g3738285
BLAST score 168
E value 8.0e-12
Match length 47
% identity 66

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 213625



```
LIB3146-025-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g3851636
NCBI GI
                   438
BLAST score
                   2.0e-43
E value
                   100
Match length
                   82
% identity
                   (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   213626
Seq. No.
                   LIB3146-025-Q1-K1-A12
Seq. ID
Method
                   BLASTX
                   q2352492
NCBI GI
                   379
BLAST score
                   1.0e-36
E value
Match length
                   131
% identity
                   60
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
Seq. No.
                   213627
                   LIB3146-025-Q1-K1-A2
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   37
E value
                   3.0e-11
                   37
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   213628
Seq. No.
                   LIB3146-025-Q1-K1-A4
Seq. ID
Method
                   BLASTX
                   g2688824
NCBI GI
                   253
BLAST score
                   4.0e-22
E value
Match length
                   67
                   73
% identity
                   (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
                   213629
Seq. No.
Seq. ID
                   LIB3146-025-Q1-K1-A5
                   BLASTX
Method
                   g3738285
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
                   47
Match length
                   89
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   213630
Seq. No.
Seq. ID
                   LIB3146-025-Q1-K1-A6
```

29735

BLASTX

q2661840

Method NCBI GI

```
BLAST score
                  4.0e-46
E value
                  143
Match length
                  62
% identity
                  (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
Seq. No.
                  213631
                  LIB3146-025-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729275
BLAST score
                  146
E value
                  4.0e-09
Match length
                  59
                  46
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (PPIASE C) (ROTAMASE
NCBI Description
                  C) (PARVULIN) >gi 1084110 pir S48658 parvulin -
                  Escherichia coli >gi 693800 bbs 156242 (S73874) parvulin,
                  peptidyl- prolyl cis/trans isomerase, PPIase [Escherichia
                  coli, K-12 HB101, Peptide, 93 aa] [Escherichia coli]
                  >qi 836657 (M87049) peptidyl-prolyl cis-trans isomerase C
                   [Escherichia coli] >gi 1790211 (AE000454) peptidyl-prolyl
                  cis-trans isomerase C (rotamase C) [Escherichia coli]
Seq. No.
                  213632
                  LIB3146-025-Q1-K1-A8
Seq. ID
                  BLASTX
Method
                  q3721926
NCBI GI
                   356
BLAST score
E value
                   3.0e-34
                   84
Match length
                   87
% identity
                  (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
NCBI Description
Seq. No.
                   213633
                  LIB3146-025-Q1-K1-B12
Seq. ID
Method
                   BLASTX
                   g3550661
NCBI GI
BLAST score
                   466
                   9.0e-47
E value
                   117
Match length
% identity
                   40
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
NCBI Description
                   tuberosum]
                   213634
Seq. No.
Seq. ID
                   LIB3146-025-Q1-K1-B5
Method
                   BLASTN
NCBI GI
                   g2558961
BLAST score
                   37
                   2.0e-11
E value
```

109 Match length 84 % identity

NCBI Description Gossypium hirsutum histone H2B1 mRNA, complete cds

213635 Seq. No.

LIB3146-025-Q1-K1-B7 Seq. ID

BLASTX Method



```
q1076668
NCBI GI
BLAST score
                  363
                  6.0e-35
E value
Match length
                  92
                   80
% identity
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >qi 639834 emb CAA58823 (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   213636
Seq. No.
                  LIB3146-025-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245077
                   692
BLAST score
                   3.0e-73
E value
                   148
Match length
                   85
% identity
                  (Z97343) glucanase homolog [Arabidopsis thaliana]
NCBI Description
                   213637
Seq. No.
                   LIB3146-025-Q1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076668
BLAST score
                   758
E value
                   6.0e-81
                 _<u>~</u>147
Match length
% identity
                   NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   213638
Seq. No.
Seq. ID
                   LIB3146-025-Q1-K1-C11
Method
                   BLASTX
                   g3150415
NCBI GI
                   593
BLAST score
                   1.0e-61
E value
                   128
Match length
                   25
% identity
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
                   213639
Seq. No.
                   LIB3146-025-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g133940
                   241
BLAST score
                   6.0e-21
E value
Match length
                   55
                   91
% identity
                   40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851 pir__R3XL3A
NCBI Description
                   ribosomal protein S3a - African clawed frog
```

[Xenopus Taevis]

>gi 65091\_emb\_CAA40592\_ (X57322) ribosomal protein Sla



```
LIB3146-025-Q1-K1-C3
Seq. ID
                  BLASTX
Method
                  g2970556
NCBI GI
                  623
BLAST score
                  4.0e-65
E value
                  141
Match length
                  83
% identity
                   (AF049708) aspartokinase-homoserine dehydrogenase [Glycine
NCBI Description
                  max]
                  213641
Seq. No.
                  LIB3146-025-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                   q4455239
NCBI GI
BLAST score
                   213
                   3.0e-17
E value
Match length
                   68
                   50
% identity
                  (AL035523) abscisic acid-induced-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   213642
Seq. No.
                   LIB3146-025-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g2130088
NCBI GI
BLAST score
                   172
                   2.0e-12
E value
Match length
                   34
                   91
% identity
                   ubiquitin conjugating enzyme - rice >gi 1373001 (U15971)
NCBI Description
                   ubiquitin conjugating enzyme [Oryza sativa]
                   213643
Seq. No.
                   LIB3146-025-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   g1906830
NCBI GI
                   354
BLAST score
                   1.0e-33
E value
                   108
Match length
                   65
% identity
                   (Y11829) heat shock protein [Arabidopsis thaliana]
NCBI Description
                   213644
Seq. No.
                   LIB3146-025-Q1-K1-D11
Seq. ID
                   BLASTX
Method
                   g4508073
NCBI GI
                   437
BLAST score
                   2.0e-43
E value
                   130
Match length
                   64
 % identity
                  (AC005882) 43220 [Arabidopsis thaliana]
NCBI Description
                   213645
 Seq. No.
                   LIB3146-025-Q1-K1-D2
 Seq. ID
```

29738

BLASTX

g3158376 388

Method NCBI GI

BLAST score

Seq. ID Method

NCBI GI

E value

BLAST score



```
2.0e-37
E value
Match length
                  109
% identity
                   72
                  (AF035385) unknown [Arabidopsis thaliana]
NCBI Description
                  213646
Seq. No.
                  LIB3146-025-Q1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1173187
BLAST score
                   405
                   1.0e-59
E value
                   124
Match length
                   90
% identity
                   40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi_643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
                   213647
Seq. No.
                   LIB3146-025-Q1-K1-D4
Seq. ID
                   BLASTX
Method
                   g3004550
NCBI GI
                   225
BLAST score
                   2.0e-18
E value
Match length
                   73
                   62
% identity
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   213648
Seq. No.
                   LIB3146-025-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   g730583
NCBI GI
BLAST score
                   245
                   5.0e-21
E value
Match length
                   62
                   79
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb_CAA55047_
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                   argentatum]
                   213649
Seq. No.
Seq. ID
                   LIB3146-025-Q1-K1-D8
                   BLASTX
Method
NCBI GI
                   g1938424
BLAST score
                   235
                   1.0e-19
E value
Match length
                   86
                   57
% identity
                   (U97002) similar to acyl-CoA dehydrogenases and epoxide
NCBI Description
                   hydrolases [Caenorhabditis elegans]
 Seq. No.
                   213650
```

29739

LIB3146-025-Q1-K1-E12

BLASTX

g70772

.283 2.0e-25



```
Match length
% identity
                  100
                  histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden
NCBI Description
                  213651
Seq. No.
```

LIB3146-025-Q1-K1-E4 Seq. ID Method BLASTX g3169180 NCBI GI BLAST score 455 2.0e-45 E value Match length 97 % identity 89

(AC004401) putative casein kinase II catalytic subunit NCBI Description [Arabidopsis thaliana]

213652 Seq. No. LIB3146-025-Q1-K1-E5 Seq. ID

Method BLASTX g1771160 NCBI GI 224 BLAST score 3.0e-18 E value 64 Match length

% identity NCBI Description (X98929) SBT1 [Lycopersicon esculentum]

>gi\_3687305\_emb\_CAA06999\_ (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 213653

LIB3146-025-Q1-K1-E6 Seq. ID

67

BLASTX Method NCBI GI g1220196 BLAST score 469 E value 4.0e-47 Match length 125 74 % identity

(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum] NCBI Description

213654 Seq. No.

LIB3146-025-Q1-K1-F12 Seq. ID

Method BLASTX NCBI GI g1076389 BLAST score 632 3.0e-66 E value Match length 131 % identity

protein phosphatase 2A pDF1 - Arabidopsis thaliana NCBI Description

>qi 683502 emb CAA57528 (X82002) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 213655

LIB3146-025-Q1-K1-F2 Seq. ID

Method BLASTX NCBI GI g1097877 BLAST score 481 3.0e-60 E value Match length 132



```
% identity
NCBI Description aminolevulinate dehydratase [Lycopersicon esculentum]
Seq. No.
                  213656
                  LIB3146-025-Q1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4104931
BLAST score
                  144
                  6.0e-09
E value
Match length
                  27
% identity
                  93
NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]
                  213657
Seq. No.
                  LIB3146-025-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  g2914706
NCBI GI
BLAST score
                  275
                  1.0e-25
E value
                  81
Match length
                  75
% identity
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
Seq. No.
                  213658
                  LIB3146-025-Q1-K1-G10
Seq. ID
                  BLASTX
Method
                  q2677830
NCBI GI
                   564
BLAST score
E value
                   3.0e-58
                   122
Match length
                   92
% identity
NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]
                   213659
Seq. No.
Seq. ID
                   LIB3146-025-Q1-K1-G2
Method
                  BLASTX
                   q421826
NCBI GI
                   304
BLAST score
                   4.0e-28
E value
                   60
Match length
                   87
% identity
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                   >gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
                   213660
Seq. No.
                   LIB3146-025-Q1-K1-G3
Seq. ID
Method
                   BLASTX
                   g3914015
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
                   149
Match length
                   26
% identity
                   TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
NCBI Description
```

coupling factor [Synechocystis sp.]

>gi\_1001661\_dbj\_BAA10395\_ (D64002) transcription-repair

```
Seq. No. 213661
Seq. ID LIB3146-025-Q1-K1-G4
Method BLASTX
NCBI GI g4322948
BLAST score 235
```

% identity 84
%NCBI Description (AF097180) cystathionine gamma-synthase precursor

[Nicotiana tabacum]

51

5.0e-20

 Seq. No.
 213662

 Seq. ID
 LIB3146-025-Q1-K1-G6

 Method
 BLASTX

 NCBI GI
 g544242

 BLAST score
 482

 E value
 1.0e-48

E value 1.0e-48
Match length 109
% identity 82

E value

Match length

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi 485498 pir S33533 heat shock protein 90 homolog

precursor - barley >gi\_22652\_emb\_CAA48143\_ (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 213663

Seq. ID LIB3146-025-Q1-K1-G8

Method BLASTX
NCBI GI g1742951
BLAST score 449
E value 1.0e-44
Match length 96
% identity 92

NCBI Description (Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 213664

Seq. ID LIB3146-025-Q1-K1-H2

Method BLASTX
NCBI GI g3242785
BLAST score 491
E value 1.0e-49
Match length 108
% identity 84

NCBI Description (AF055355) respiratory burst oxidase protein C [Arabidopsis

thaliana]

Seq. No. 213665

Seq. ID LIB3146-025-Q1-K1-H3

Method BLASTX
NCBI GI g3608147
BLAST score 321
E value 1.0e-29
Match length 146
% identity 37

NCBI Description (AC005314) putative chloroplast 31 kDa ribonucleoprotein

precursor [Arabidopsis thaliana]

Seq. No. 213666

```
LIB3146-025-Q1-K1-H5
Seq. ID
Method
                  BLASTX
                  q3551838
NCBI GI
                  231
BLAST score
E value
                  1.0e-19
                  74
Match length
                   69
% identity
                  (AF070967) SKP1-like protein [Nicotiana clevelandii]
NCBI Description
                   213667
Seq. No.
                  LIB3146-025-Q1-K2-A1
Seq. ID
```

Method BLASTX
NCBI GI g1813329
BLAST score 150
E value 4.0e-10
Match length 30
% identity 90

NCBI Description (AB000637) HMG-1 [Canavalia gladiata]

213668

Seq. ID LIB3146-025-Q1-K2-A11 Method BLASTX NCBI GI g2760327 BLAST score 154 E value 4.0e-10 Match length 30 93

Seq. No.

NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]

 Seq. No.
 213669

 Seq. ID
 LIB3146-025-Q1-K2-A2

 Method
 BLASTX

 NCBI GI
 g4126401

 BLAST score
 412

 E value
 2.0e-40

Match length 93 % identity 85

NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis]

Seq. No. 213670 Seq. ID LIB3146-025-Q1-K2-A3 Method BLASTX

NCBI GI g4538913 BLAST score 170 E value 5.0e-12 Match length 78 % identity 51

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 213671

Seq. ID LIB3146-025-Q1-K2-A4 Method BLASTX

NCBI GI g481818
BLAST score 282
E value 3.0e-25
Match length 52
% identity 98

% identity

NCBI Description

64

[Nicotiana sylvestris]



```
NCBI Description coproporphyrinogen oxidase - soybean
                    213672
 Seq. No.
                    LIB3146-025-Q1-K2-A8
 Seq. ID
                    BLASTX
 Method
                    g2465434
 NCBI GI
 BLAST score
                    369
                    2.0e-35
 E value
                    94
 Match length
                    74
 % identity
 NCBI Description (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
 Seq. No.
                    213673
                    LIB3146-025-Q1-K2-A9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2245136
                    342
 BLAST score
                    2.0e-32
 E value
                    96
 Match length
                    71
 % identity
                    (Z97344) trehalose-6-phosphate synthase homolog
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    213674
                    LIB3146-025-Q1-K2-B1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2245136
 BLAST score
                    554
                    5.0e-57
 E value
                    137
 Match length
                    76
  % identity
                    (Z97344) trehalose-6-phosphate synthase homolog
  NCBI Description
                    [Arabidopsis thaliana]
                    213675
  Seq. No.
  Seq. ID
                    LIB3146-025-Q1-K2-B10
  Method
                    BLASTN
                    q619750
  NCBI GI
  BLAST score
                    33
  E value
                    5.0e-09
                    33
  Match length
                    100
  % identity
                    Arabidopsis thaliana phosphoribosylanthranilate isomerase
  NCBI Description
                     (PAI1) gene, complete cds
                    213676
  Seq. No.
  Seq. ID
                    LIB3146-025-Q1-K2-B11
  Method
                    BLASTX
                    g2326772
  NCBI GI
  BLAST score
                     473
                    1.0e-47
  E value
  Match length
                    136
```

29744

(Y14507) anther-specific protein [Nicotiana sylvestris]

>gi\_2326774\_emb\_CAA74846\_ (Y14506) anther-specific protein



```
Seq. No.
Seq. ID
                  LIB3146-025-Q1-K2-B2
Method
                  BLASTX
NCBI GI
                  q3860255
BLAST score
                   302
                   2.0e-27
E value
Match length
                  136
                   49
% identity
                  (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213678
Seq. ID
                  LIB3146-025-Q1-K2-B4
Method
                  BLASTX
NCBI GI
                   g2736147
                   409
BLAST score
                   3.0e-40
E value
                   112
Match length
% identity
                   64
                   (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
NCBI Description
                   thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase,
                   FAH1 [Arabidopsis thaliana]
Seq. No.
                   213679
Seq. ID
                   LIB3146-025-Q1-K2-B9
Method
                   BLASTX
                   g4324967
NCBI GI
BLAST score
                   688
                   9.0e-73
E value
Match length
                   136
                   99
% identity
                  (AF114796) ADP-ribosylation factor [Glycine max]
NCBI Description
                   213680
Seq. No.
                   LIB3146-025-Q1-K2-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2342735
BLAST score
                   351
E value
                   4.0e-40
Match length
                   116
% identity
                   66
                   (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   213681
Seq. No.
                   LIB3146-025-Q1-K2-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4580389
BLAST score
                   223
                   1.0e-18
E value
                   56
Match length
```

75 % identity

(AC007171) unknown protein [Arabidopsis thaliana] NCBI Description

213682 Seq. No.

Seq. ID LIB3146-025-Q1-K2-C6

BLASTX Method g1730171 NCBI GI BLAST score 509

4000

ر المائد



253

122

43

9.0e-22

BLAST score

Match length

% identity

E value

```
E value
Match length
                  120
                  82
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi_1370066_emb_CAA61574_ (X89394)
                  glucose-6-phosphate isomerase [Clarkia williamsonii]
                  213683
Seq. No.
                  LIB3146-025-Q1-K2-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2208944
BLAST score
                  529
                  4.0e-54
E value
                  134
Match length
                  74
% identity
NCBI Description (Y11120) nodulin-35 homologue [Arabidopsis thaliana]
                  213684
Seq. No.
                  LIB3146-025-Q1-K2-C9
Seq. ID
                  BLASTX
Method
                  q3914685
NCBI GI
BLAST score
                   637
E value
                  8.0e-67
                  132
Match length
% identity
                   91
                  60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
NCBI Description
                  protein L17 [Zea mays]
                   213685
Seq. No.
                  LIB3146-025-Q1-K2-D11
Seq. ID
                   BLASTX
Method
                   q3402704
NCBI GI
BLAST score
                   318
                   2.0e-29
E value
Match length
                   130
% identity
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   213686
Seq. No.
                   LIB3146-025-Q1-K2-D4
Seq. ID
Method
                   BLASTX
                   g3860258
NCBI GI
BLAST score
                   145
                   4.0e-09
E value
Match length
                   38
% identity
                   68
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213687
                   LIB3146-025-Q1-K2-D7
Seq. ID
                   BLASTX
Method
                   g2213594
NCBI GI
```



NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

 Seq. No.
 213688

 Seq. ID
 LIB3146-025-Q1-K2-D8

 Method
 BLASTX

 NCBI GI
 g629692

 PLAST score
 212

BLAST score 212 E value 6.0e-17 Match length 121 % identity 42

NCBI Description hypothetical protein - common tobacco

>gi\_506471\_emb\_CAA56189\_ (X79794) unnamed protein product

[Nicotiana tabacum]

Seq. No. 213689

Seq. ID LIB3146-025-Q1-K2-E1

Method BLASTX
NCBI GI g2832628
BLAST score 429
E value 2.0e-42
Match length 125
% identity 70

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 213690

Seq. ID LIB3146-025-Q1-K2-E10

Method BLASTX
NCBI GI g537639
BLAST score 175
E value 1.0e-12
Match length 91
% identity 41

NCBI Description (U14168) lipid transfer protein [Nicotiana tabacum]

Seq. No. 213691

Seq. ID LIB3146-025-Q1-K2-E11

Method BLASTX
NCBI GI g2984709
BLAST score 385
E value 2.0e-37
Match length 115
% identity 66

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 213692

Seq. ID LIB3146-025-Q1-K2-E2

Method BLASTX
NCBI GI g729470
BLAST score 182
E value 2.0e-13
Match length 51
% identity 71

NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor



## [Solanum tuberosum]

```
213693
Seq. No.
                   LIB3146-025-Q1-K2-E5
Seq. ID
                   BLASTX
Method
                   q1708971
NCBI GI
BLAST score
                   148
E value
                   1.0e-09
Match length
                   60
                   50
% identity
                   (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
NCBI Description
                   (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                   >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
                   black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                   (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                   serotina] >gi_1090776_prf__2019441A mandelonitrile lyase
                   [Prunus serotina]
                   213694
Seq. No.
                   LIB3146-025-Q1-K2-E6
Seq. ID
Method
                   BLASTX
                   q20739
NCBI GI
BLAST score
                   496
                   3.0e-50
E value
Match length
                   106
                   85
% identity
                   (X54377) P-protein subunit of glycine decarboxylase enzyme
NCBI Description
                   complex [Pisum sativum]
                   213695
Seq. No.
                   LIB3146-025-Q1-K2-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3859534
                   193
BLAST score
E value
                   5.0e-15
Match length
                    43
% identity
                   (AF095452) asparagine synthetase [Arabidopsis thaliana]
NCBI Description
                    213696
Seq. No.
                   LIB3146-025-Q1-K2-F10
Seq. ID
                   BLASTN
Method
NCBI GI
                    q939859
                    34
BLAST score
                    2.0e-10
E value
Match length
                    58
                    90
% identity
NCBI Description B.pilosa mRNA for calmodulin
                    213697
Seq. No.
                    LIB3146-025-Q1-K2-F11
Seq. ID
                    BLASTX
Method
                    g125271
NCBI GI
                    479
BLAST score
                    2.0e-48
E value
                    97
Match length
```



% identity CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA) NCBI Description >gi 100860 pir\_\_S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize >gi 3318993 pdb 1A60 Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays >gi 22117\_emb\_CAA43659\_ (X61387) casein kinase II alpha subunit [Zea mays] 213698 Seq. No. LIB3146-025-Q1-K2-F2 Seq. ID BLASTN Method g2264310 NCBI GI 35 BLAST score 3.0e-10 E value 43 Match length 95 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MKP11, complete sequence [Arabidopsis thaliana] 213699 Seq. No. LIB3146-025-Q1-K2-F4 Seq. ID Method BLASTX NCBI GI g2809246 BLAST score 163 E value 3.0e-11 Match length 51 61 % identity (AC002560) F2401.15 [Arabidopsis thaliana] NCBI Description 213700 Seq. No. LIB3146-025-Q1-K2-G1 Seq. ID BLASTX Method g3860255 NCBI GI BLAST score 185 4.0e-14 E value 73 Match length 60 % identity (AC005824) hypothetical protein [Arabidopsis thaliana] NCBI Description 213701 Seq. No. Seq. ID LIB3146-025-Q1-K2-G11 BLASTN Method g3702724 NCBI GI BLAST score 60 2.0e-25 E value Match length 104 89 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K17N15, complete sequence [Arabidopsis thaliana] 213702 Seq. No. LIB3146-025-Q1-K2-G3 Seq. ID Method BLASTN

Method BLASTN
NCBI GI g22553
BLAST score 78
E value 6.0e-36
Match length 86
% identity 98



## NCBI Description Tomato 25S ribosomal RNA gene

 Seq. No.
 213703

 Seq. ID
 LIB3146-025-Q1-K2-G8

 Method
 BLASTX

Method BLASTX
NCBI GI 94115915
BLAST score 316
E value 4.0e-37
Match length 124
% identity 65

% identity 65
NCBI Description (AF118222) contains similarity to Helix pomatia br-1

protein (GB: X96994) [Arabidopsis thaliana]

Seq. No. 213704

Seq. ID LIB3146-025-Q1-K2-H2

Method BLASTX
NCBI GI g3894172
BLAST score 414
E value 1.0e-40
Match length 122
% identity 60

NCBI Description (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Seq. No. 213705

Seq. ID LIB3146-025-Q1-K2-H3

Method BLASTX
NCBI GI g1001607
BLAST score 168
E value 8.0e-12
Match length 53
% identity 55

NCBI Description (D64000) hypothetical protein [Synechocystis sp.]

Seq. No. 213706

Seq. ID LIB3146-025-Q1-K2-H7

Method BLASTX
NCBI GI g2935300
BLAST score 552
E value 5.0e-57
Match length 112
% identity 96

NCBI Description (AF038046) 3-hydroxy-3-methylglutaryl-coenzyme A reductase

2 [Gossypium hirsutum]

Seq. No. 213707

Seq. ID LIB3146-025-Q1-K2-H8

Method BLASTN
NCBI GI g3236479
BLAST score 33
E value 5.0e-09
Match length 65

% identity 88
NCBI Description Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 213708

LIB3146-026-Q1-K2-A11 Seq. ID BLASTX Method g3851636 NCBI GI 415 BLAST score 8.0e-41 E value Match length 95 % identity 81 (AF098519) unknown [Avicennia marina] >gi 4128206 NCBI Description (AF056316) 40S ribosome protein S7 [Avicennia marina] Seq. No. 213709 Seq. ID LIB3146-026-Q1-K2-A3 Method BLASTX

NCBI GI q729275 BLAST score 150 1.0e-09 E value 59 Match length % identity 47

PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (PPIASE C) (ROTAMASE NCBI Description

C) (PARVULIN) >gi\_1084110\_pir\_\_S48658 parvulin -

Escherichia coli >gi 693800 bbs 156242 (S73874) parvulin, peptidyl- prolyl cis/trans isomerase, PPIase [Escherichia coli, K-12 HB101, Peptide, 93 aa] [Escherichia coli] >qi 836657 (M87049) peptidyl-prolyl cis-trans isomerase C [Escherichia coli] >gi 1790211 (AE000454) peptidyl-prolyl cis-trans isomerase C (rotamase C) [Escherichia coli]

213710 Seq. No.

LIB3146-026-Q1-K2-A4 Seq. ID

BLASTX Method g2688824 NCBI GI BLAST score 272 E value 4.0e-26 Match length 95 72 % identity

(U93273) putative auxin-repressed protein [Prunus NCBI Description

armeniaca]

Seq. No. 213711

LIB3146-026-Q1-K2-A6 Seq. ID

Method BLASTX g2661840 NCBI GI 337 BLAST score 1.0e-31 E value 110 Match length 60 % identity

(Y15430) adenosine kinase [Physcomitrella patens] NCBI Description

213712 Seq. No.

Seq. ID LIB3146-026-Q1-K2-A8

BLASTX Method g3721926 NCBI GI BLAST score 563 4.0e-58 E value 127 Match length 89 % identity

NCBI Description (AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Method

NCBI GI

BLASTX g1076668



```
Seq. No.
                  213713
                  LIB3146-026-Q1-K2-A9
Seq. ID
                  BLASTX
Method
                  g2245119
NCBI GI
                  428
BLAST score
                  3.0e-42
E value
Match length
                  134
                  65
% identity
NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]
                  213714
Seq. No.
                  LIB3146-026-Q1-K2-B1
Seq. ID
Method
                  BLASTX
                  q1263291
NCBI GI
                   532
BLAST score
                  1.0e-54
E value
                  117
Match length
% identity
                   84
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
                   213715
Seq. No.
                  LIB3146-026-Q1-K2-B10
Seq. ID
Method
                  BLASTX
                   g3212869
NCBI GI
BLAST score
                   446
                   2.0e-44
E value
                   118
Match length
                   68
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                   213716
Seq. No.
                   LIB3146-026-Q1-K2-B11
Seq. ID
Method
                   BLASTX
                   q1082801
NCBI GI
BLAST score
                   146
E value
                   4.0e-18
                   133
Match length
                   45
% identity
                  splicing factor SF3a60 - human >gi_551450_emb_CAA57388_
NCBI Description
                   (X81789) splicing factor SF3a60 [Homo sapiens]
                   213717
Seq. No.
                   LIB3146-026-Q1-K2-B12
Seq. ID
Method
                   BLASTX
                   g3550661
NCBI GI
                   466
BLAST score
                   9.0e-47
E value
Match length
                   117
                   40
% identity
                   (AJ001310) 39 kDa EF-Hand containing protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   213718
                   LIB3146-026-Q1-K2-B7
Seq. ID
```



```
BLAST score
E value
                  3.0e-74
                  136
Match length
% identity
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                  [Solanum tuberosum]
Seq. No.
                  213719
                  LIB3146-026-Q1-K2-B8
Seq. ID
Method
                  BLASTX
                  g2245077
NCBI GI
BLAST score
                  630
E value
                  5.0e-66
                  132
Match length
                  86
% identity
                  (Z97343) glucanase homolog [Arabidopsis thaliana]
NCBI Description
                  213720
Seq. No.
                  LIB3146-026-Q1-K2-C11
Seq. ID
                  BLASTX
Method
                  g3150415
NCBI GI
                   605
BLAST score
                   5.0e-63
E value
Match length
                   130
                   25
% identity
                  (ACO04165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
Seq. No.
                   213721
                   LIB3146-026-Q1-K2-C2
Seq. ID
                   BLASTX
Method -
NCBI GI
                   g1173253
BLAST score
                   462
                   2.0e-46
E value
                   107
Match length
% identity
                   90
                   40S RIBOSOMAL PROTEIN S3 >gi 543317 pir S41170 ribosomal
NCBI Description
                   protein S3 - mouse >gi_57728_emb_CAA35916_ (X51536)
                   ribosomal protein S3 (AA 1-243) [Rattus rattus]
                   >gi_439522_emb_CAA54167_ (X76772) ribosomal protein S3 [Mus
                   musculus]
                   213722
Seq. No.
                   LIB3146-026-Q1-K2-C3
Seq. ID
                   BLASTX
Method
                   g2130088
NCBI GI
BLAST score
                   144
                   4.0e-09
E value
```

Match length 34 82 % identity

ubiquitin conjugating enzyme - rice >gi\_1373001 (U15971) NCBI Description

ubiquitin conjugating enzyme [Oryza sativa]

Seq. No. 213723

LIB3146-026-Q1-K2-C5 Seq. ID



```
BLASTX
Method
NCBI GI
                   q2970556
BLAST score
                   571
                   5.0e-59
E value
                   131
Match length
                   82
% identity
                   (AF049708) aspartokinase-homoserine dehydrogenase [Glycine
NCBI Description
                   213724
Seq. No.
                   LIB3146-026-Q1-K2-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455239
BLAST score
                   213
                   4.0e-17
E value
Match length
                   68
                   50
% identity
NCBI Description
                   (AL035523) abscisic acid-induced-like protein [Arabidopsis
                   thaliana]
                   213725
Seq. No.
                   LIB3146-026-Q1-K2-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1906830
BLAST score
                   354
                   1.0e-33
E value
                   108
Match length
                   65
% identity
                  (Y11829) heat shock protein [Arabidopsis thaliana]
NCBI Description
                   213726
Seq. No.
                   LIB3146-026-Q1-K2-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3046731
                   288
BLAST score
E value
                   7.0e-26
Match length
                   71
                   79
% identity
                  (AJ005373) protein kinase [Craterostigma plantagineum]
NCBI Description
                   213727
Seq. No.
                   LIB3146-026-Q1-K2-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3152618
BLAST score
                   544
                   6.0e-56
E value
                   127
Match length
% identity
                   (AC004482) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   >qi 3242724 (AC003040) putative pectinesterase [Arabidopsis
                   thaliana]
```

213728 Seq. No.

LIB3146-026-Q1-K2-D11 Seq. ID

Method BLASTX g4508073 NCBI GI BLAST score 447



E value 2.0e-44
Match length 136
% identity 62

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 213729

Seq. ID LIB3146-026-Q1-K2-D2

Method BLASTX
NCBI GI g542200
BLAST score 306
E value 5.0e-28
Match length 125
% identity 54

NCBI Description hypothetical protein - garden asparagus

>gi 452714 emb CAA54526\_ (X77320) unknown [Asparagus

officinalis]

Seq. No. 213730

Seq. ID LIB3146-026-Q1-K2-D4

Method BLASTX
NCBI GI g4185153
BLAST score 234
E value 1.0e-19
Match length 73

% identity 63

NCBI Description (AC005724) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213731

Seq. ID LIB3146-026-Q1-K2-D5

Method BLASTX
NCBI GI g1173187
BLAST score 569
E value 8.0e-59
Match length 112
% identity 96

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi\_1362041\_pir\_\_S56673

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 213732

Seq. ID LIB3146-026-Q1-K2-D8

Method BLASTX
NCBI GI g1938424
BLAST score 235
E value 1.0e-19
Match length 86
% identity 57

NCBI Description (U97002) similar to acyl-CoA dehydrogenases and epoxide

hydrolases [Caenorhabditis elegans]

Seq. No. 213733

Seq. ID LIB3146-026-Q1-K2-D9

Method BLASTN
NCBI GI g2564049
BLAST score 50
E value 4.0e-19



Match length 161 % identity 86 NCBI Description Ara

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLE2, complete sequence [Arabidopsis thaliana]

Seq. No. 213734

Seq. ID LIB3146-026-Q1-K2-E1

Method BLASTX
NCBI GI g1771160
BLAST score 217
E value 1.0e-17
Match length 64
% identity 66

NCBI Description (X98929) SBT1 [Lycopersicon esculentum]

>gi 3687305 emb CAA06999 (AJ006378) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 213735

Seq. ID LIB3146-026-Q1-K2-E12

Method BLASTX
NCBI GI g70772
BLAST score 283
E value 3.0e-25
Match length 56
% identity 100

NCBI Description histone H4 - wheat >gi\_70773\_pir\_\_HSPM4 histone H4 - garden

pea

Seq. No. 213736

Seq. ID LIB3146-026-Q1-K2-E4

Method BLASTX
NCBI GI g3169180
BLAST score 455
E value 2.0e-45
Match length 97
% identity 89

NCBI Description (AC004401) putative casein kinase II catalytic subunit

[Arabidopsis thaliana]

Seq. No. 213737

Seq. ID LIB3146-026-Q1-K2-E6

Method BLASTX
NCBI GI g1220196
BLAST score 543
E value 6.0e-56
Match length 109
% identity 96

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 213738

Seq. ID LIB3146-026-Q1-K2-E7

Method BLASTX
NCBI GI g3169180
BLAST score 187
E value 5.0e-14
Match length 97
% identity 51



(AC004401) putative casein kinase II catalytic subunit NCBI Description [Arabidopsis thaliana] Seq. No. 213739 LIB3146-026-Q1-K2-F12 Seq. ID Method BLASTX NCBI GI q3928142 224 BLAST score 6.0e-19 E value 49 Match length % identity 92 NCBI Description (AJ131045) protein phosphatase [Cicer arietinum] 213740 Seq. No. LIB3146-026-Q1-K2-F3 Seq. ID BLASTX Method g4104931 NCBI GI BLAST score 144 5.0e-09 E value Match length 27 93 % identity NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana] Seq. No. 213741 LIB3146-026-Q1-K2-F4 Seq. ID Method BLASTX a434765 NCBI GI 216 BLAST score E value 2.0e-17 75 Match length 59 % identity NCBI Description (D21262) ORF [Homo sapiens] Seq. No. 213742 Seq. ID LIB3146-026-Q1-K2-G1 Method BLASTX NCBI GI q167970 BLAST score 306 E value 6.0e-28 Match length 110 % identity 56 NCBI Description (L05915) [GST1] gene product [Dianthus caryophyllus] Seq. No. 213743 LIB3146-026-Q1-K2-G10 Seq. ID

Method BLASTX NCBI GI g3986695 BLAST score 582 2.0e-60 E value 126 Match length 92 % identity

(AF101423) ribosomal protein L12 [Cichorium intybus] NCBI Description

Seq. No. 213744

Seq. ID LIB3146-026-Q1-K2-G2

BLASTX Method NCBI GI g3075488



BLAST score 398 E value 2.0e-45 Match length 105 % identity 87

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 213745

Seq. ID LIB3146-026-Q1-K2-G4

Method BLASTX
NCBI GI g4322948
BLAST score 235
E value 1.0e-19
Match length 51
% identity 84

NCBI Description (AF097180) cystathionine gamma-synthase precursor

[Nicotiana tabacum]

Seq. No. 213746

Seq. ID LIB3146-026-Q1-K2-G6

Method BLASTX
NCBI GI g544242
BLAST score 151
E value 2.0e-10
Match length 50
% identity 58

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_485498\_pir\_\_\$33533 heat shock protein 90 homolog

precursor - barley >gi\_22652\_emb\_CAA48143\_ (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 213747

Seq. ID LIB3146-026-Q1-K2-G8

Method BLASTX
NCBI GI g1943751
BLAST score 449
E value 8.0e-45
Match length 96

Match length 96 % identity 92

NCBI Description (U93845) Arabidopsis thaliana ER-type calcium pump

protein, complete sequence >gi 2078292 (U96455) ER-type

Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No. 213748

Seq. ID LIB3146-026-Q1-K2-H2

Method BLASTX
NCBI GI g3242785
BLAST score 482
E value 1.0e-48
Match length 108
% identity 82

NCBI Description (AF055355) respiratory burst oxidase protein C [Arabidopsis

thaliana]

Seq. No. 213749

Seq. ID LIB3146-026-Q1-K2-H3

Method BLASTX NCBI GI g3242785



```
BLAST score
                  3.0e-09
E value
Match length
                  67
                  49
% identity
                  (AF055355) respiratory burst oxidase protein C [Arabidopsis
NCBI Description
                  thaliana]
                  213750
Seq. No.
Seq. ID
                  LIB3146-026-Q1-K2-H5
Method
                  BLASTX
NCBI GI
                  q3551838
                  181
BLAST score
                  2.0e-13
E value
                  48
Match length
                  75
% identity
                  (AF070967) SKP1-like protein [Nicotiana clevelandii]
NCBI Description
                  213751
Seq. No.
Seq. ID
                  L:IB3146-026-Q1-K2-H9
                  BLASTX
Method
NCBI GI
                  g1076316
                  234
BLAST score
                  7.0e-29
E value
                  120
Match length
                  53
% identity
                  drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                  >gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis
                  thaliana]
                  213752
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-A10
Method
                  BLASTN
                  g4210947
NCBI GI
                  39
BLAST score
E value
                  2.0e-12
Match length
                  67
                  90
% identity
NCBI Description Hevea brasiliensis DnaJ protein mRNA, complete cds
Seq. No.
                  213753
Seq. ID
                  LIB3146-027-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g541825
BLAST score
                  664
                  6.0e-70
E value
Match length
                  141
% identity
                  protein kinase - spinach >gi 457711 emb CAA82993 (Z30332)
NCBI Description
                  protein kinase [Spinacia oleracea]
                  213754
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-A12
```

Method BLASTX

NCBI GI g3056595 BLAST score 180 E value 3.0e - 13Match length 44



% identity (AC004255) T1F9.16 [Arabidopsis thaliana] NCBI Description Seq. No. 213755 LIB3146-027-Q1-K1-A2 Seq. ID Method BLASTX NCBI GI q3402704 BLAST score 148 E value 2.0e-09 Match length 121 % identity 32 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana] Seq. No. 213756 LIB3146-027-Q1-K1-A5 Seq. ID Method BLASTX NCBI GI q266579 BLAST score 193 1.0e-14 E value 49 Match length 67 % identity METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 169713 (L02306) NCBI Description metallothionein [Ricinus communis] 213757 Seq. No. LIB3146-027-Q1-K1-A7 Seq. ID Method BLASTX NCBI GI q4102861 BLAST score 544 E value 7.0e-56 Match length 115 87 % identity (AF016893) copper/zinc-superoxide dismutase [Populus NCBI Description tremuloides] Seq. No. 213758 Seq. ID LIB3146-027-Q1-K1-B1 Method BLASTX NCBI GI q4567202 BLAST score 513 3.0e-52 E value Match length 132 % identity 78 NCBI Description (AC007168) putative myo-inositol 1-phosphate synthase [Arabidopsis thaliana] Seq. No. 213759 Seq. ID LIB3146-027-Q1-K1-B10 Method BLASTX NCBI GI g4490739

BLAST score 473 1.0e-47 E value Match length 131 73 % identity

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 213760

NCBI GI

BLAST score



```
LIB3146-027-Q1-K1-B4
Seq. ID
                  BLASTX
Method
                  g1871176
NCBI GI
                  273
BLAST score
                  4.0e-24
E value
Match length
                  101
% identity
                  55
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
                  213761
Seq. No.
                  LIB3146-027-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3688123
BLAST score
                  577
                  9.0e-60
E value
Match length
                  132
% identity
                  81
                  (AJ006293) granule-bound starch synthase [Antirrhinum
NCBI Description
                  majus]
Seq. No.
                  213762
Seq. ID
                  LIB3146-027-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  q2586083
BLAST score
                  200
E value
                  1.0e-31
Match length
                  141
% identity
                  57
                   (U72725) receptor kinase-like protein [Oryza
NCBI Description
                  longistaminata]
                  213763
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
                  246
                   4.0e-26 ·
E value
Match length
                  91
                  70
% identity
                   (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  213764
Seq. ID
                  LIB3146-027-Q1-K1-C11
                  BLASTX
Method
NCBI GI
                  g1495366
BLAST score
                   304
                  1.0e-27
E value
Match length
                  139
                   42
% identity
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
Seq. No.
                   213765
Seq. ID
                  LIB3146-027-Q1-K1-C12
                  BLASTX
Method
```

29761

g1064929

```
E value 3.0e-56 Match length 124 85
```

NCBI Description (X92967) cyclin A-like protein [Nicotiana tabacum]

Seq. No. 213766

Seq. ID LIB3146-027-Q1-K1-C8

Method BLASTX
NCBI GI g4544372
BLAST score 152
E value 6.0e-10
Match length 62
% identity 42

NCBI Description (AC006920) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 213767

Seq. ID LIB3146-027-Q1-K1-C9

Method BLASTX
NCBI GI g3668082
BLAST score 199
E value 2.0e-15
Match length 39
% identity 95

NCBI Description (AC004667) putative DAL1 protein [Arabidopsis thaliana]

Seq. No. 213768

Seq. ID LIB3146-027-Q1-K1-D1

Method BLASTX
NCBI GI g4191255
BLAST score 587
E value 6.0e-61
Match length 137
% identity 85

NCBI Description (AJ132323) chalcone synthase [Casuarina glauca]

Seq. No. 213769

Seq. ID LIB3146-027-Q1-K1-D11

Method BLASTX
NCBI GI g3461833
BLAST score 375
E value 3.0e-36
Match length 76
% identity 86

NCBI Description (AC004138) putative expansin [Arabidopsis thaliana]

Seq. No. 213770

Seq. ID LIB3146-027-Q1-K1-D3

Method BLASTX
NCBI GI g951427
BLAST score 527
E value 6.0e-54
Match length 130
% identity 77

NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus

communis]



```
Seq. No.
                   213771
                  LIB3146-027-Q1-K1-D6
Seq. ID
                  BLASTX
Method
                  g4490937
NCBI GI
                  173
BLAST score
E value
                  2.0e-12
                  107
Match length
                                                                     150
% identity
                  30
                   (AJ132261) hypothetical helicase K12H4.8-like protein [Homo
NCBI Description
                   sapiens]
                   213772
Seq. No.
                  LIB3146-027-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3924603
BLAST score
                   262
E value
                   3.0e-26
Match length
                   77
                   79
% identity
                   (AF069442) putative WD-repeat protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   213773
                   LIB3146-027-Q1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2739010
BLAST score
                   294
                   1.0e-26
E value
Match length
                   132
                   46
% identity
                  (AF022464) CYP77A3p [Glycine max]
NCBI Description
Seq. No.
                   213774
Seq. ID
                   LIB3146-027-Q1-K1-E11
Method
                   BLASTX
                   q2738949
NCBI GI
BLAST score
                   667
                   3.0e-70
E value
Match length
                   138
                   88
% identity
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                   ananassa]
                   213775
Seq. No.
Seq. ID
                   LIB3146-027-Q1-K1-E12
Method
                   BLASTN
NCBI GI
                   g4539402
BLAST score
                   33
                   6.0e-09
E value
                   93
Match length
                   62
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13
NCBI Description
                   (ESSA project)
```

Seq. No. 213776
Seq. ID LIB3146-027-Q1-K1-E3

Method BLASTX



```
NCBI GI
                     g416641
  BLAST score
                    128
                    7.0e-11
  E value
  Match length
                    50
  % identity
                    74
  NCBI Description
                    INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4
                    >gi_287568_dbj_BAA03309_ (D14413) ORF [Vigna radiata]
Seq. No.
                    213777
  Seq. ID
                    LIB3146-027-Q1-K1-E8
  Method
                    BLASTX
  NCBI GI
                    q2979546
  BLAST score
                    197
  E value
                    3.0e-15
  Match length
                    58
                     62
  % identity
  NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
                    213778
  Seq. No.
                    LIB3146-027-Q1-K1-F1
  Seq. ID
  Method
                    BLASTX
                    q3860258
  NCBI GI
  BLAST score
                    159
                    7.0e-11
  E value
  Match length
                    101
  % identity
                     37
  NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
  Seq. No.
                    213779
                    LIB3146-027-Q1-K1-F10
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q100481
  BLAST score
                     247
  E value
                    5.0e-21
  Match length
                     69
  % identity
                     67
  NCBI Description fill protein - garden snapdragon
  Seq. No.
                     213780
  Seq. ID
                    LIB3146-027-Q1-K1-F12
  Method
                    BLASTX
  NCBI GI
                    g3746060
  BLAST score
                    262
  E value
                    8.0e-23
  Match length
                    93
  % identity
                    58
  NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
                    213781
  Seq. No.
  Seq. ID
                    LIB3146-027-Q1-K1-F9
  Method
                    BLASTX
  NCBI GI
                    q2895576
  BLAST score
                    142
  E value
                    9.0e-09
  Match length
                    88
                    28
  % identity
  NCBI Description (AF041337) vacuolar proton pump subunit SFD beta isoform
```



## [Bos taurus]

```
213782
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g139780
BLAST score
                  202
                  9.0e-16
E value
Match length
                  66
                  67
% identity
                  WOUND-INDUCED PROTEIN 1 >gi 82293 pir _JQ0398 wun1 protein
NCBI Description
                  - potato
                  213783
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3885515
BLAST score
                  240
                  1.0e-20
E value
                  46
Match length
% identity
                  96
                   (AF084202) similar to ribosomal protein S26 [Medicago
NCBI Description
                  sativa]
                  213784
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-G4
Method
                  BLASTX
                  g167367
NCBI GI
BLAST score
                  579
                  5.0e-60
E value
                  135
Match length
                  84
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  213785
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3065835
BLAST score
                  151
                   5.0e-10
E value
Match length
                  89
                   42
% identity
                  (AF058800) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                   213786
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-G8
Method
                  BLASTX
                  q1706377
NCBI GI
                   351
BLAST score
                   2.0e-33
E value
Match length
                  100
                   69
% identity
                  DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
NCBI Description
```

4-REDUCTASE) >gi\_499018\_emb\_CAA53578\_ (X75964) dihydroflavonol reductase [Vitis vinifera]



```
213787
Seq. No.
Seq. ID
                  LIB3146-027-Q1-K1-H1
                  BLASTX
Method
NCBI GI
                  g3065835
BLAST score
                  503
E value
                  4.0e-51
Match length
                  131
                  75
% identity
                  (AF058800) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  213788
                  LIB3146-027-Q1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213789
Seq. ID
                  LIB3146-027-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q1173456
BLAST score
                  330
E value
                  7.0e-31
Match length
                  97
% identity
                  58
NCBI Description
                  SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN
                  D3) (SM-D3) >gi 600750 (U15009) Sm D3 [Homo sapiens]
Seq. No.
                  213790
Seq. ID
                  LIB3146-027-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3510253
BLAST score
                  401
E value
                  4.0e-39
Match length
                  130
% identity
                  64
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  213791
Seq. ID
                  LIB3146-027-Q1-K1-H5
                  BLASTX
Method
NCBI GI
                  q3065835
BLAST score
                  272
                  4.0e-24
E value
Match length
                  102
                  55
% identity
                  (AF058800) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  213792
Seq. ID
                  LIB3146-027-Q1-K1-H6
```

29766

BLASTX

g2660664

Method NCBI GI



```
BLAST score
                   5.0e-12
E value
                   111
Match length
                   40
% identity
                  (AC002342) unknown protein [Arabidopsis thaliana]
NCBI Description
                   213793
Seq. No.
                  LIB3146-027-Q1-K1-H9
Seq. ID
                                                                 -- :
                  BLASTX
Method
NCBI GI
                   g2341034
                   547
BLAST score
E value
                   3.0e-56
Match length
                   111
                   97
% identity
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213794
                   LIB3146-028-Q1-K1-A1
Seq. ID
Method
                   BLASTX
                   g4107099
NCBI GI
BLAST score
                   453
E value
                   3.0e-45
Match length
                   129
% identity
                   65
NCBI Description
                   (AB015141) AHP1 [Arabidopsis thaliana]
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
                   213795
Seq. No.
                   LIB3146-028-Q1-K1-A10
Seq. ID
                   BLASTX
Method
                   q3860272
NCBI GI
BLAST score
                   668
                   2.0e-70
E value
                   140
Match length
                   91
% identity
                   (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                   protein [Arabidopsis thaliana]
                   213796
Seq. No.
Seq. ID
                   LIB3146-028-Q1-K1-A3
                   BLASTX
Method
                   g3377801
NCBI GI
BLAST score
                   264
                   5.0e-23
E value
                   70
Match length
                   66
% identity
                   (AF075597) contains similarity to pectinesterases
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 213797

Seq. ID LIB3146-028-Q1-K1-A4

Method BLASTX
NCBI GI g3293547
BLAST score 150
E value 1.0e-09



```
Match length
% identity
                  41
                  (AF072709) putative oxidoreductase [Streptomyces lividans]
NCBI Description
                  213798
Seq. No.
                  LIB3146-028-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730456
BLAST score
                  450
                  7.0e-45
E value
Match length
                  102
% identity
                  77
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                  213799
                  LIB3146-028-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q441457
                  630
BLAST score
                  5.0e-66
E value
                  118
Match length
                  98
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  213800
Seq. No.
Seq. ID
                  LIB3146-028-Q1-K1-B10
                  BLASTX
Method
NCBI GI
                  q4325338
BLAST score
                  310
E value
                  2.0e-28
Match length
                  96
% identity
                  66
                  (AF128392) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213801
Seq. ID
                  LIB3146-028-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4115918
BLAST score
                  379
                  2.0e-36
E value
Match length
                  116
% identity
NCBI Description
                  (AF118222) similar to nascent polypeptide associated
                  complex alpha chain [Arabidopsis thaliana]
Seq. No.
                  213802
```

Seq. ID LIB3146-028-Q1-K1-B2

Method BLASTX NCBI GI g3327245 BLAST score 270 9.0e-24 E value 79 Match length 62 % identity

NCBI Description (AB016083) Ntc12 [Nicotiana tabacum]

Seq. No. 213803

Seq. No.

213808



```
LIB3146-028-Q1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2791896
                  135
BLAST score
                   2.0e-17
E value
Match length
                  110
                   62
% identity
                  (Y08997) 146kDa nuclear protein [Xenopus laevis]
NCBI Description
Seq. No.
                   213804
Seq. ID
                  LIB3146-028-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                   q3881976
                   280
BLAST score
                   5.0e-25
E value
Match length
                   60
                   85
% identity
NCBI Description
                  (AJ012409) hypothetical protein [Homo sapiens]
Seq. No.
                   213805
                  LIB3146-028-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3645985
BLAST score
                   212
                   6.0e-17
E value
Match length
                   36
% identity
                   94
                   (AL031581) 1-evidence=predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-method_score=23.36;
                   1-evidence_end; 2-evidence=predicted by match;
                   2-match_accession=AA141041;
                   2-match_description=CK01110.3prime CK Drosophila
                   melanogaster
Seq. No.
                   213806
Seq. ID
                   LIB3146-028-Q1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1345785
BLAST score
                   664
E value
                   6.0e-70
Match length
                   131
% identity
                   98
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                   >gi_567935_dbj_BAA05640_ (D26593) chalcone synthase
                   [Camellia sinensis]
Seq. No.
                   213807
Seq. ID
                   LIB3146-028-Q1-K1-C12
                   BLASTX
Method
NCBI GI
                   g2832625
BLAST score
                   355
                   1.0e-33
E value
Match length
                   137
                   47
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
```



```
Seq. ID
                  LIB3146-028-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q3738311
BLAST score
                  287
E value
                  9.0e-26
Match length
                  121
% identity
                  49
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  >gi_4249406 (AC006072) putative WD-40 repeat protein
                  [Arabidopsis thaliana]
Seq. No.
                  213809
Seq. ID
                  LIB3146-028-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q3738306
BLAST score
                  232
E value
                  2.0e-19
Match length
                  129
% identity
                  40
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  213810
Seq. No.
Seq. ID
                  LIB3146-028-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  g231503
BLAST score
                  529
                  4.0e-54
E value
Match length
                  127
% identity
                  82
                  ACTIN 97 >gi_100417_pir__ S20098 actin - potato
NCBI Description
                  >gi_21544_emb_CAA39280_ (X55751) actin [Solanum tuberosum]
Seq. No.
                  213811
Seq. ID
                  LIB3146-028-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4572674
BLAST score
                  443
E value
                  4.0e-44
Match length
                  117
% identity
                  68
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                  213812
Seq. ID
                  LIB3146-028-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2493144
BLAST score
                  453
E value
                  3.0e-45
Match length
                  125
% identity
                  54
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
NCBI Description
                  16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir S60132
```

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi 926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]



```
Seq. No.
                  213813
Seq. ID
                  LIB3146-028-Q1-K1-D12
Method
                  BLASTX
                  g3021485
NCBI GI
BLAST score
                  489
E value
                  2.0e-49
Match length
                  102
                  95
% identity
                  (AJ224932) histone H2B-3 [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  213814
Seq. ID
                  LIB3146-028-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q1255954
BLAST score
                   343
E value
                  2.0e-32
Match length
                  79
% identity
                  80
                  (Z70677) thioredoxin [Ricinus communis]
NCBI Description
                  213815
Seq. No.
Seq. ID
                  LIB3146-028-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2492519
BLAST score
                   339
                   7.0e-32
E value
                   66
Match length
                   100
% identity
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi 1395191 dbj_BAA13021_ (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
Seq. No.
                   213816
                   LIB3146-028-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4102839
BLAST score
                   588
E value
                   5.0e-61
Match length
                   140
% identity
                   80
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
NCBI Description
                   213817
Seq. No.
                   LIB3146-028-Q1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2708743
BLAST score
                   148
                   2.0e-09
E value
Match length
                   103
% identity
                   32
                   (AC003952) putative Tal-1-like reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
                   213818
Seq. No.
```

BLASTX NCBI GI g3551838

LIB3146-028-Q1-K1-E3

Seq. ID

Method

Match length

NCBI Description

% identity

95 54



```
BLAST score
E value.
                  1.0e-50
                  127
Match length
                  78
% identity
                  (AF070967) SKP1-like protein [Nicotiana clevelandii]
NCBI Description
                  213819
Seq. No.
                  LIB3146-028-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3551838
BLAST score
                  420
                  2.0e-41
E value
Match length
                  105
% identity
                  78
NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]
                  213820
Seq. No.
                  LIB3146-028-Q1-K1-E5
Seq. ID
Method
                  BLASTX
                  g2959781
NCBI GI
BLAST score
                  568
                  1.0e-58
E value
                  125
Match length
                  85
% identity
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                  213821
Seq. No.
                  LIB3146-028-Q1-K1-E6
Seq. ID
                  BLASTX
Method
                   g3204125
NCBI GI
BLAST score
                   299
                   3.0e-27
E value
Match length
                   72
                   81
% identity
                  (AJ006766) putative Pi starvation-induced protein [Cicer
NCBI Description
                   arietinum]
                   213822
Seq. No.
Seq. ID
                   LIB3146-028-Q1-K1-E7
Method
                   BLASTX
                   g2224731
NCBI GI
                   287
BLAST score
                   8.0e-26
E value
Match length
                   98
% identity
                   62
                  (AB004932) Aux22d [Vigna radiata]
NCBI Description
                   213823
Seq. No.
Seq. ID
                   LIB3146-028-Q1-K1-E9
                   BLASTX
Method
NCBI GI
                   q1001135
BLAST score
                   276
                   2.0e-24
E value
```

29772

(D64001) acetolactate synthase [Synechocystis sp.]



79

% identity

NCBI Description

```
Seq. No.
                     213824
                     LIB3146-028-Q1-K1-F10
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q133872
  BLAST score
                     600
  E value
                     2.0e-62
  Match length
                     131
                     93
  % identity
                     30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                     >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                     spinach >gi_322404 pir_A44121 small subunit ribosomal
                     protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                     (X66135) ribosomal protein S1 [Spinacia oleracea]
                     >qi 170143 (M82923) chloroplast ribosomal protein S1
                     [Spinacia oleracea]
                     213825
  Seq. No.
  Seq. ID
                     LIB3146-028-Q1-K1-F11
                     BLASTX
  Method
                     q3738092
  NCBI GI
                     242
  BLAST score
                     2.0e-20
  E value
  Match length
                     58
  % identity
                     79
                     (AC005617) similar to glyoxysomal malate dehydrogenase
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                     213826
  Seq. ID
                     LIB3146-028-Q1-K1-F12
  Method
                     BLASTX
                     q3860020
  NCBI GI
  BLAST score
                     281
                     5.0e-25
  E value
  Match length
                     103
  % identity
                     53
                     (AF091091) unknown [Homo sapiens]
  NCBI Description
  Seq. No.
                     213827
  Seq. ID
                     LIB3146-028-Q1-K1-F4
  Method
                     BLASTX
                     g2253442
  NCBI GI
  BLAST score
                     256
                     4.0e-22
  E value
  Match length
                     63
  % identity
                     63
                     (AF007784) LTCOR11 [Lavatera thuringiaca]
  NCBI Description
  Seq. No.
                     213828
  Seq. ID
                     LIB3146-028-Q1-K1-F5
  Method
                     BLASTX
  NCBI GI
                     g1707017
                     247
  BLAST score
                     4.0e-21
  E value
  Match length
                     57
```

29773

(U78721) RNA helicase isolog [Arabidopsis thaliana]



```
Seq. No.
                  213829
Seq. ID
                  LIB3146-028-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1841468
BLAST score
                  608
E value
                  2.0e-63
Match length
                  129
% identity
                  88
                  (Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]
NCBI Description
Seq. No.
Seq. ID
                  LIB3146-028-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3298544
BLAST score
                  207
E value
                  2.0e-16
Match length
                  59
% identity
                  61
NCBI Description
                  (AC004681) unknown protein [Arabidopsis thaliana]
                  213831
Seq. No.
Seq. ID
                  LIB3146-028-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3415115
BLAST score
                  223
                  3.0e-18
E value
                  55
Match length
                  75
% identity
NCBI Description
                  (AF081202) villin 2 [Arabidopsis thaliana]
Seq. No.
                  213832
Seq. ID
                  LIB3146-028-Q1-K1-G6
Method
                  BLASTX
                  g4155128
NCBI GI
BLAST score
                  221
                  5.0e-18
E value
Match length
                  113
% identity
                  41
NCBI Description
                   (AE001491) putative 3-HYDROXYACID DEHYDROGENASE
                   [Helicobacter pylori J99]
Seq. No.
                  213833
Seq. ID
                  LIB3146-028-Q1-K1-G9
Method
                  BLASTX
                  g3763916
NCBI GI
BLAST score
                  463
E value
                  2.0e-46
Match length
                  134
% identity
                  66
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
```

Seq. No. 213834

Seq. ID LIB3146-028-Q1-K1-H1

Method BLASTX NCBI GI g2443890

E value

Match length

NCBI Description

% identity

1.0e-22

100

57



```
BLAST score
                  9.0e-09
E value
Match length
                  101
% identity
                  40
                  (AC002294) similar to NAM (gp X92205 1321924) and CUC2
NCBI Description
                  (gp_AB002560 1944132) proteins [Arabidopsis thaliana]
Seq. No.
                  213835
Seq. ID
                  LIB3146-028-Q1-K1-H4
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  36
E value
                  9.0e-11
Match length
                  36
% identity
                  38
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  213836
Seq. ID
                  LIB3146-028-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q1353239
BLAST score
                  156
E value
                  2.0e-10
Match length
                  58
% identity
                  59
NCBI Description (U10245) putative RNA helicase A [Arabidopsis thaliana]
Seq. No.
                  213837
                  LIB3146-028-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  453
E value
                  3.0e-45
Match length
                  111
% identity
                  77
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                  213838
Seq. ID
                  LIB3146-028-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4467124
BLAST score
                  285
E value
                  1.0e-25
                  100
Match length
% identity
                  61
NCBI Description
                  (AL035538) hypothetical protein [Arabidopsis thaliana]
                  213839
Seq. No.
                  LIB3146-028-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467124
BLAST score
                  261
```

29775

(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. ID

Method



```
Seq. No.
                  213840
Seq. ID
                  LIB3146-030-Q1-K1-A12
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  37
% identity
                  61
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213841
Seq. ID
                  LIB3146-030-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  q559684
BLAST score
                  620
E value
                  8.0e-65
Match length
                  131
% identity
                  90
NCBI Description
                  (L36097) aquaporin [Mesembryanthemum crystallinum]
Seq. No.
                  213842
Seq. ID
                  LIB3146-030-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q3334140
BLAST score
                  482
E value
                  1.0e-48
Match length
                  117
                  77
% identity
NCBI Description
                  CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5
                   (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)
                  >gi 2737888 (U59148) nucleolar protein AnCbf5p [Emericella
                  nidulans]
Seq. No.
                  213843
Seq. ID
                  LIB3146-030-Q1-K1-A8
Method
                  BLASTX
                  g2570827
NCBI GI
BLAST score
                  566
E value
                  2.0e-58
Match length
                  132
% identity
                  75
                  (AF026058) anthocyanidin synthase [Matthiola incana]
NCBI Description
Seq. No.
                  213844
Seq. ID
                  LIB3146-030-Q1-K1-A9
Method
                  BLASTN
NCBI GI
                  g2696018
BLAST score
                  35
E value
                  4.0e-10
Match length
                  79
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213845
```

29776

LIB3146-030-Q1-K1-B10

BLASTX



NCBI GI g3355480 BLAST score 148 E value 2.0e-09 Match length 58 % identity 47

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

213846

Seq. No.

Seq. ID LIB3146-030-Q1-K1-B3

Method BLASTX
NCBI GI g122085
BLAST score 483
E value 9.0e-49
Match length 114
% identity 85

NCBI Description HISTONE H3 >gi\_81641\_pir\_S06250 histone H3 - Arabidopsis

thaliana >gi\_82482\_pir\_\_S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253\_emb\_CAA31970\_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi\_168506

(M35388) histone H3 [Zea mays] >gi\_169655 (M77493) histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3

[Petroselinum crispum] >gi\_169659 (M77495) histone H3
[Petroselinum crispum] >gi\_387565 (M17130) histone H3
[Arabidopsis thaliana] >gi\_387567 (M17131) histone H3
[Arabidopsis thaliana] >gi\_886738\_emb\_CAA59111\_ (X84377) histone 3 [Zea mays] >gi\_1040764 (M35387) histone H3
[Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3
homolog [Brassica napus] >gi\_1531754\_emb\_CAA57811\_ (X82414)
Histone H3 [Asparagus officinalis] >gi\_1667592 (U77296) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana.

ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb\_N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana]
>gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea]
>gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 213847

Seq. ID LIB3146-030-Q1-K1-B8

Method BLASTX
NCBI GI g2880043
BLAST score 172
E value 1.0e-15
Match length 95
% identity 47

NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A

hydrolase [Arabidopsis thaliana]

Seq. No. 213848

Seq. ID LIB3146-030-Q1-K1-C1

Method BLASTX NCBI GI g1064929 BLAST score 536



```
E value
                  5.0e-55
Match length
                  117
% identity
                  88
                  (X92967) cyclin A-like protein [Nicotiana tabacum]
NCBI Description
Seq. No.
                  213849
                  LIB3146-030-Q1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3775989
BLAST score
                  183
E value
                  5.0e-15
Match length
                  85
% identity
                  60
NCBI Description
                  (AJ010458) RNA helicase [Arabidopsis thaliana]
                  213850
Seq. No.
                  LIB3146-030-Q1-K1-C5
Seq. ID
Method
                  BLASTN
                  q2618602
NCBI GI
                  47
BLAST score
                  2.0e-17
E value
                  160
Match length
% identity
                  89
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213851
                  LIB3146-030-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1730108
BLAST score
                  370
                  1.0e-35
E value
Match length
                  90
% identity
                  78
                  LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                  HYDROXYLASE) >gi_486848_pir__S36233 flavanone 3-hydroxylase
                  homolog - garden petunia
                  213852
Seq. No.
Seq. ID
                  LIB3146-030-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g142742
BLAST score
                  709
E value
                  3.0e-75
Match length
                  136
% identity
                  100
NCBI Description
                  (M73248) cryIA(c)3 [Bacillus thuringiensis]
Seq. No.
                  213853
Seq. ID
                  LIB3146-030-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4115386
BLAST score
                  174
                  2.0e-12
E value
Match length
                  93
                  47
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
```

% identity

NCBI Description

90



```
Seq. No.
                  213854
Seq. ID
                  LIB3146-030-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1076515
BLAST score
                  188
E value
                  3.0e-14
                  91
Match length
                  45
% identity
                  pectinesterase precursor - kidney bean
NCBI Description
                  >gi 732913 emb CAA59482 (X85216) pectinesterase [Phaseolus
                  vulgaris]
                  213855
Seq. No.
Seq. ID
                  LIB3146-030-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4467137
                  582
BLAST score
                  2.0e-60
E value
                  126
Match length
% identity
                  84
NCBI Description
                  (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                  213856
Seq. ID
                  LIB3146-030-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q1345698
                  587
BLAST score
                  5.0e-61
E value
Match length
                  117
                  93
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
                  (CAB-151) (LHCP) >gi 99601 pir S20917 chlorophyll
                  a/b-binding protein - upland cotton
                  >gi 452314_emb_CAA38025_ (X54090) chlorophyll ab binding
                  protein [Gossypium hirsutum]
                  213857
Seq. No.
Seq. ID
                  LIB3146-030-Q1-K1-E1
                  BLASTX
Method
NCBI GI
                  g541935
BLAST score
                  419
                  3.0e-41
E value
Match length
                  90
% identity
                  90
                  4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL13) -
NCBI Description
                  soybean (fragment)
Seq. No.
                  213858
Seq. ID
                  LIB3146-030-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1408460
BLAST score
                  602
E value
                  1.0e-62
Match length
                  129
```

(U40161) type 2A protein serine/threonine phosphatase 55

BLAST score

425



## kDa B regulatory subunit [Arabidopsis thaliana]

```
Seq. No.
                  213859
Seq. ID
                  LIB3146-030-Q1-K1-E12
                  BLASTX
Method
NCBI GI
                  g3608137
BLAST score
                  183
                  1.0e-13
E value
                  71
Match length
% identity
                  52
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213860
Seq. ID
                  LIB3146-030-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2065531
BLAST score
                  330
E value
                  8.0e-31
Match length
                  67
% identity
                  91
NCBI Description
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
Seq. No.
                  213861
Seq. ID
                  LIB3146-030-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3080439
BLAST score
                   400
E value
                  5.0e-39
Match length
                  109
% identity
                  69
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213862
Seq. ID
                  LIB3146-030-Q1-K1-E7
                  BLASTX
Method
                  g3153902
NCBI GI
BLAST score
                  433
E value
                  5.0e-43
Match length
                  114
                  76
% identity
                  (AF066076) 14-3-3-like protein [Helianthus annuus]
NCBI Description
Seq. No.
                  213863
Seq. ID
                  LIB3146-030-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3892057
BLAST score
                  562
E value
                  5.0e-58
                  125
Match length
                  45
% identity
                  (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  213864
Seq. ID
                  LIB3146-030-Q1-K1-F1
Method
                  BLASTX
                  g266567
NCBI GI
```

```
E value 6.0e-42

Match length 129
% identity 65

NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
(ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
>gi_421956_pir__S23558 mitochondrial processing peptidase
(EC 3.4.99.41) alpha chain precursor - potato
>gi_21493_emb_CAA46990_ (X66284) mitochondrial processing
peptidase [Solanum tuberosum]
```

Seq. No. 213865 Seq. ID LIB3146-030-Q1-K1-F10

Method BLASTX
NCBI GI g485742
BLAST score 651
E value 2.0e-68
Match length 134

% identity 99
NCBI Description (L32791) pyrophosphatase [Beta vulgaris]

Seq. No. 213866

Seq. ID LIB3146-030-Q1-K1-F11

Method BLASTX
NCBI GI g1076776
BLAST score 204
E value 3.0e-16
Match length 50
% identity 84

NCBI Description histone H2A - wheat >gi\_536888\_dbj\_BAA07276\_ (D38087)

protein H2A [Triticum aestivum] >gi 1095224 prf 2108279A

4

histone H2A:ISOTYPE=2 [Triticum aestivum]

Seq. No. 213867

Seq. ID LIB3146-030-Q1-K1-F4

Method BLASTX
NCBI GI g1172597
BLAST score 226
E value 1.0e-18
Match length 47
% identity 91

NCBI Description WOUND-INDUCED BASIC PROTEIN >gi 81888 pir JS0731

wound-inducible basic protein - kidney bean >gi\_169365

(L00625) basic protein [Phaseolus vulgaris]

>gi\_217989\_dbj\_BAA02299\_ (D12914) 5.8 kb basic protein

[Phaseolus vulgaris]

Seq. No. 213868

Seq. ID LIB3146-030-Q1-K1-F6

Method BLASTX
NCBI GI g2565010
BLAST score 431
E value 1.0e-42
Match length 133
% identity 59

NCBI Description (AC002983) putative microfibril-associated protein [Arabidopsis thaliana] >gi 3377811 (AF076275) contains

similarity to ATP synthase B/B' (Pfam: ATP-synt B.hmm,



```
score: 11.71) [Arabidopsis thaliana]
```

```
Seq. No.
                  213869
Seq. ID
                  LIB3146-030-Q1-K1-F7
                  BLASTX
Method
NCBI GI
                  q320552
BLAST score
                  465
                  1.0e-46
E value
                  124
Match length
                  76
% identity
NCBI Description
                  anthranilate synthase (EC 4.1.3.27) alpha-1 chain -
                  Arabidopsis thaliana
Seq. No.
                  213870
Seq. ID
                  LIB3146-030-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q548774
BLAST score
                  240
                  2.0e-20
E value
Match length
                  88
                  56
% identity
                  60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__$38360 ribosomal
NCBI Description
                  protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  213871
Seq. ID
                  LIB3146-030-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  q4455334
                  221
BLAST score
                  2.0e-18
E value
                  51
Match length
                  78
% identity
NCBI Description
                  (AL035525) myosin-like protein [Arabidopsis thaliana]
   2. 2.
                  213872
Seq. No.
Seq. ID
                  LIB3146-030-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1351271
BLAST score
                  545
E value
                  4.0e-56
Match length
                  113
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
                  >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi_806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
Seq. No.
                  213873
Seq. ID
                  LIB3146-030-Q1-K1-H6
Method
                  BLASTX
                  g4090533
NCBI GI
BLAST score
                  591
E value
                  2.0e-61
Match length
                  119
```

92

% identity



```
NCBI Description (U68215) ACC oxidase [Carica papaya]
                   213874
Seq. No.
Seq. ID
                   LIB3146-032-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g4538959
BLAST score
                   145
                   2.0e-09
E value
Match length
                   48
% identity
                   52
                  (AL049488) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213875
                   LIB3146-032-Q1-K1-A10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2182286
BLAST score
                   43
E value
                   3.0e-15
Match length
                   119
                   84
% identity
                   Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   213876
Seq. ID
                   LIB3146-032-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   q629735
BLAST score
                   246
                   6.0e-21
E value
Match length
                   69
% identity
                   67
                   fill protein - garden snapdragon >gi 406309 emb_CAA40553_
NCBI Description
                   (X57296) FIL1 [Antirrhinum majus]
Seq. No.
                   213877
                   LIB3146-032-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2369766
BLAST score
                   399
                   8.0e-39
E value
                   75
Match length
                   96
% identity
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
Seq. No.
                   213878
Seq. ID
                   LIB3146-032-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2996096
BLAST score
                   511
                   3.0e-52
E value
                   99
Match length
                   98
% identity
                   (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                   alpha [Oryza sativa]
```

29783

213879

LIB3146-032-Q1-K1-A8

Seq. No. Seq. ID



```
Method
                   BLASTX
NCBI GI
                   q2506931
BLAST score
                   267
E value
                   1.0e-23
                   92
Match length
                   55
% identity
NCBI Description
                   APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE
                   DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE)
                   >gi_2129977_pir__JC4616 apyrase (EC 3.6.1.5) - potato
                   >gi 1381633 (U58597) ATP-diphosphohydrolase [Solanum
                   tuberosum]
Seq. No.
                   213880
                   LIB3146-032-Q1-K1-B10
Seq. ID
Method
                   BLASTX
                   a1702983
NCBI GI
                   297
BLAST score
E value
                   4.0e-28
                   112
Match length
% identity
                   58
                   AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850
NCBI Description
                   hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria
                   x ananassa] >gi_927034 (L44142) auxin-repressed protein
                   [Fragaria ananassa]
Seq. No.
                   213881
                   LIB3146-032-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2618698
BLAST score
                   406
                   7.0e-40
E value
                   111
Match length
% identity
                   72
                   (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213882
Seq. ID
                   LIB3146-032-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   q4455207
BLAST score
                   420
E value
                   3.0e-41
Match length
                   91
% identity
                   89
                   (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   213883
Seq. ID
                   LIB3146-032-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g4033735
BLAST score
                   394
                   2.0e-49
E value
```

Match length

NCBI Description

% identity

Seq. No.

137

213884

75

(AF054284) spliceosomal protein SAP 155 [Homo sapiens]

% identity

57



```
Seq. ID
                  LIB3146-032-Q1-K1-B7
                  BLASTX
Method
NCBI GI
                  q4033735
BLAST score
                   492
E value
                  8.0e-50
Match length
                   116
% identity
                  78
NCBI Description (AF054284) spliceosomal protein SAP 155 [Homo sapiens]
Seq. No.
                  213885
Seq. ID
                  LIB3146-032-Q1-K1-B9
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
                  8.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  213886
Seq. ID
                  LIB3146-032-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3056595
BLAST score
                  344
E value
                  2.0e-32
Match length
                  114
% identity
                  66
NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]
Seq. No.
                  213887
Seq. ID
                  LIB3146-032-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1345571
BLAST score
                  154
E value
                  3.0e-10
Match length
                   41
% identity
                  73
NCBI Description (X80010) starch branching enzyme II [Pisum sativum]
Seq. No.
                  213888
Seq. ID
                  LIB3146-032-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1742951
BLAST score
                  449
                  9.0e-45
E value
Match length
                  96
% identity
                  92
NCBI Description (Y09817) Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.
                  213889
Seq. ID
                  LIB3146-032-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4558591
BLAST score
                  379
E value
                  1.0e-36
Match length
                  127
```



```
NCBI Description
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
                   thaliana]
                   213890
Seq. No.
Seq. ID
                   LIB3146-032-Q1-K1-D1
Method
                   BLASTN
NCBI GI
                   g4115332
BLAST score
                   36
E value
                   4.0e-11
Match length
                   44
% identity
                   95
NCBI Description Pisum sativum (Alaska) ubiquitin (PUB1) gene, complete cds
Seq. No.
                   213891
Seq. ID
                   LIB3146-032-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   q4249410
BLAST score
                   290
E value
                   4.0e-26
Match length
                   91
% identity
                   65
NCBI Description
                  (AC006072) unknown protein [Arabidopsis thaliana]
Seq. No.
                   213892
Seq. ID
                   LIB3146-032-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   a3983665
BLAST score
                   374
E value
                   5.0e-36
Match length
                   111
% identity
NCBI Description
                  (AB011271) importin-beta2 [Oryza sativa]
Seq. No.
                   213893
Seq. ID
                   LIB3146-032-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   q728949
BLAST score
                   167
E value
                   1.0e-11
Match length
                   127
% identity
                   BLUE COPPER PROTEIN PRECURSOR >gi_99665_pir__$25555 blue
NCBI Description
                   copper protein - Arabidopsis thaliana >gi_2147156_pir__I39698 blue copper-binding protein -
                   Arabidopsis thaliana >gi_16203_emb_CAA78771_ (Z15058) blue
                   copper-binding protein [unidentified bacterium]
                   >gi 739987_prf__2004275A blue copper-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   213894
Seq. ID
                   LIB3146-032-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3868758
```

Method BLASTX
NCBI GI g3868758
BLAST score 163
E value 9.0e-12
Match length 34
% identity 94



Ory

```
(D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                  213895
Seq. No.
Seq. ID
                  LIB3146-032-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  g398966
BLAST score
                  188
E value
                   3.0e-14
Match length
                   39
% identity
                   92
NCBI Description
                  4-COUMARATE--COA LIGASE 2 (4CL) (CLONE 4CL16)
                  >gi_541937_pir__PQ0772 4-coumarate--CoA ligase (EC
                   6.2.1.12) (clone GM4CL1B) - soybean (fragment)
                  >gi 18520 emb CAA49576 (X69955) 4-coumarate--CoA ligase
                   [Glycine max]
                  213896
Seq. No.
Seq. ID
                  LIB3146-032-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3983665
BLAST score
                   427
E value
                   3.0e-42
Match length
                   111
% identity
                   76
NCBI Description (AB011271) importin-beta2 [Oryza sativa]
                   213897
Seq. No.
Seq. ID
                  LIB3146-032-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   g1332579
BLAST score
                   458
E value
                  1.0e-47
Match length
                  10,5
% identity
                   10
NCBI Description
                  (X98063) polyubiquitin [Pinus sylvestris]
                  213898
Seq. No.
                  LIB3146-032-Q1-K1-E12
Seq. ID
Method
                  BLASTX
                   q2760349
NCBI GI
                   203
BLAST score
                   2.0e-16
E value
Match length
                  73
% identity
                   15
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  213899
Seq. ID
                  LIB3146-032-Q1-K1-E2
Method
                  BLASTX
                  g1008984
NCBI GI
BLAST score
                  119
                   1.0e-11
E value
Match length
                  73
                   55
% identity
NCBI Description
                  (X91811) chalcone synthase-like [Oryza sativa]
```

29787

213900

Seq. No.



```
Seq. ID
                  LIB3146-032-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  g124226
BLAST score
                  424
                  8.0e-42
E value
Match length
                  103
% identity
                  81
                  INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 100278 pir__S21059 translation initiation factor
                  eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                  (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
                  plumbaginifolia]
Seq. No.
                  213901
Seq. ID
                  LIB3146-032-01-K1-F10
Method
                  BLASTX
NCBI GI
                  g2995384
BLAST score
                  172
E value
                  2.0e-12
Match length
                  70
% identity
                  56
                  (AJ004810) cytochrome P450 monooxygenase [Zea mays]
NCBI Description
Seq. No.
                  213902
Seq. ID
                  LIB3146-032-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3914658
BLAST score
                  246
E value
                  3.0e-21
Match length
                  65
% identity
                  74
                  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1694974 emb CAA70851 (Y09635) plastid ribosomal
                  protein [Arabidopsis thaliana]
                  213903
Seq. No.
Seq. ID
                  LIB3146-032-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4574320
BLAST score
                  206
                  3.0e-16
E value
Match length
                  62
% identity
                  66
NCBI Description
                  (AF117224) wound-induced protein WI12 [Mesembryanthemum
                  crystallinum]
Seq. No.
                  213904
```

Seq. ID LIB3146-032-Q1-K1-F7

Method BLASTX NCBI GI g2995384 BLAST score 173 1.0e-12 E value 70 Match length 56 % identity

(AJ004810) cytochrome P450 monooxygenase [Zea mays] NCBI Description

Seq. No. 213905

BLAST score

E value

162 1.0e-11



```
LIB3146-032-Q1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2564237
BLAST score
                  346
                  9.0e-33
E value
                  73
Match length
                  85
% identity
NCBI Description
                  (Y10112) omega-6 desaturase [Gossypium hirsutum]
Seq. No.
                  213906
Seq. ID
                  LIB3146-032-Q1-K1-G11
Method
                  BLASTX
                  g4325324
NCBI GI
                  401
BLAST score
                  2.0e-39
E value
                  89
Match length
% identity
                  88
                  (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  213907
Seq. ID
                  LIB3146-032-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1946362
BLAST score
                  201
E value
                  9.0e-21
Match length
                  101
% identity
                  59
                  (U93215) photosystem II reaction center 6.1KD protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  213908
Seq. ID
                  LIB3146-032-Q1-K1-G5
                  BLASTX
Method
NCBI GI
                  g3860333
BLAST score
                  232
                  2.0e-19
E value
Match length
                  68
% identity
                  63
NCBI Description
                  (AJ012693) basic blue copper protein [Cicer arietinum]
Seq. No.
                  213909
                  LIB3146-032-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539371
BLAST score
                  167
                  1.0e-11
E value
Match length
                  124
                  37
% identity
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                  213910
Seq. ID
                  LIB3146-032-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4538959
```



```
Match length 67
% identity 58
NCBI Description (AL049488) putative protein [Arabidopsis thaliana]
Seq. No. 213911
Seq. ID LIB3146-032-Q1-K1-H7
Method BLASTX
NCBI GI g3860319
BLAST score 393
```

BLAST score 393 E value 2.0e-38 Match length 83 % identity 92

NCBI Description (AJ012686) nucleolar protein [Cicer arietinum]

Seq. No. 213912

Seq. ID LIB3146-032-Q1-K1-H8

Method BLASTX
NCBI GI g231509
BLAST score 246
E value 3.0e-21
Match length 88
% identity 57

NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935

actin-depolymerizing factor - trumpet lily

>gi\_22748\_emb\_CAA78483\_ (Z14110) actin depolymerizing

factor [Lilium longiflorum]

Seq. No. 213913

Seq. ID LIB3146-032-Q1-K1-H9

Method BLASTX
NCBI GI g1703380
BLAST score 233
E value 1.0e-19
Match length 46
% identity 93

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)

ADP-ribosylation factor [Oryza sativa]

Seq. No. 213914

Seq. ID LIB3146-033-Q1-K1-A10

Method BLASTX
NCBI GI g3914343
BLAST score 362
E value 8.0e-35
Match length 95
% identity 73

NCBI Description PHYTOCHROME A >gi\_2664190\_emb\_CAA04679\_ (AJ001318) phytochrome A [Populus tremula x Populus tremuloides]

Seq. No. 213915

Seq. ID LIB3146-033-Q1-K1-A11

Method BLASTX
NCBI GI g2982322
BLAST score 379
E value 3.0e-40
Match length 107
% identity 73



```
NCBI Description
                   (AF051246) probable proteasome subunit [Picea mariana]
                     213916
Seq. No.
Seq. ID
                     LIB3146-033-Q1-K1-A4
Method
                     BLASTX
NCBI GI
                     q2865394
BLAST score
                     190
E value
                     2.0e-14
Match length
                     85
% identity
                     52
NCBI Description
                    (AF036949) basic leucine zipper protein [Zea mays]
Seq. No.
                     213917
Seq. ID
                     LIB3146-033-Q1-K1-A5
Method
                     BLASTX
NCBI GI
                     q1345933
BLAST score
                     364
                     7.0e-35
E value
Match length
                     73
% identity
                     92
                    CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS) >gi_1084323_pir__S53007 citrate synthase - cucurbit
NCBI Description
                     >gi_975633_dbj_BAA07328_ (D38132) glyoxysomal citrate
                     synthase [Cucurbita sp.]
Seq. No.
                     213918
Seq. ID
                     LIB3146-033-01-K1-A7
Method
                     BLASTX
NCBI GI
                     q2499498
BLAST score
                     499
E value
                     1.0e-50
Match length
                     131
% identity
                     76
NCBI Description
                    PHOSPHOGLYCERATE KINASE, CYTOSOLIC
                     >gi_1161602_emb_CAA88840_ (Z48976) phosphoglycerate kinase
                     (PGK) [Nicotiana tabacum]
                     213919
Seq. No.
Seq. ID
                    LIB3146-033-Q1-K1-A9
Method
                    BLASTX
NCBI GI
                     g1708971
BLAST score
                     203
E value
                     6.0e-16
Match length
                     64
% identity
                     52
NCBI Description
                     (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
                     (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                    >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -black cherry >gi_288116_emb_CAA51194_ (X72617) mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                     (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                    serotina] >gi 1090776 prf 2019441A mandelonitrile lyase
```

Seq. No. 213920

Seq. ID LIB3146-033-Q1-K1-B10

[Prunus serotina]

Method BLASTX



NCBI GI g4406780
BLAST score 304
E value 3.0e-28
Match length 75
% identity 76
NCBI Description (AC00653)

NCBI Description (AC006532) putative multispanning membrane protein

[Arabidopsis thaliana]

Seq. No. 213921

Seq. ID LIB3146-033-Q1-K1-B11

Method BLASTX
NCBI GI g3123745
BLAST score 164
E value 1.0e-11
Match length 83
% identity 41

NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 213922

Seq. ID LIB3146-033-Q1-K1-B5

Method BLASTX
NCBI GI g2961346
BLAST score 217
E value 1.0e-17
Match length 49
% identity 76

NCBI Description (AL022140) pectinesterase like protein [Arabidopsis

thaliana]

Seq. No. 213923

Seq. ID LIB3146-033-Q1-K1-B9

Method BLASTX
NCBI GI g1170747
BLAST score 194
E value 4.0e-18
Match length 69

Match length 69 % identity 77

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi 167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 213924

Seq. ID LIB3146-033-Q1-K1-C1

Method BLASTX
NCBI GI g3540195
BLAST score 670
E value 1.0e-70
Match length 134
% identity 45

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 213925

Seq. ID LIB3146-033-Q1-K1-C11

Method BLASTX NCBI GI g1181589 BLAST score 202



```
E value
Match length
% identity
                  75
                   (D83070) high mobility group protein [Canavalia gladiata]
NCBI Description
                  >gi 1483173 dbj BAA13133 (D86594) high mobility group
                  protein [Canavalia gladiata]
                  213926
Seq. No.
Seq. ID
                  LIB3146-033-Q1-K1-C3
Method
                  BLASTN
NCBI GI
                  q2351069
                  40
BLAST score
                  4.0e-13
E value
Match length
                  92
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  213927
Seq. ID
                  LIB3146-033-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q320565
BLAST score
                  179
                  2.0e-13
E value
Match length
                  73
                   49
% identity
NCBI Description transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
                  213928
Seq. No.
Seq. ID
                  LIB3146-033-Q1-K1-C7
Method
                  BLASTX
                  q975888
NCBI GI
                   305
BLAST score
                   4.0e-28
E value
                   100
Match length
% identity
                   65
                   (U32511) myo-inositol-1-phosphate synthase
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                   213929
Seq. ID
                  LIB3146-033-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   q3395427
BLAST score
                   180
                   2.0e-13
E value
Match length
                   77
% identity
                   52
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   213930
Seq. ID
                   LIB3146-033-Q1-K1-D1
```

Method BLASTX NCBI GI g4512699 BLAST score 440 E value 1.0e-43 Match length 133 % identity 67



NCBI Description (AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No. 213931

Seq. ID LIB3146-033-Q1-K1-D10

Method BLASTN
NCBI GI g2267582
BLAST score 293
È value 1.0e-164
Match length 307
% identity 99

NCBI Description Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA,

complete cds

Seq. No. 213932

Seq. ID LIB3146-033-Q1-K1-D11

Method BLASTX
NCBI GI g3123264
BLAST score 432
E value 5.0e-43
Match length 91
% identity 89

NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi\_2244857\_emb\_CAB10279\_

(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 213933

Seq. ID LIB3146-033-Q1-K1-D12

Method BLASTX
NCBI GI g3482918
BLAST score 401
E value 4.0e-39
Match length 94
% identity 83

NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 213934

Seq. ID LIB3146-033-Q1-K1-D5

Method BLASTX
NCBI GI g3063396
BLAST score 506
E value 2.0e-51
Match length 114
% identity 83

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 213935

Seq. ID LIB3146-033-Q1-K1-D6

Method BLASTX
NCBI GI 94210712
BLAST score 595
E value 7.0e-62
Match length 129
% identity 81

NCBI Description (AJ006870) purple acid phosphatase [Ipomoea batatas]

Seq. No. 213936



```
LIB3146-033-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914131
BLAST score
                  147
                  2.0e-09
E value
Match length
                  79
% identity
                  38
NCBI Description
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR
                   (LTP 2) (MAJOR POLLEN ALLERGEN PAR J 2.0102) (PAR J II) (P8
                  PROTEIN) >gi_1532056_emb_CAA65122 (X95866) P8 protein
                  [Parietaria judaica]
Seq. No.
                  213937
Seq. ID
                  LIB3146-033-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1708971
BLAST score
                  191
E value
                  1.0e-14
Match length
                  58
% identity
                  53
                  (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
NCBI Description
                  (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                  >gi_421871 pir S32156 mandelonitrile lyase (EC 4.1.2.10) -
                  black cherry >gi_288116_emb_CAA51194 (X72617)
                  mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                  (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                  serotina] >gi 1090776 prf 2019441A mandelonitrile lyase
                  [Prunus serotina]
Seq. No.
                  213938
Seq. ID
                  LIB3146-033-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q729671
BLAST score
                  243
E value
                  1.0e-20
Match length
                  71
% identity
                  70
NCBI Description
                  HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
Seq. No.
                  213939
Seq. ID
                  LIB3146-033-Q1-K1-E5
Method
                  BLASTX
                  g123379
                  156
                  2.0e-10
                  32
```

NCBI GI BLAST score E value Match length % identity 91

NCBI Description HMG1/2-LIKE PROTEIN (SB11 PROTEIN) >qi 99914 pir S22309

HMG-1-like protein - soybean >qi 18645 emb CAA41200

(X58245) HMG-1 like protein gene [Glycine max]

Seq. No. 213940

Seq. ID LIB3146-033-Q1-K1-E6

Method BLASTX NCBI GI q1706377 BLAST score 563 E value 4.0e-58